

Childhood Cancer Data Initiative (CCDI) Webinar Series

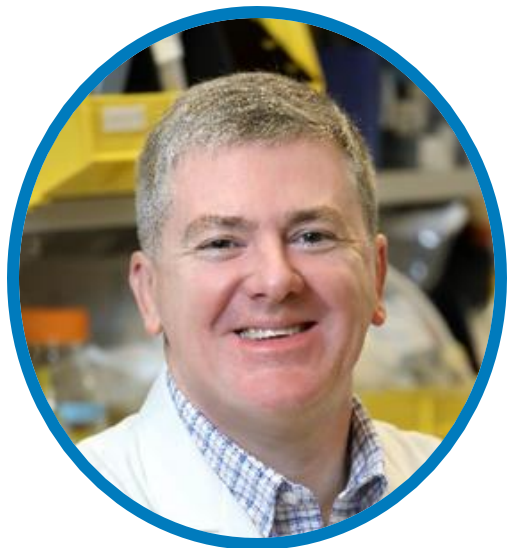
# MCI Update: Pediatric Soft Tissue Sarcomas

*Jack Shern, M.D.*

## Agenda

1. *Molecular Characterization Initiative (MCI): Creating a National Strategy*
2. *MCI Data Flow: Enabling Access to Data for Research and Analysis*
3. *MCI Soft Tissue Sarcoma Data: Clinical Impact*
4. Q&A

# Today's Speaker

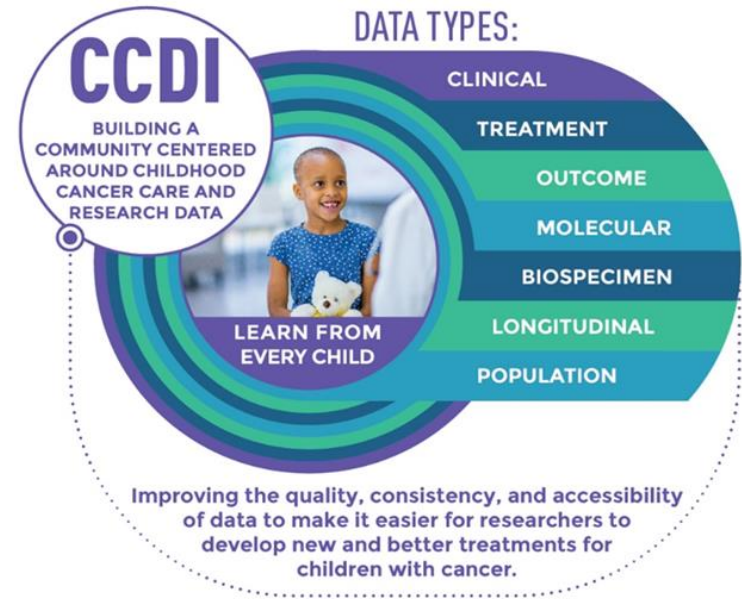


## Jack Shern, M.D.

- Lasker Clinical Research Scholar
- Head of the Tumor Evolution and Genomics Section, National Cancer Institute

# CCDI Goals

- Gather **data from every child, adolescent, and young adult** diagnosed with a childhood cancer
- **Create a national strategy** of molecular characterization to inform diagnosis and treatment
- **Develop a platform and tools** to bring together clinical and research data that will inform new insights in biology/etiology to improve preventive measures, treatment, quality of life, and survivorship for childhood cancers
- **Engage the entire** childhood cancer care and research community



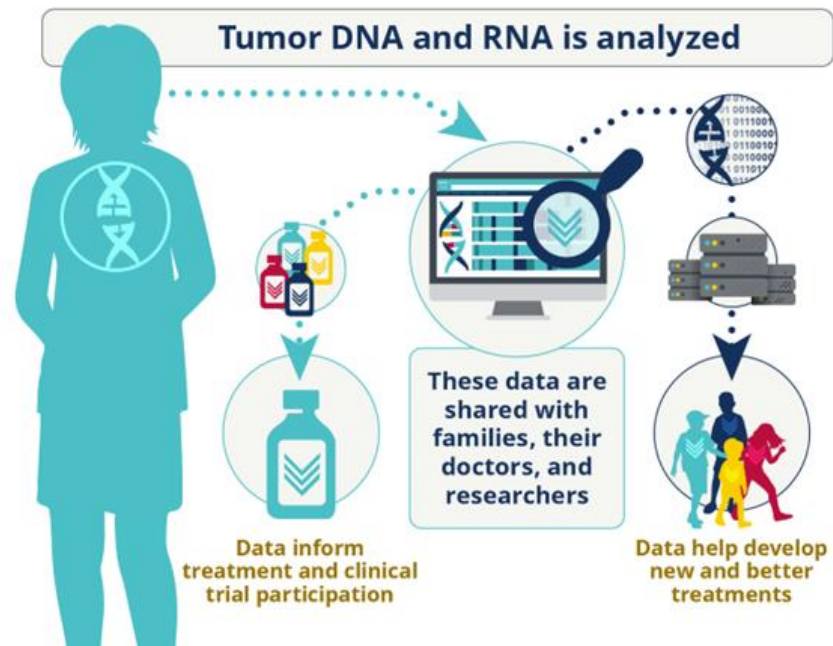
*Flores-Toro JA et al., J Clin Oncol, 2023 (PMID:37267580);  
Jagu S et al., Pediatr Blood Cancer, 2024 (PMID: 37889049)*

# Molecular Characterization Initiative

*Creating a National Strategy*

# CCDI Molecular Characterization Initiative (MCI)

- Launched in partnership with Children's Oncology Group's (COG) Project:EveryChild
- State-of-the-art molecular characterization at diagnosis (WES, fusions, methylation) in a CLIA-testing environment at no cost to participants
- Results returned to participants and treating physicians within 14-21 days
- Enrolled more than 4,500 participants from all 50 states, Canada, Australia, and New Zealand
- Learn more: [ccdi.cancer.gov/MCI](https://ccdi.cancer.gov/MCI)





# Expanding MCI

- Plan to add Ewing sarcoma and relapsed or refractory tumors
- Expand to include AYAs outside of COG for the Coordinated Pediatric, Adolescent, and Young Adult Rare Cancer Initiative
- Prioritize diseases for **research characterization** and determine which assays (WGS, RNA Seq, single cell, epigenetics, proteomics/metabolomics) are appropriate to deepen our understanding of cancer biology
  - Partnering with COG disease-specific scientific committees and other subject matter experts





# MCI Data Flow

*Enabling Access to Data for  
Research and Analysis*

# CCDI Data Ecosystem: A Connected Network of Resources

**GDC & cBioPortal:  
Visualization Tools**

**Federation & CPI APIs:  
Data Discovery & Integration**

**Cancer Genomics Cloud:  
Data Integration &  
Analysis**

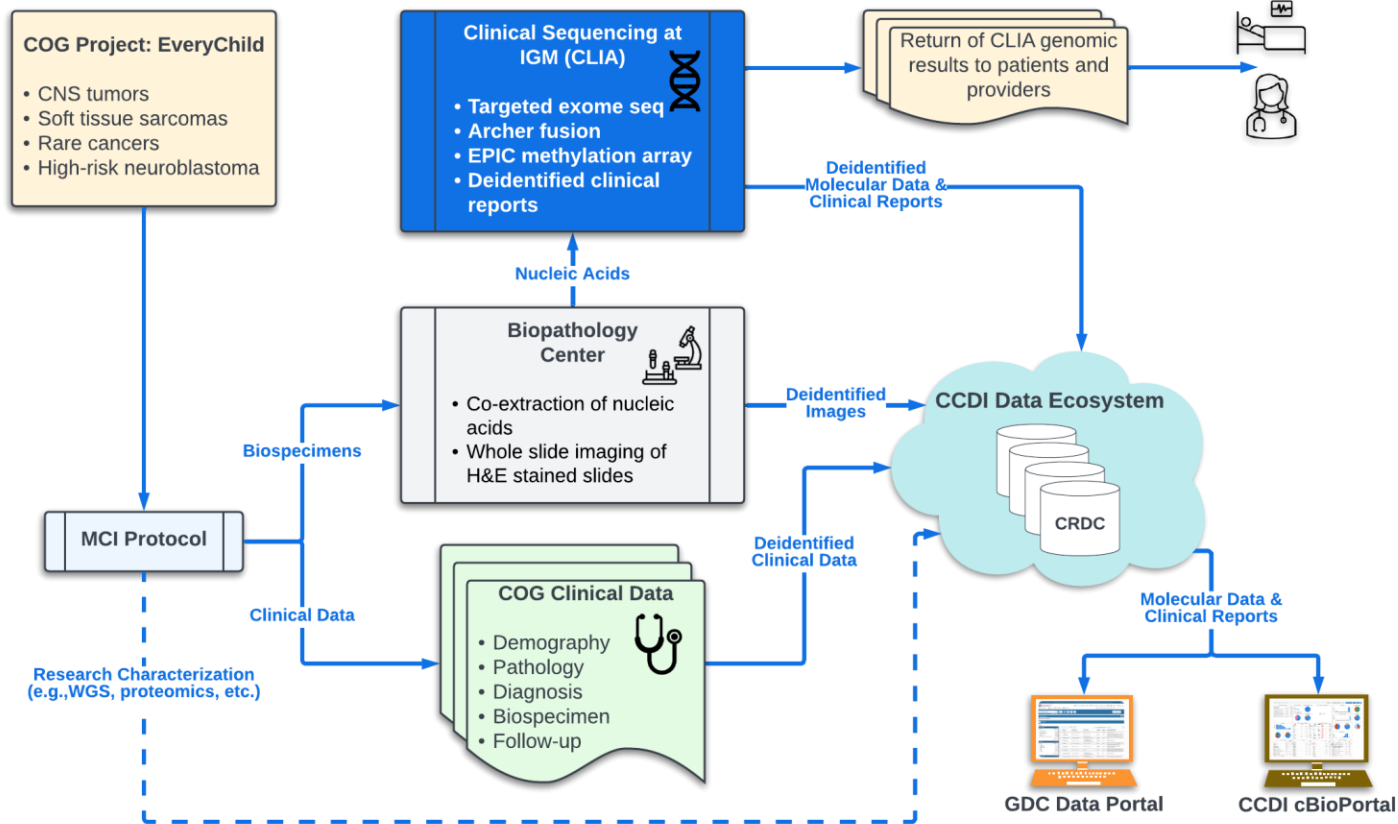
**C3DC & NCCR:  
Clinical & Real World Data**

**Hub Explore: Build Cohorts**

**Catalog, MTP, & CIViC:  
Knowledgebases**

**Hub: Entry Point**

# MCI Data Flow



# MCI: Assay Types & Data File Formats

Sample	Assay	Analytics	Result Type	File Description	File Format
Tumor + normal DNA	Enhanced WES  <b>Note: &gt; 10-fold less input DNA requirement for exome</b>	250x Churchill alignment to GRCh38; IGMseq Pipeline Analysis in AWS	Germline + somatic SNVs, INDELs, CNV, and LOH  <b>Note: Clinical report will include tumor mutational burden (TMB)</b>	Germline and Somatic Read Alignments	.FASTQ, .cram, .crai;
				Germline and Somatic VCFs	.vcf.gz
				PII Redacted Report	.pdf, .json
Tumor RNA	Archer Dx Pan-Solid FusionPlex  <b>Note: RNAseq will replace Archer panel for fusion calling</b>	Archer Analysis v. 6.0 in AWS	Fusion/ITD detection	Targeted RNA Read Alignment	.cram, .crai
				Archer Fusion Results	.txt
				PII Redacted Report	.pdf, .json
Tumor DNA	Illumina 850K EPIC methyl array	DKFZ Classifier v. 12.5	Disease classification	Illumina EPIC Array Intensity File	.idat
				DKFZ Classification	.html
				PII Redacted Report	.pdf, .json
				Biospecimen and clinical data	.json

Institutional reimbursement for completion of data submission

# CCDI Hub Explore Dashboard: Inventory of Data Sets

- An inventory of CCDI-managed childhood cancer data
- Provides:
  - Faceted search
  - Visualization of search results
  - Export results for further analysis
- Facilitates data discovery across studies, enabling the building of cohorts



# CCDI Hub Explore: Faceted Filtering

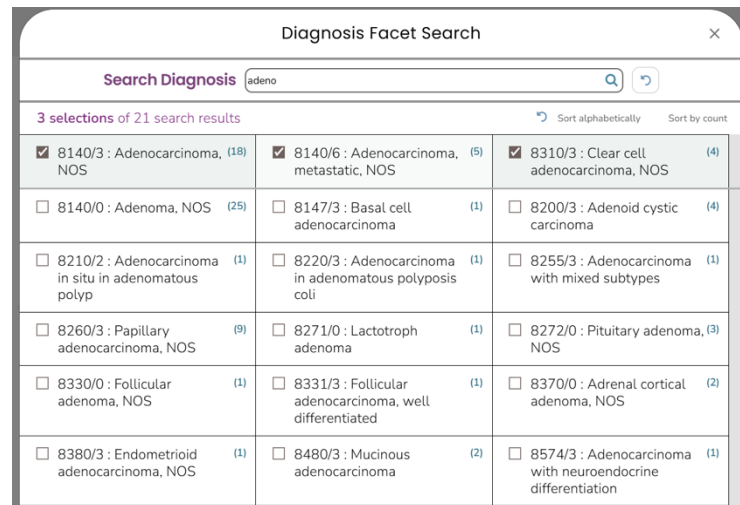
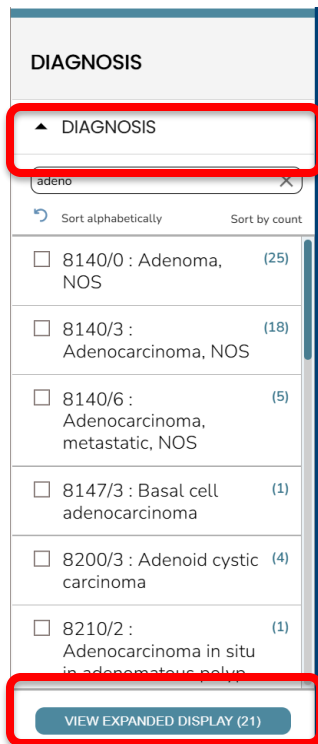
- Filter available data by various annotations of interest
  - Diagnosis
  - Demographics
  - Treatment
  - Treatment response
  - Survival
  - Samples
  - Data category
  - Study
- Facet selections dynamically reload visualization dashboard and tabular lists

The screenshot displays the CCDI Hub Explore interface. On the left, a sidebar contains a list of facets: DEMOGRAPHICS, SEX, RACE, DIAGNOSIS, SAMPLES, DATA CATEGORY, STUDY, and SEQUENCING LIBRARY. The main area features a dashboard with several charts: a donut chart for 'CCDI\_M3\_jh003319' (29 participants), a donut chart for 'Subepidemiology' (1 participant), a bar chart for 'Age at Diagnosis (years)', a donut chart for 'Sex' (12 participants), a donut chart for 'Race' (37 participants), and a donut chart for 'Assay Type' (555 participants). Below the charts is a table with columns for Participant ID, Study ID, Sex, Race, and Synonym Participant ID. The table lists 12 participants with their respective IDs and demographic information.

Participant ID	Study ID	Sex	Race	Synonym Participant ID
<input type="checkbox"/> 00301d7891573761d0f	phs002431	Female	White	
<input type="checkbox"/> 0061cb0846973206cf1	phs002431	Male	White	
<input type="checkbox"/> 0065a9f1e89ec2859595	phs002431	Female	Hispanic or Latino/White	
<input type="checkbox"/> 008b0484717e7d007d4	phs002431	Male	White	
<input type="checkbox"/> 0099ef6cd49602a28fb	phs002431	Female	White	
<input type="checkbox"/> 00c5e4372375eb362793	phs002431	Female	White	
<input type="checkbox"/> 00df38f09994eada22	phs002431	Male	White	
<input type="checkbox"/> 00e3d1d383c8c08a25d2	phs002431	Male	White	
<input type="checkbox"/> 00ef950ac98a210da9f9	phs002431	Male	White	1131296
<input type="checkbox"/> 01504e3b7031af9ec2b2	phs002431	Female	White	


# CCDI Hub Explore: Diagnosis Search


- By default, first several diagnoses are listed sorted by numeric code
- Entering a search term will reduce the space of listed diagnoses to the first several matches
- Clicking the “View Expanded Display” button will show all possible matches
- Checking the associated checkbox will update the visual dashboard and table lists accordingly




# Additional Facet Types


Checkbox selection

DEMOGRAPHICS 

Participant ID Search 

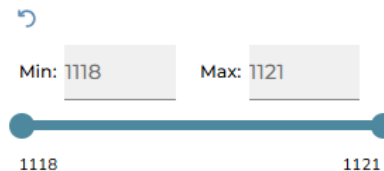
**UPLOAD PARTICIPANTS SET** 

Participant ID upload



STUDY	
▲ DBGAP ACCESSION	
 Sort alphabetically	Sort by count
<input type="checkbox"/> phs000720	(403)
<input type="checkbox"/> phs001437	(267)
<input type="checkbox"/> phs002371	(30)

## Age sliders

▲ AGE AT DIAGNOSIS (DAYS)



### Upload Participants Set

Add a list of Participant IDs:  **or** Choose a file to upload: 

*e.g. PARTICIPANT-101025,  
PARTICIPANT-101026,  
PARTICIPANT-101027*

**BROWSE**

**CANCEL CLEAR SUBMIT**

## SAMPLES

▲ AGE AT COLLECTION (DAYS)





# CCDI Hub Explore: File-based Access

- Files can be added to the My Files cart from any of the tab lists
- Options differ by table
  - Example 1:** add all the files for a Participant from the “Participants” tab
  - Example 2:** add single files from “Files” tab
- Download study metadata from Studies tab

The screenshot shows the CCDI Hub Explore interface. At the top, there are tabs for 'Participants (4615)', 'Diagnosis (12416)', 'Studies (1)', 'Samples (6720)', and 'Files (36572)'. The 'Files' tab is highlighted with a red box. Below the tabs, there are two buttons: 'ADD ALL FILTERED FILES' and 'ADD SELECTED FILES', both highlighted with red boxes. The interface shows '3 row(s) selected' and 'Results per Page: 10' with '1-10 of 36572' items. A table of files is displayed with columns: File Name, File Category, File Description, File Type, File Size, Study ID, Participant ID, Sample ID, GUID, and MD5sum. Three rows are highlighted with red boxes, each with a checked checkbox in the first column.

File Name	File Category	File Description	File Type	File Size	Study ID	Participant ID	Sample ID	GUID	MD5sum
IGM_PBCNBA-0DVSBN_20240329.clinical_report.json	Clinical data	IGM Clinical JSON	json	517 Bytes	phs002790	PBCNBA		dg.4DFC/a48632eb-fc7a-4527-b62a-1d067c9e2679	b3f693931ecb285621f5e7bd7a55558
IGM_PBCNBA-0DVSBW_20240402.clinical_report.json	Clinical data	IGM Clinical JSON	json	11.81 KB	phs002790	PBCNBA		dg.4DFC/dca0a1a1-adc6-44e1-b5a2-9e1e552c1a00	a8098e1a9306904e22c333e3cb1cc3de
IGM_PBCNBB-0DVSSBO_20240329.clinical_report.json	Clinical data	IGM Clinical JSON	json	517 Bytes	phs002790	PBCNBB		dg.4DFC/b40996b8-d607-46a9-9b75-2926113fe90e	78e0fde284cae727981ed8909d8bca

# Obtain Controlled-access Files

**1. The database of Genotypes and Phenotypes (dbGaP) access is given using eRA Commons accounts.**

- Go to the [eRA Commons site](#) and create an account under your organization or institution.

**2. Go to the dbGaP Controlled Access Data section and select Authorized Access. Log in with your eRA Commons account.**

**3. Create a Research Project.**

- Select the projects you would like controlled access to.
- Create a Research Use Statement explaining the need for the projects.
- Confirm project structure and send off for review to the Data Access Committee.

**4. Go to the My Requests tab to see all current access that is linked to your eRA Commons Account.**

- Go to the “Downloaders” tab and search for other members in your lab/group and add them to the selected Research Projects

1. eRA Commons account



2. dbGaP access



3. Access to projects through dbGaP



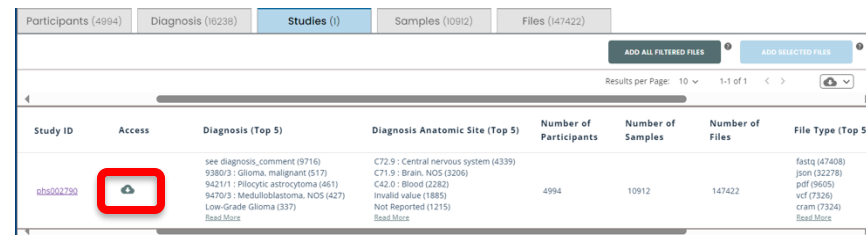
4. Grant access to others in your lab/group


**How to Apply for Controlled Access on dbGaP:** [https://www.youtube.com/watch?v=m0xp\\_cCO7kA](https://www.youtube.com/watch?v=m0xp_cCO7kA)

# How Do I Access MCI FASTQ Files for Rhabdomyosarcoma?

## Go to [ccdi.cancer.gov/explore](https://ccdi.cancer.gov/explore)

- Select "Molecular Characterization Initiative" under Study Name or choose "phs002790" under Study dbGaP Accession
- Download the Study Manifest
- Find the tabs ending with "\_file" (look for FASTQ, JSON, etc.)

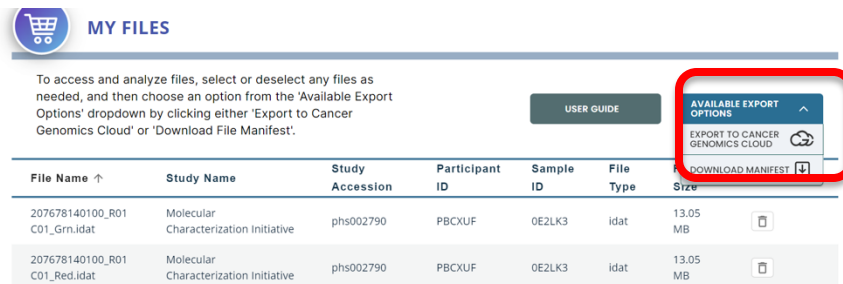


Participants (4994)	Diagnosis (16238)	Studies (1)	Samples (10912)	Files (147422)			
ADD ALL FILTERED FILES							
ADD SELECTED FILES							
Results per Page: 10 1:1 of 1							
Study ID	Access	Diagnosis (Top 5)	Diagnosis Anatomic Site (Top 5)	Number of Participants	Number of Samples	Number of Files	File Type (Top 5)
phs002790		see diagnosis_comment (9716) 9380:3 : Glioma, malignant (517) 9421:1 : Pilocytic astrocytoma (461) 9470:3 : Medulloblastoma, NOS (427) Low-Grade Glioma (337) Read:None	C72.9 : Central nervous system (4339) C71.9 : Brain, NOS (3204) C42.0 : Blood (2282) Invalid value (1885) Not Reported (1215) Read:None	4994	10912	147422	fastq (47408) json (32278) pdf (9605) vcf (7326) cram (7324) Read:None

## Create a Data Repository Service Manifest for Cloud Analysis

## Export the manifest to Cancer Genomics Cloud (CGC):

- In CGC, go to your Project → Files → Add Files → GA4GH Data Repository Service (DRS)
- Files will load into your project for analysis



MY FILES



To access and analyze files, select or deselect any files as needed, and then choose an option from the 'Available Export Options' dropdown by clicking either 'Export to Cancer Genomics Cloud' or 'Download File Manifest'.

USER GUIDE

AVAILABLE EXPORT OPTIONS

EXPORT TO CANCER GENOMICS CLOUD

DOWNLOAD MANIFEST

File Name ↑	Study Name	Study Accession	Participant ID	Sample ID	File Type	File Size	
207678140100_R01 CD1_Grn.idat	Molecular Characterization Initiative	phs002790	PBCXUF	0E2LK3	idat	13.05 MB	
207678140100_R01 CD1_Red.idat	Molecular Characterization Initiative	phs002790	PBCXUF	0E2LK3	idat	13.05 MB	

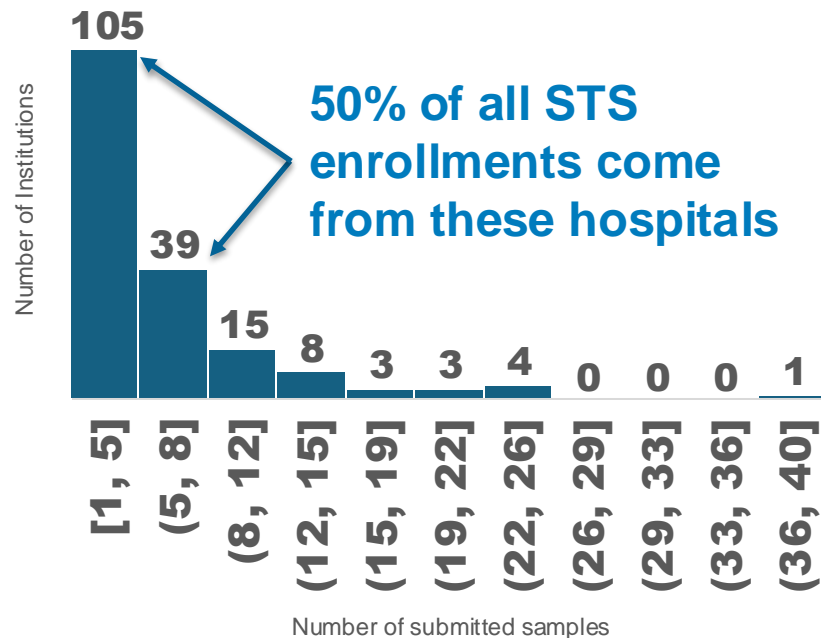
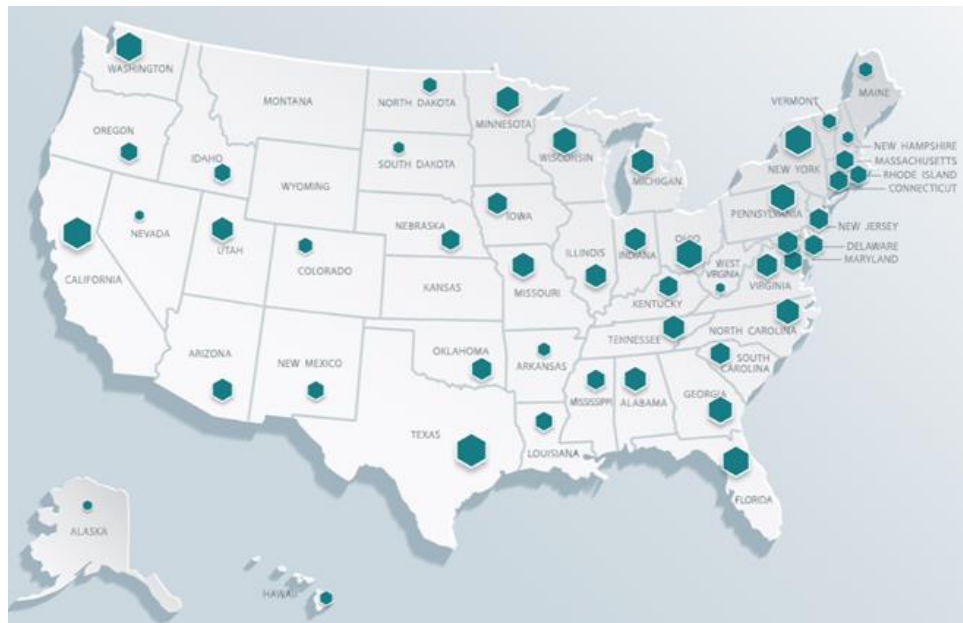
# MCI Data Access: FAQs

- **Does the lab data exist in a structured format, or is it expected that we use NLP on the PDF documents to make it computable?**
  - Deidentified clinical sample reports are available in both PDF and JSON formats.
- **Are there institutional IDs attached to the data so we can organize it by institutions in the platform?**
  - Institutional IDs are not attached to the data to reduce the risk of re-identification, especially for extremely rare pediatric cancers.
- **Is it possible to download the de-identified summary reports directly without going through the dbGaP approval process?**
  - The summary reports were not provided in this manner due to potential inclusion of sensitive information.

# MCI-Soft Tissue Sarcoma Data

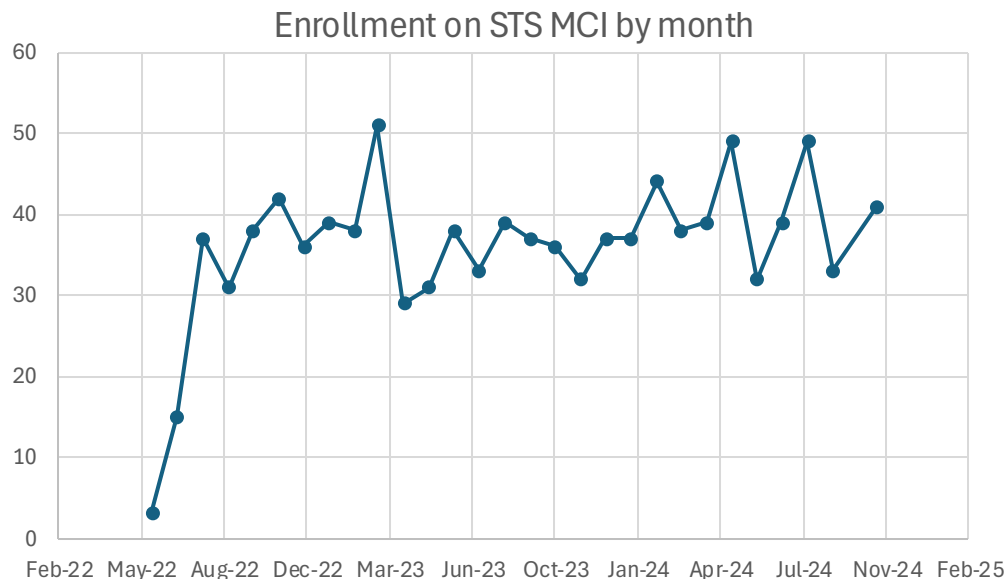
*Clinical Impact*

# Distribution of Enrollment of Soft Tissue Sarcoma (STS) Patients

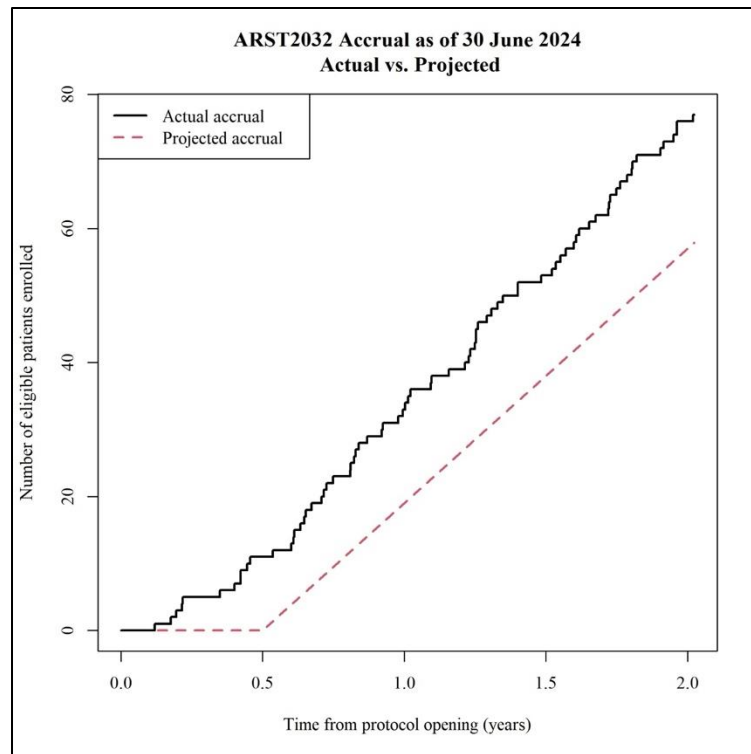
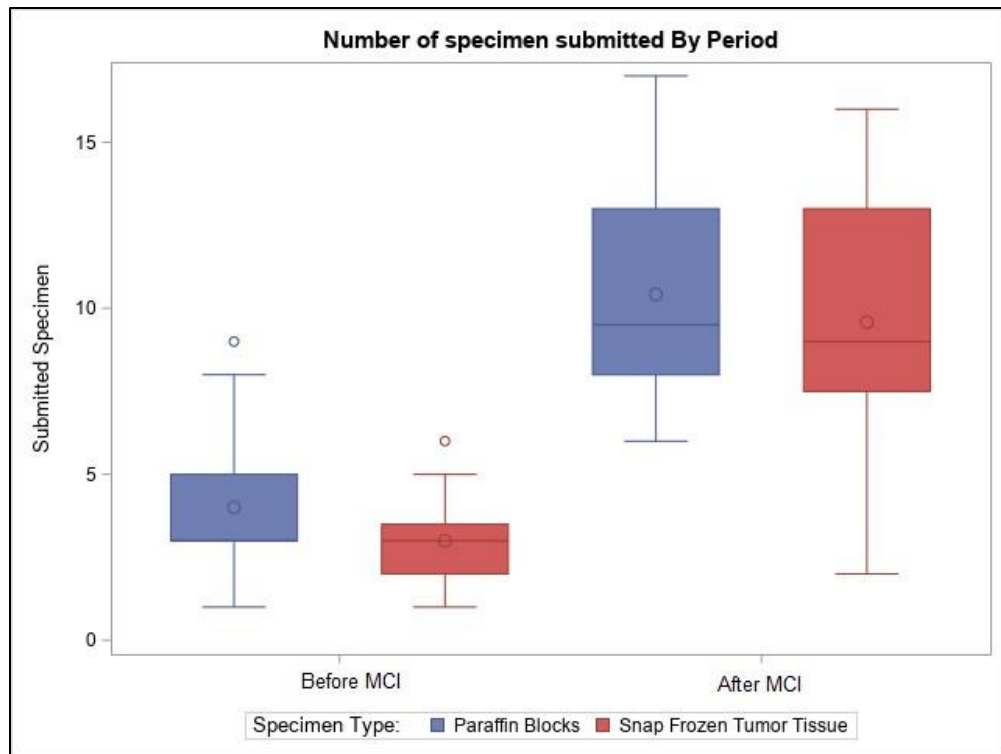


# MCI - STS Study: As of 10/29/2024

- 1,043 enrolled patients
- 851 (82%) of enrollees have a submitted paired blood/tumor specimen
- 777 (75%) pass QC and have completed profiling
- 2,170 completed assays



# Increased Submission of Samples with Opening of MCI



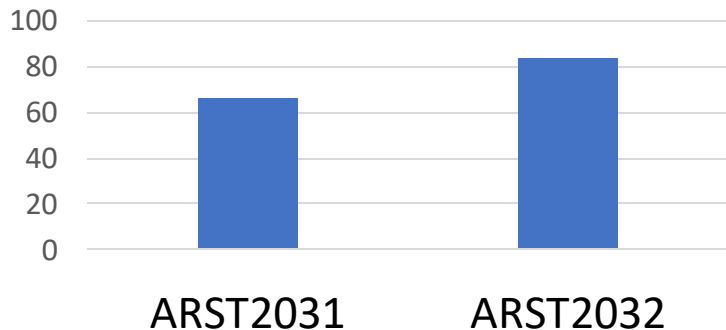
Sapna Oberoi; Wei Xu COG



# Co-enrollment on Soft Tissue Sarcoma Clinical Trials

- MCI is required for eligibility on ARST2032 for low-risk rhabdomyosarcoma
- Transition to “Regimen M” for patients with *MYOD1* or *TP53* mutant tumors allowed at Week 3 or 6

**Patients co-enrolled on APEC MCI and clinical trials**



## 2. SOMATIC CANCER-ASSOCIATED SEQUENCE VARIATION IN THE TUMOR

Variant Information	Genomic Change (GRCh38)	Etiology	Germline Variant Allele Fraction (%)	Tumor Variant Allele Fraction (%)	Variant Classification (AMP/ASCO/CAP)
<i>NRAS</i> (NM_002524.5) c.35G>C p.Gly12Ala	chr1:114716126 C>G	Somatic	not detected	66%	Tier I (Level B)
<i>TP53</i> (NM_000546.6) c.404G>T p.Cys135Phe	chr17:7675208 C>A	Somatic	not detected	2%**	Tier I (Level B)
<i>NF1</i> (NM_001042492.3) c.6420_6427+18del p.?	chr17:31336907_31336932del	Somatic	not detected	24%*	Tier I (Level B)

\*The variant allele frequency/fraction for this variant may be underestimated due to its nature as a deletion event.

## 3. PERTINENT NEGATIVES

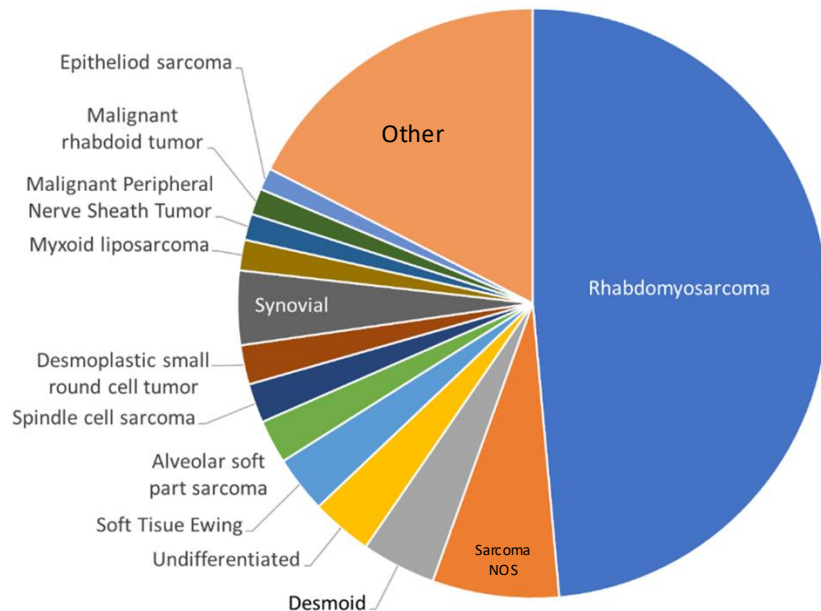
***TP53* Germline Sequence Variants** - No pathogenic or likely pathogenic germline single nucleotide variants or small insertion-deletion events were detected.

***TP53* Copy Number** - No biallelic loss detected. However, a single copy loss of *TP53* was detected on 17p in the tumor specimen.

# Soft Tissue Sarcoma patients enrolled in the first year of MCI

Total Number of patients is 425

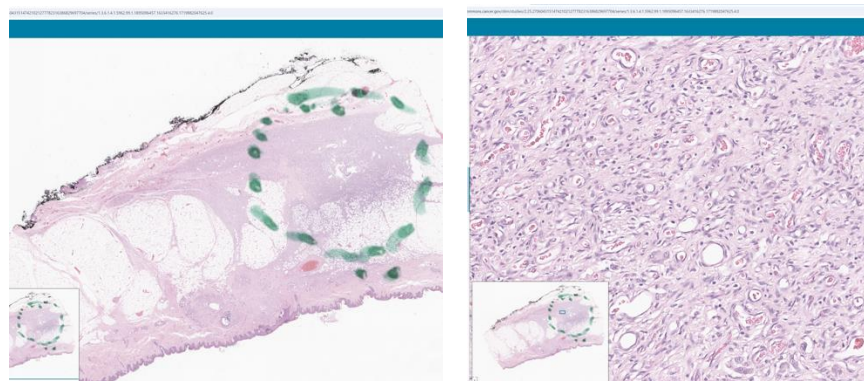
Variable	Frequency	Percentage
<b>Median age at diagnosis</b>	11.2 (0.07, 25.86)	
<b>Age at diagnosis</b>		
≤ 18 years	382	89.9
> 18 years	43	10.1
<b>Sex</b>		
Female	196	46.1
Male	229	53.9
<b>Race</b>		
American Indian or Alaska Native	5	1.2
Asian	18	4.2
Black or African American	61	14.4
Multiple Races	7	1.7
Native Hawaiian or other Pacific Islander	6	1.4
White	270	63.5
Not Reported or UKN	58	13.7
<b>Ethnicity</b>		
Hispanic or Latino	79	18.6
Not Hispanic or Latino	301	70.8
Not Reported or UKN	45	10.6



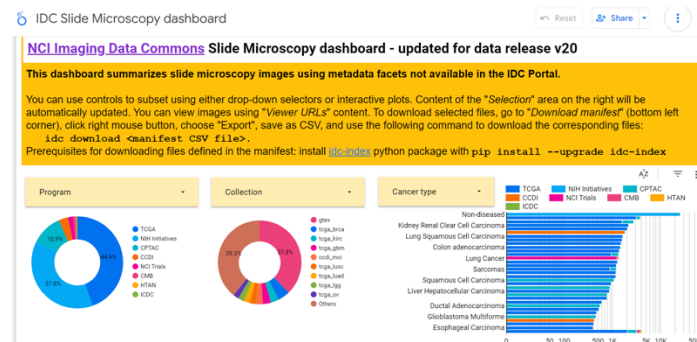
# MCI H&E Images Now Available in Imaging Data Commons

## [Imaging Data Commons Collections](#)

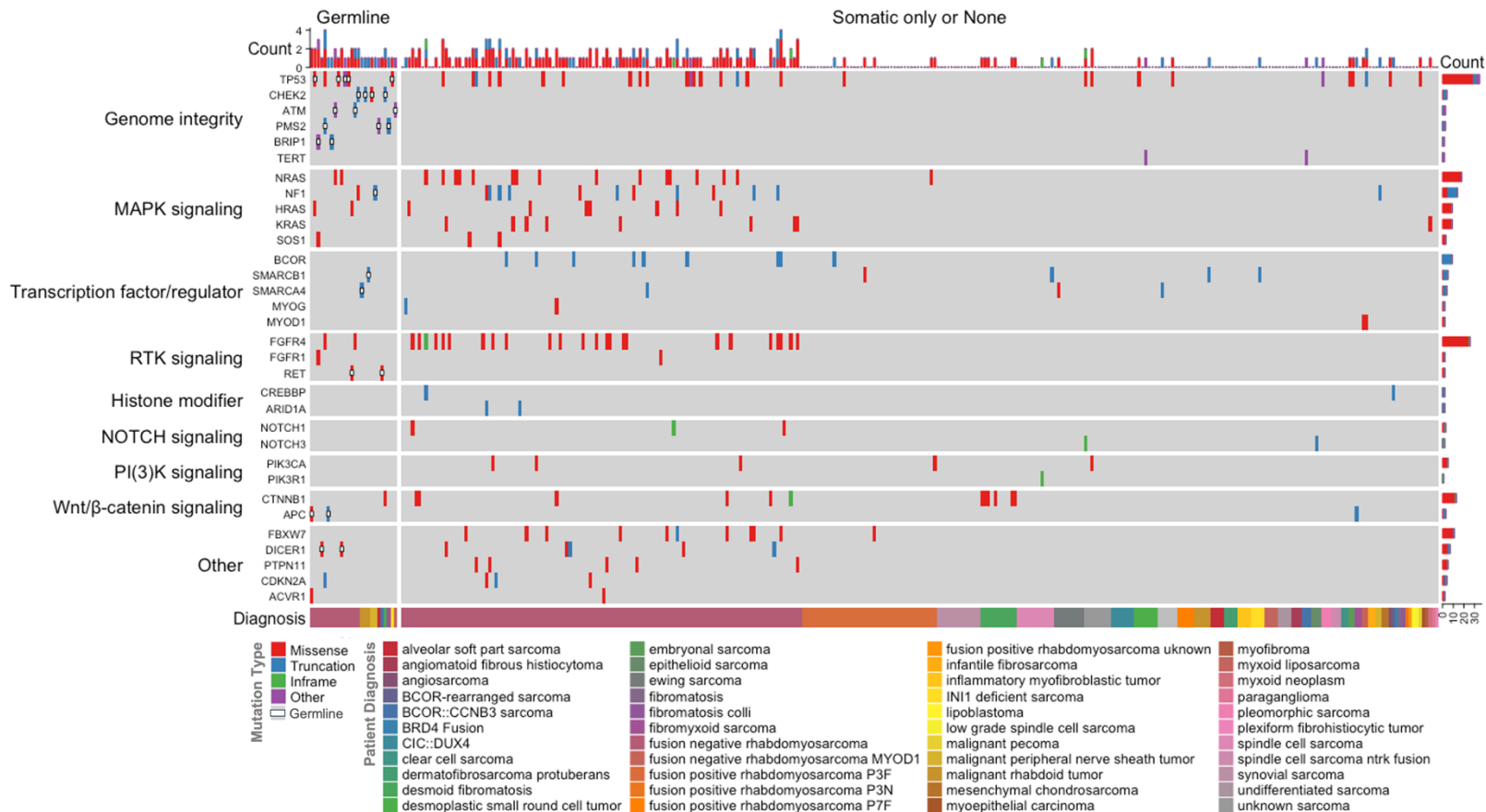
- Hematoxylin and eosin (H&E) stained images in Digital Imaging and Communications in Medicine (DICOM) format are now accessible as open-access through the Imaging Data Commons (IDC)
- Additional images associated will be released in the coming months, new images will be periodically added as participants are enrolled
- Links to images on IDC are accessible through CCDI Hub



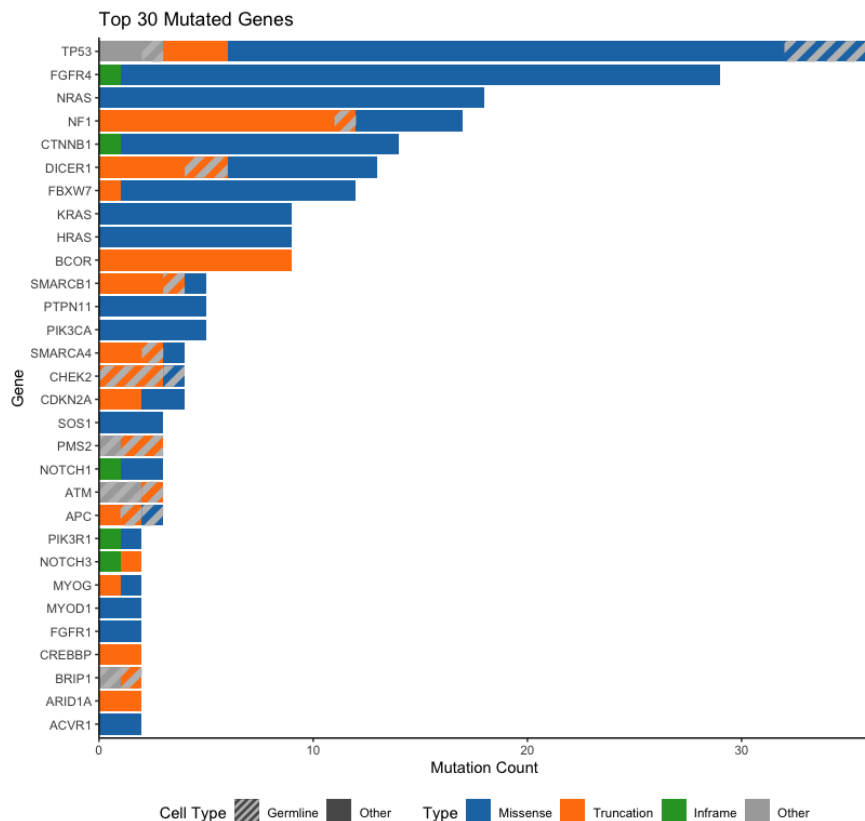
## [IDC Slide Microscopy Dashboard](#)



# Soft Tissue Sarcoma Mutational Summary

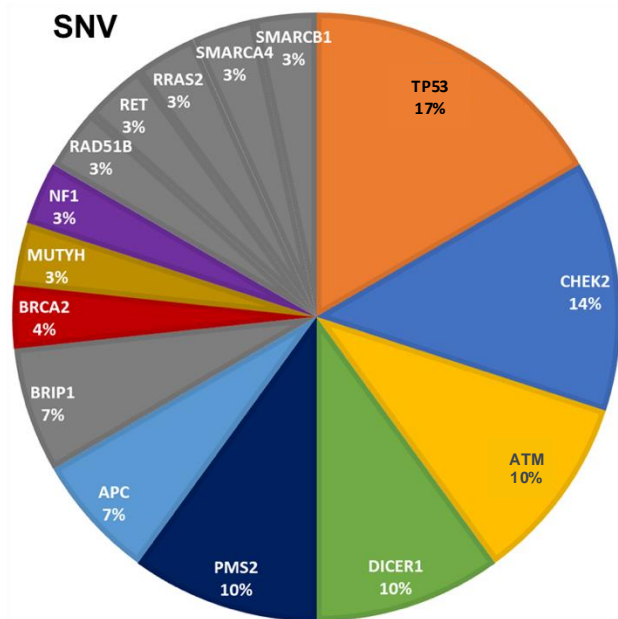


# Recurrently Mutated Genes in the STS cohort



- Recurrent gene rank list is largely driven by fusion negative RMS
- Mutation of *FGFR4* is common in fusion negative RMS
- *MYOD1* L122R mutations are uncommon (at least at the time of diagnosis)

# 11% of profiled STS patients have a reportable germline finding



\*Single nucleotide variants reported in 1 or more patients

## 1. GERMLINE CANCER-ASSOCIATED SEQUENCE VARIATION

Gene (Transcript ID)	Genomic Change (GRCh38)	Nucleotide Change	Etiology/Zygosity	Predicted Protein Change	Associated Disease/Condition	Variant Interpretation (ACMG/AMP Evidence)
<i>RET</i> (NM_020975.6)	chr10:43114598 G>C	c.1998G>C	Het	p.Lys666Asn	(AD) Medullary thyroid carcinoma (OMIM: 155240) (AD) Multiple endocrine neoplasia IIA (OMIM: 171400) (AD) Multiple endocrine neoplasia IIB (OMIM: 162300) (AD) Pheochromocytoma (OMIM: 171300)	Pathogenic (PS1, PS3_Moderate, PS4_Moderate, PM2, PM5)

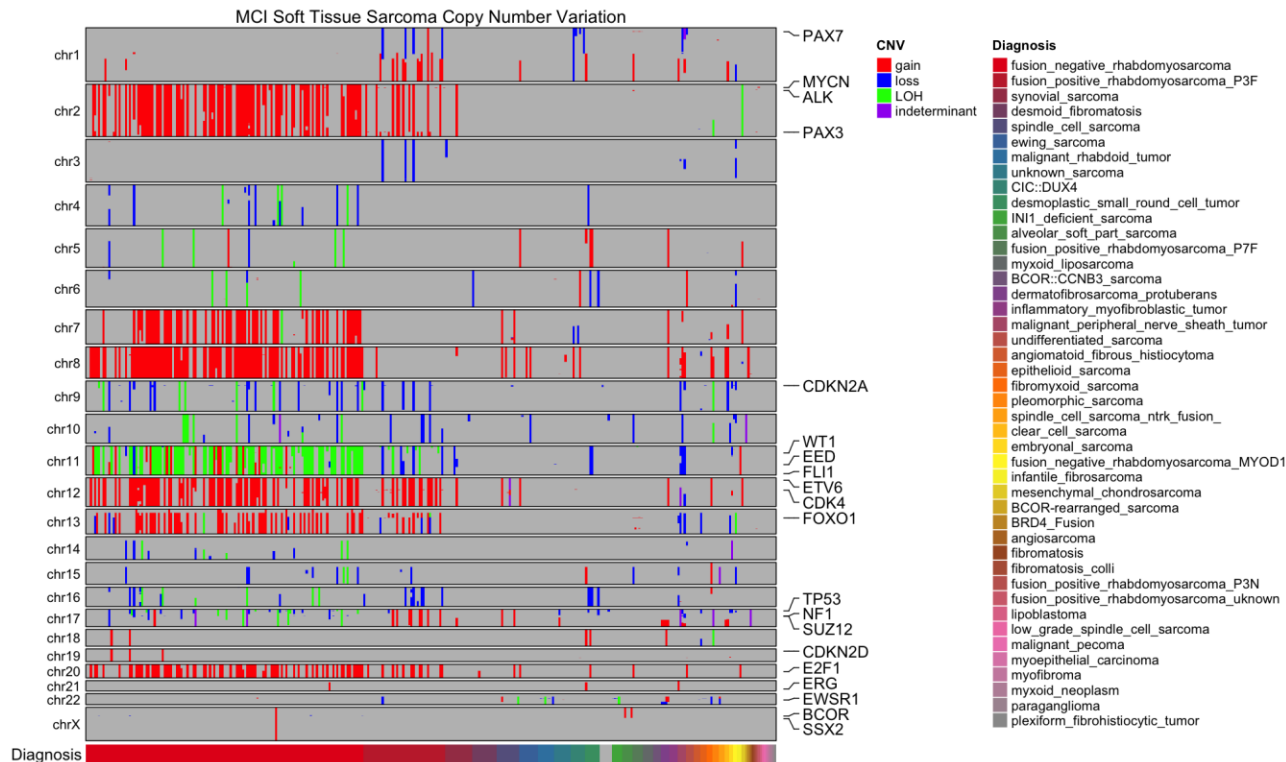
### NM\_020975.6(*RET*):c.1998G>C p.(Lys666Asn)

This individual's comparator peripheral blood specimen harbors a heterozygous missense variant in the *RET* gene, which is one of the receptor tyrosine kinases that plays a key role in cell proliferation and differentiation (PMID: 16979782). Pathogenic variants in this gene are associated with autosomal dominant disorders; medullary thyroid carcinoma (OMIM: 155240), multiple endocrine neoplasia IIA (OMIM: 171400), multiple endocrine neoplasia IIB (OMIM: 162300) and pheochromocytoma (OMIM: 171300). A germline *RET* variant has also been reported in the setting of relapsed leukemia (PMID: 30936199).

This missense variant (p.Lys666Asn) is a well-described pathogenic variant as it has been reported in the setting of medullary thyroid carcinoma in multiple unrelated individuals in the literature. *In-vitro* studies showed that this variant results in increase phosphorylation of ERK and high kinase activity (ACMG/AMP: PS4\_Moderate, PS3\_Moderate; PMIDs: 27673361, 15858153, 20103606). This variant is present at an extremely low frequency in gnomAD, a large-scale control population database (ACMG/AMP: PM2) and this same amino acid change resulting from a different nucleotide change (c.1998G>T) has been reported as pathogenic in literature and in ClinVar by multiple clinical laboratories (ACMG/AMP: PS1; ClinVar ID: 24932). Additionally, a different amino acid change at this same residue (Lys666Glu) has been reported as pathogenic in literature and ClinVar (ACMG/AMP: PM5; ClinVar ID: 24931). Together, and in accordance with ACMG/AMP guidelines, this variant is classified as pathogenic.

“Rhabdomyosarcoma NOS”

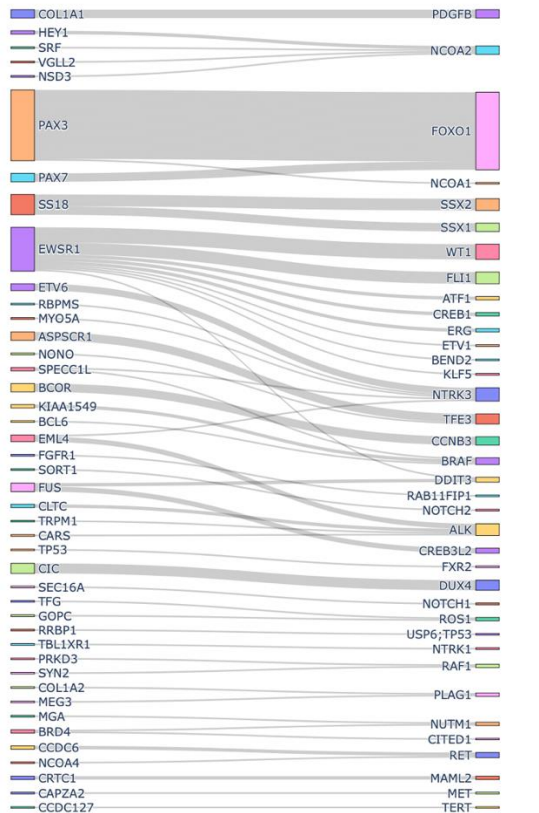
# Soft Tissue Sarcoma Copy Number Summary



- Fusion Negative RMS has a very distinct CN profile
- Focal deletion and amplification of *CDKN2A/CDK4* occurs in ~20% of the population
- Multiple tumors especially patients with Li Fraumeni have evidence of chromothripsis

# STS Fusion Oncogene Summary – Archer Results

## Detected Fusion Oncogenes in MCI STS



### “Soft tissue sarcoma NOS”

**1. AMP/ASCO/CAP Tier I or Tier II Alterations (Potentially Actionable)**

Gene Fusion	5' Fusion Partner	3' Fusion Partner	Classification (AMP/ASCO/CAP)
<i>EWSR1::KLF5</i>	<i>EWSR1</i> :NM_001163287.2 [Exon: 9] (GRCh37) chr22:29686457	<i>KLF5</i> :NM_001730.4 [exon: 2] (GRCh37) chr13:73636660	Tier I (Level B)

Targeted RT-PCR followed by subsequent Sanger sequencing confirmed the presence of this event.

### “Spindle cell neoplasm”

**1. AMP/ASCO/CAP Tier I or Tier II Alterations (Potentially Actionable)**

Gene Fusion	5' Fusion Partner	3' Fusion Partner	Classification (AMP/ASCO/CAP)
<i>EML4::NTRK3</i>	<i>EML4</i> :NM_019063.4 [exon: 2] (GRCh37) chr2:42472827	<i>NTRK3</i> :NM_001012338.2 [exon: 14] (GRCh37) chr15:88576276	Tier I (Level A)

Targeted RT-PCR followed by subsequent Sanger sequencing confirmed the presence of this event.



# Resources

Access CCDI resources  
through the CCDI Hub



## CCDI Data Access:

- Access guide: [https://ccdi.cancer.gov/static/media/CCDI\\_Usage\\_Instructions\\_Nov2024\\_v2.5.0.69ea3cd5.pdf](https://ccdi.cancer.gov/static/media/CCDI_Usage_Instructions_Nov2024_v2.5.0.69ea3cd5.pdf)
- Information about CCDI study data: [datacatalog.ccdi.cancer.gov/resource/CCDI](https://datacatalog.ccdi.cancer.gov/resource/CCDI)
- Cancer Data Standards Registry and Repository: [cadsr.cancer.gov/onedata/Home.jsp](https://cadsr.cancer.gov/onedata/Home.jsp)

## Data Models and Federation API:

- CCDI: [github.com/CBIIT/ccdi-model](https://github.com/CBIIT/ccdi-model)
- CCDI template: [github.com/CBIIT/Model\\_to\\_Submission](https://github.com/CBIIT/Model_to_Submission)
- Childhood Cancer Clinical Data Commons: [github.com/CBIIT/c3dc-model](https://github.com/CBIIT/c3dc-model)
- CCDI Federation API: [cbiit.github.io/ccdi-federation-api](https://cbiit.github.io/ccdi-federation-api)

# Team Members

- Patients and Families
- Advocacy Community
- Local treatment, pathology and surgical teams
- Children's Oncology Group Project EveryChild Team
- Children's Oncology Group Soft Tissue Sarcoma Committee
- Nationwide Biopathology Center Team
- Institute for Genomic Medicine Team
- NCI Childhood Cancer Data Initiative Team

Yasmine Akkari, Institute for Genomic Medicine  
Michael A. Arnold, University of Colorado  
Natalie Bir, Biopathology Center  
Catherine E. Cottrell, Institute for Genomic Medicine  
**Avery Funkhouser**, National Cancer Institute  
Doug Hawkins, Seattle Childrens Hospital  
**Subhashini Jagu**, National Cancer Institute  
Javed Khan, National Cancer Institute  
Corinne M. Linardic, Duke School of Medicine  
Elaine R. Mardis, Institute for Genomic Medicine  
Mariam Mathew, Institute for Genomic Medicine  
Yvonne Moyer, Biopathology Center  
**Sapna Oberoi**, University of Manitoba  
Nilsa C. Ramirez, Biopathology Center  
Greg Reaman, National Cancer Institute  
**Erin R. Rudzinski**, Seattle Childrens Hospital  
Kathleen Schieffer, Institute for Genomic Medicine  
Malcolm Smith, National Cancer Institute  
Shountea Stover, Biopathology Center  
**Diana Thomas**, Biopathology Center  
Rajkumar Venkatramani, Texas Children's Hospital  
**Wei Xue**, University of Florida  
Aaron Weiss, Maine Medical Center  
**Greg Wheeler**, Institute for Genomic Medicine

# Q&A

# How You Can Engage with CCDI



**Learn about CCDI and subscribe to our monthly newsletter:**  
[cancer.gov/CCDI](https://cancer.gov/CCDI)



**Access CCDI data and resources:**  
[ccdi.cancer.gov](https://ccdi.cancer.gov)



**Questions? Email us at:**  
[NCIChildhoodCancerDataInitiative@mail.nih.gov](mailto:NCIChildhoodCancerDataInitiative@mail.nih.gov)

# Thank you for attending!



**NATIONAL  
CANCER  
INSTITUTE**

[cancer.gov](https://cancer.gov)

[cancer.gov/espanol](https://cancer.gov/espanol)