

Childhood Cancer Data Initiative Webinar Series

Impact of the Molecular Characterization Initiative on Pediatric CNS Tumors

Diana Thomas and Sarah Leary

Agenda

1. Molecular Characterization Initiative (MCI): Strategy
2. MCI Progress: Genomics and Clinical Data for CNS Subjects
3. MCI Data: Clinical Impact
4. MCI Data: Implications for Clinical Trials
5. Q&A

Today's Speakers



Diana L. Thomas, M.D., Ph.D.
Neuropathologist

- Pathology Operations Director, Biopathology Center
- Nationwide Children's Hospital

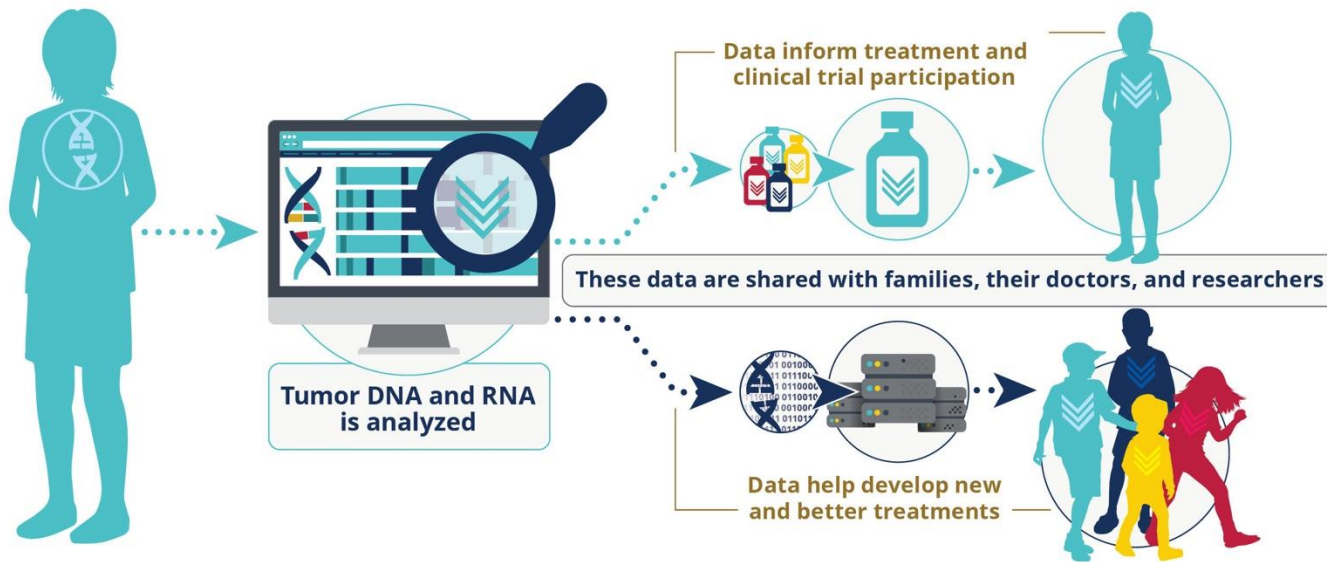


Sarah E. S. Leary, M.D., M.S.
Pediatric Oncologist

- Medical Director, Pediatric Brain Tumor Program
- Seattle Children's Hospital

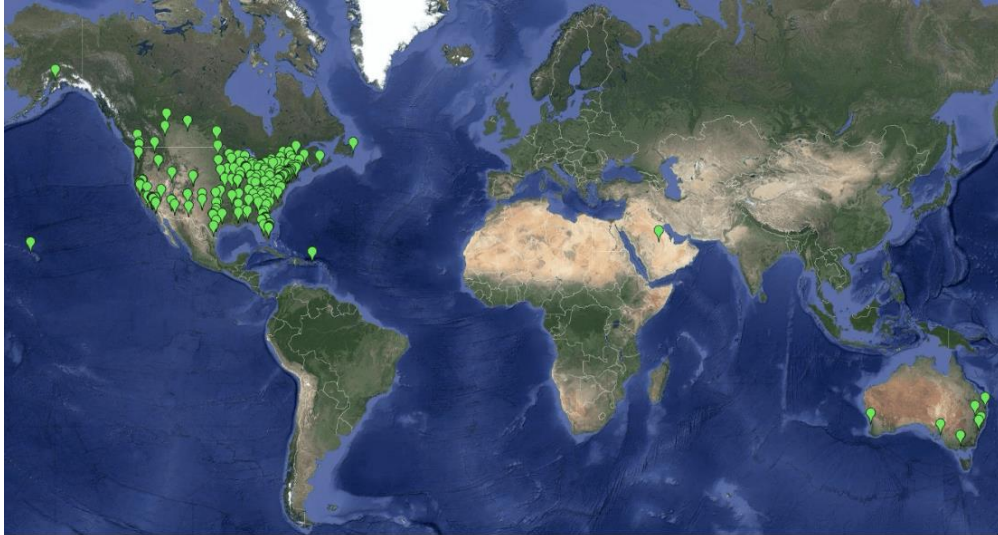
Molecular Characterization Initiative (MCI) *Strategy*

WHAT IS THE CCDI Molecular Characterization Initiative?



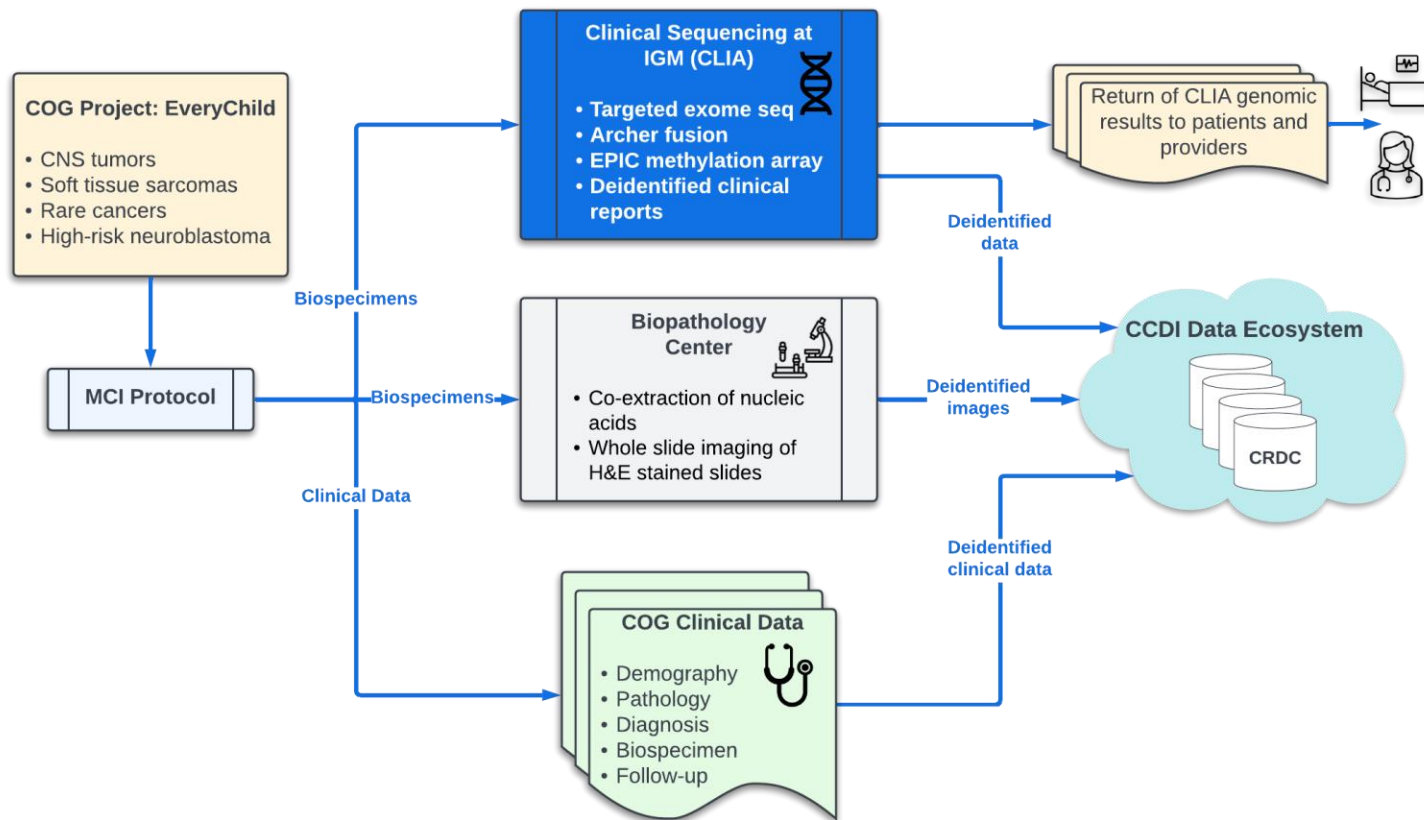
cancer.gov/CCDI-molecular

Children's Oncology Group (COG) Institutions



More than 90% of 16,000 children and adolescents diagnosed with cancer each year in the United States are cared for at Children's Oncology Group member institutions.

A Partnership Between NCI and COG Project: Every Child



MCI Progress

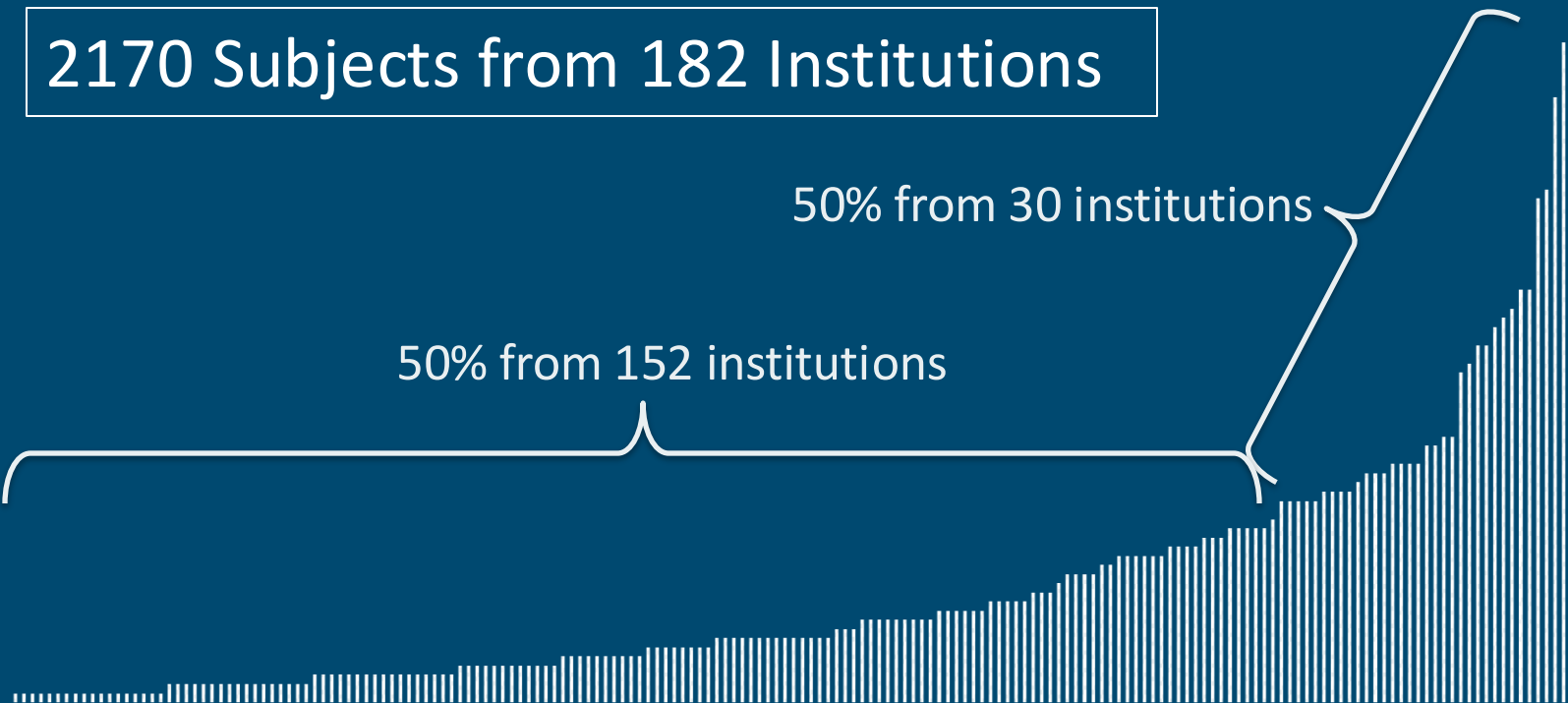
Genomics and Clinical Data for CNS Subjects

MCI CNS Enrollment by Institution as of 12/31/2023

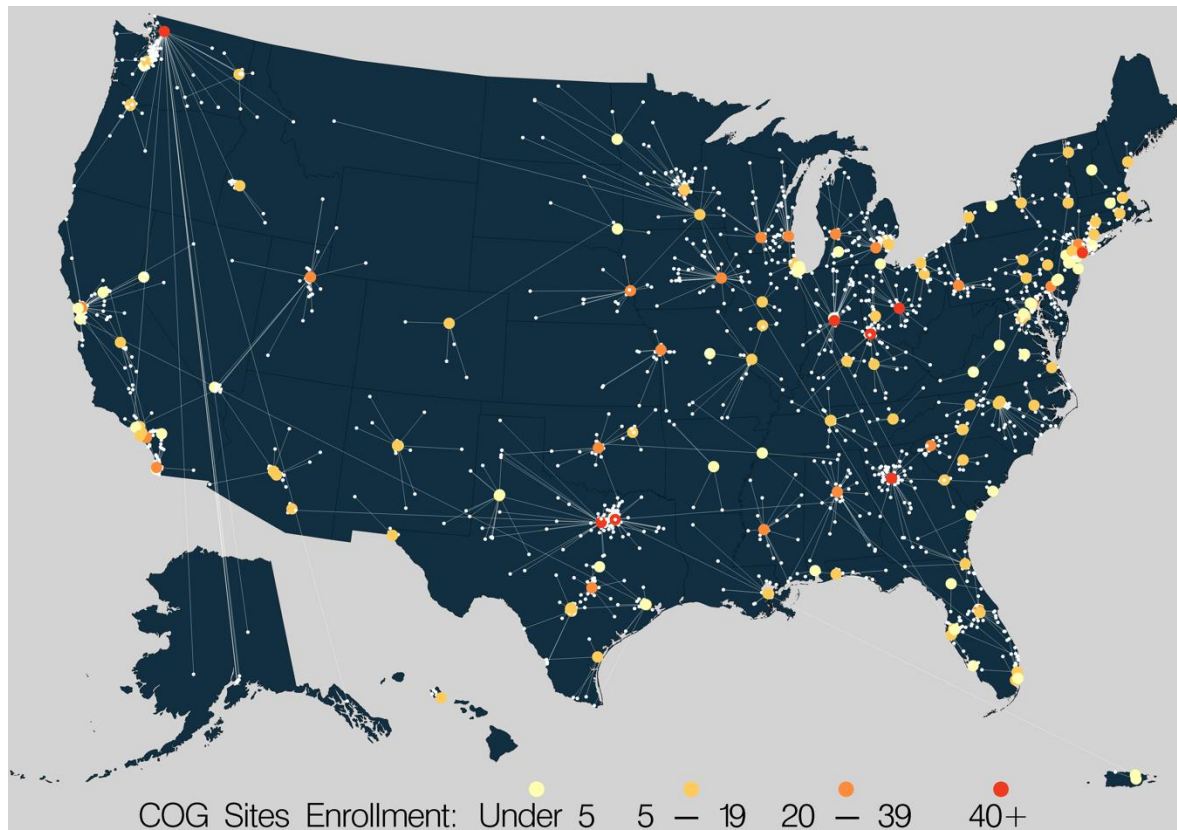
2170 Subjects from 182 Institutions

50% from 30 institutions

50% from 152 institutions

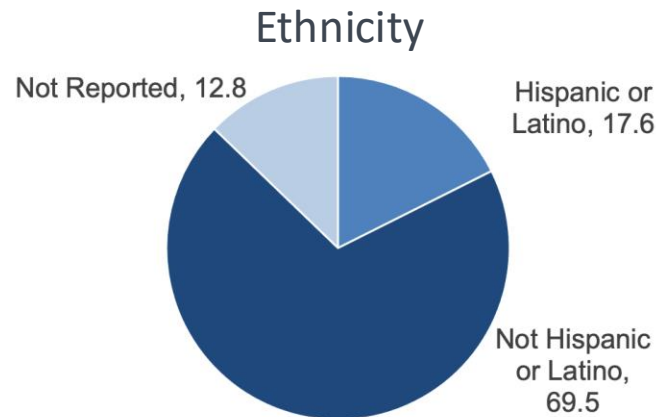
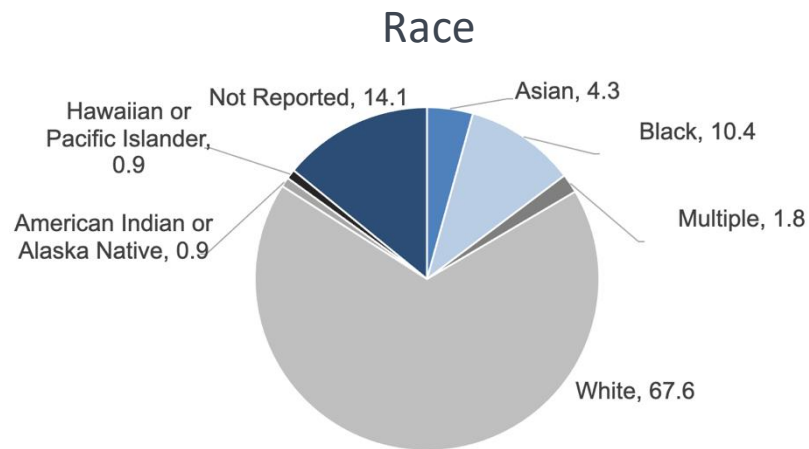


MCI CNS Enrollment (12/31/23) by Subject US Zip Code

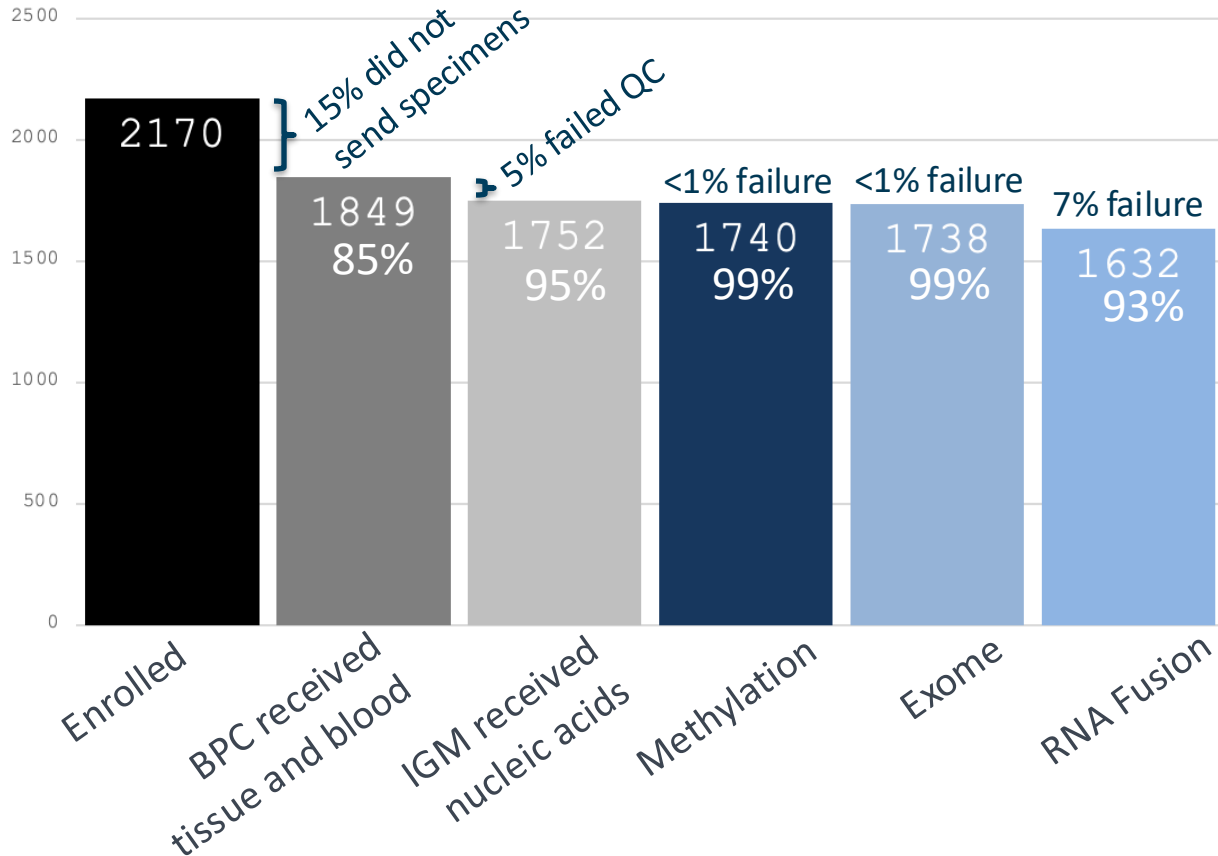


MCI CNS Patient Demographics

- Median Age: 8.9 years (range 0-25)
- Gender: 44% female, 56% male
- Country: 90% USA, 6% Canada, 1.6% Australia, 1.6% New Zealand
- Race: 4.3 % Asian, 10.4% Black, 1.8% multiple, 0.9% Hawaiian or Pacific Islander, 0.9% Native American
- Ethnicity: 17.6% Hispanic or Latino



MCI CNS Return of Results



MCI Data

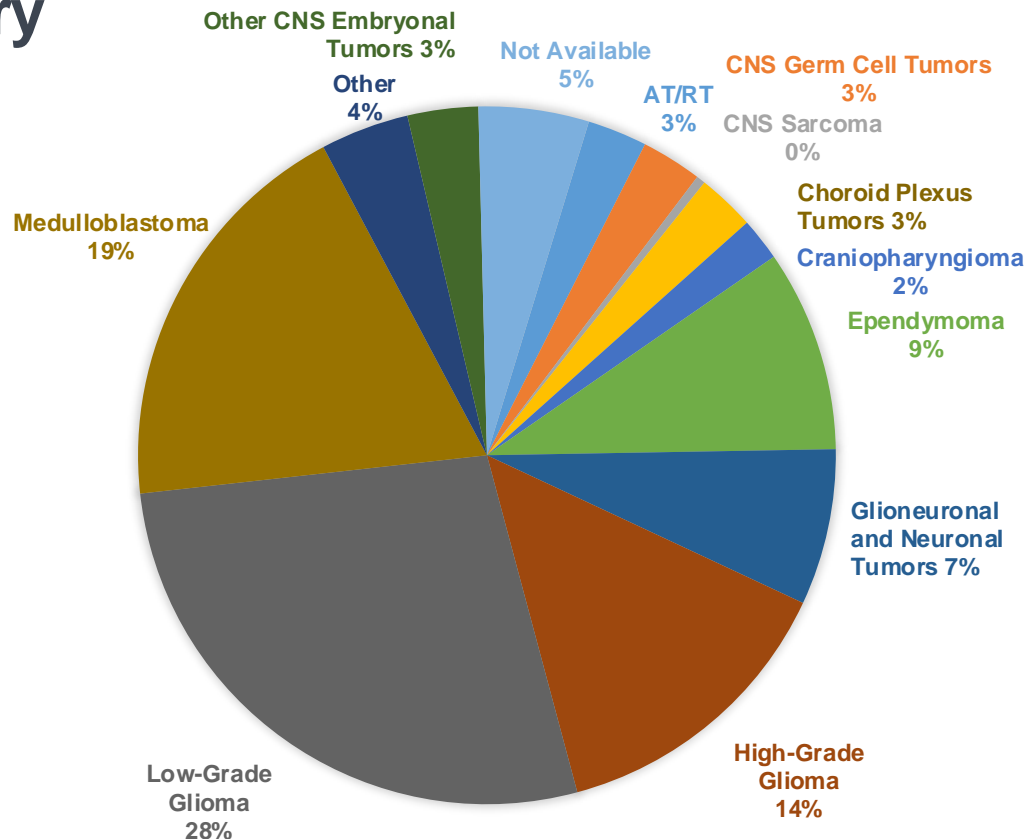
Clinical Impact

MCI CNS Diagnosis Category

CNS Diagnosis Category	Frequency Count	Percent of Total (%)
* Atypical teratoid/ rhabdoid tumor	60	2.8
* CNS Germ Cell Tumors	61	2.8
CNS Sarcoma	9	0.4
Choroid Plexus tumors	58	2.7
Craniopharyngioma	43	2.0
* Ependymoma	203	9.4
Glioneuronal and neuronal tumors	157	7.2
* High-Grade Glioma	301	13.9
* Low-Grade Glioma	595	27.4
* Medulloblastoma	412	19.0
Other	89	4.1
Other CNS Embryonal tumors	71	3.3
Not Available	111	5.1
	2170	100.0

* Current COG trial for selected patients

* Planned COG trial for selected patients

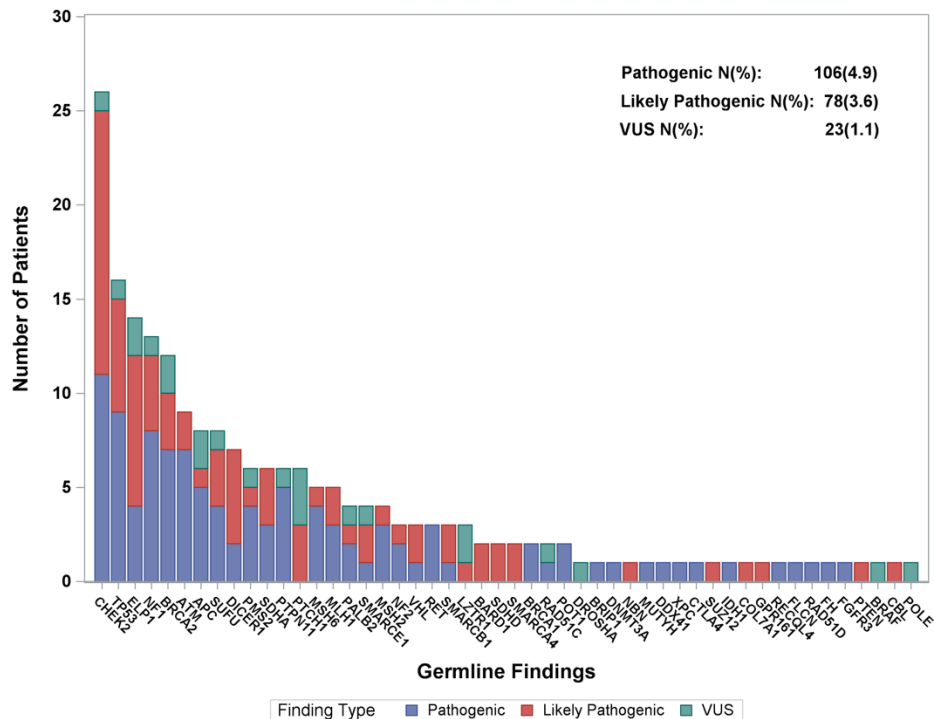


Results: Somatic Alterations Detected in CNS Tumors

- Whole exome DNA sequencing:
 - Pathogenic variants detected in 43.2% of tumors (n=1829)
 - 111 *BRAF* V600
 - 28 *IDH1*
 - Medically-informative copy number variation (CNV) or loss of heterozygosity (LOH) in 76.3% of tumors
- Archer fusion panel: fusions detected in 28.5% of tumors (n=1683)
 - 289 *BRAF::KIAA1549*
 - 36 *NTRK/ROS/ALK* fusions

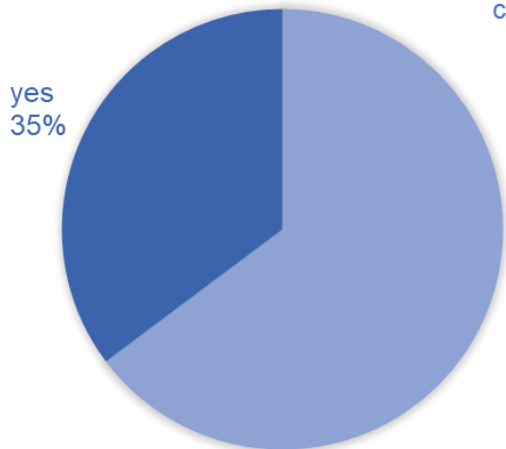
Results: 12% Germline Cancer Predisposition

- 207 of 1738 children tested found to have genetic cancer predisposition
- 49 different genes
 - CHEK2 (1.5%), TP53 (0.9%)
 - MMR defects (0.9%)
 - 12 high-grade glioma
 - 1 low-grade glioma
 - 2 medulloblastoma
 - ELP1 (0.8%), NF1 (0.7%)

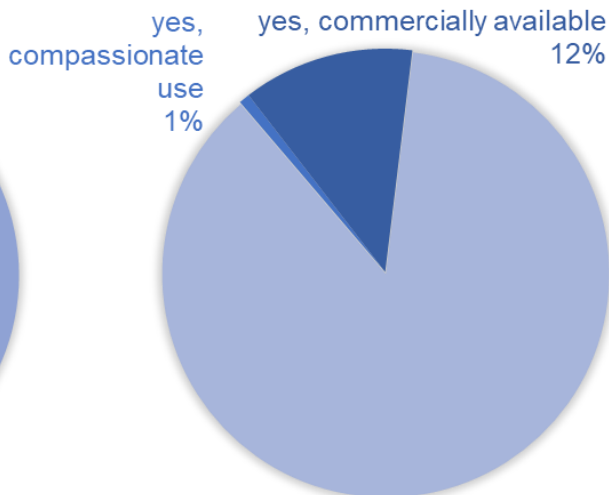


MCI CNS Follow-Up

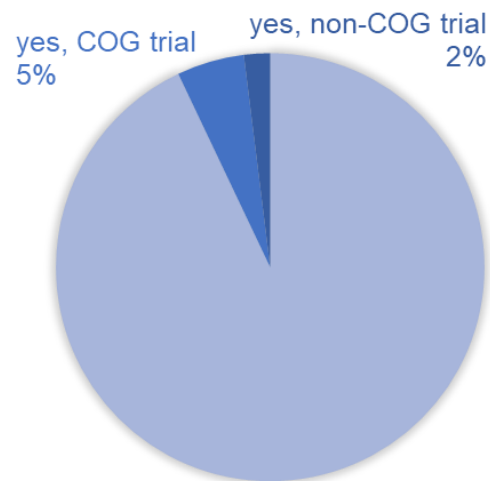
Diagnosis refined by testing?
N=965



Therapy matched by sequencing?
N=887



Trial enrolled using results?
N=964

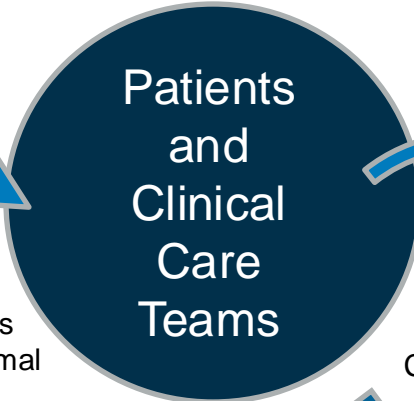


MCI Data

Implications for Clinical Trials

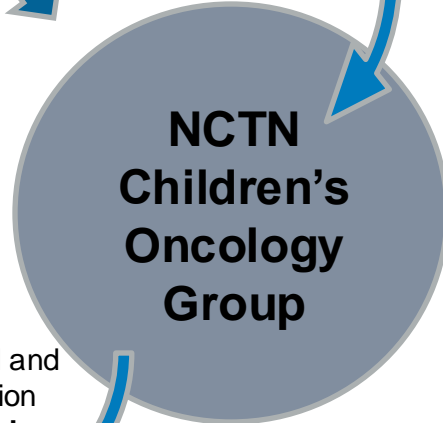
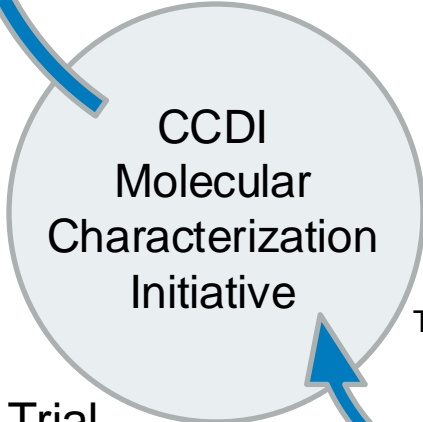
Genomic and Clinical
Data Sharing

Therapeutic Trial
Screening



Return of Clinical Results
Whole Exome, Tumor/Normal
Methylation
RNA Fusion Panel

Project:EveryChild
APEC14B1 – MCI
Consent and Enrollment



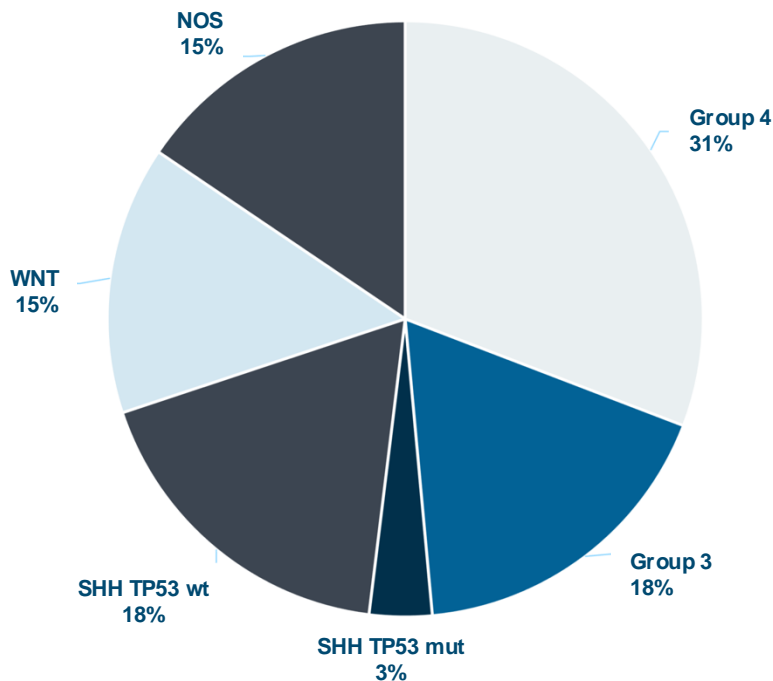
**Biopathology
Center**
Tissue Quality Control and
Nucleic Acid Extraction
**Institute for Genomic
Medicine**
Molecular Testing

Therapeutic Trial
Data

Therapeutic Trial
Enrollment

MCI CNS Diagnosis: Medulloblastoma

MCI CNS Medulloblastoma (n=412 as of 12/31/2024)



Medulloblastoma Group	Frequency	Percent (%)
Group 4	127	31%
Group 3	73	18%
SHH TP53 wt	74	18%
SHH TP53 mut	14	3%
WNT	60	15%
NOS	64	15%
Total	412	100%

COG Clinical Trial Approach for Medulloblastoma Integrated Clinical and Molecular Risk Stratification

- Clinical Risk Factors
 - Metastatic Disease
 - Incomplete Resection
 - Anaplastic Histology
 - Age < 4*
*radiation avoidance
- Molecular High-Risk
 - Group 3
 - MYC amplification
 - Isochromosome 17
 - SHH
 - TP53 mutation or deletion
 - NMYC or GLI amplification
 - Chromosome 14 loss
- Molecular Low-Risk
 - WNT
 - Group 4
 - Chromosome 11 loss

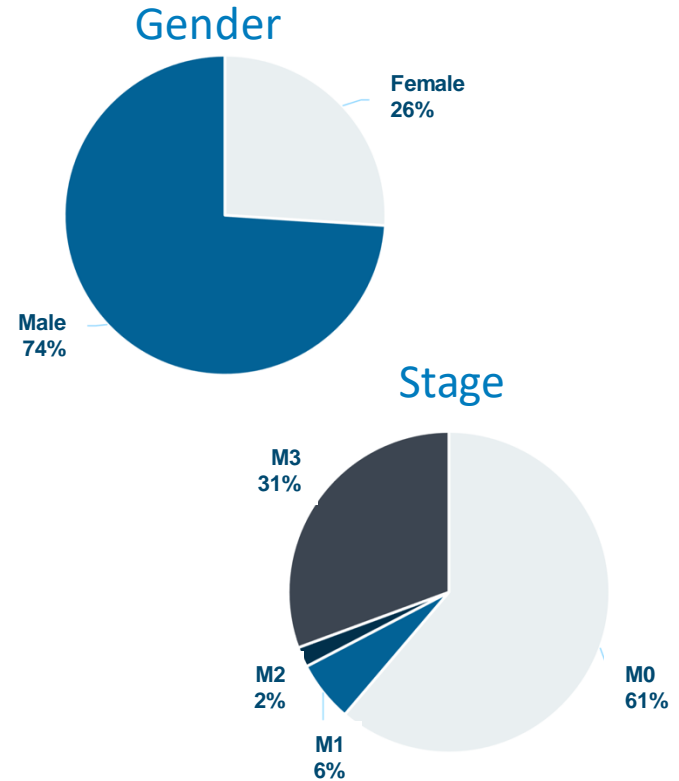
DNA Methylation

Exome Sequencing

Exome Copy Number

MCI CNS Diagnosis: Medulloblastoma Group 3 (n=73)

- Median Age: 5 years (range 1-23)
- >2:1 Male:Female
- Stage: 39% metastatic
- One Year Follow-Up (n=22)
 - Extent of Resection: 73% GTR
 - Radiation Therapy: 64% (all proton)
 - One Year Survival: 68%



NCTN COG Clinical Trial Design

**Project EveryChild Enrollment
for STUDY SCREENING and
MOLECULAR CHARACTERIZATION INITIATIVE (MCI)**

MEDULLOBLASTOMA

**INTEGRATED
RISK STRATIFICATION
(Exome, Methylation)**

WNT

**LOW/AVG
RISK**

**HIGH
RISK**

HIGH-GRADE GLIOMA

H3K27, BRAF, No IDH

**BRAF
V600**

**No
BRAF V600**

LOW-GRADE GLIOMA

BRAF, No IDH

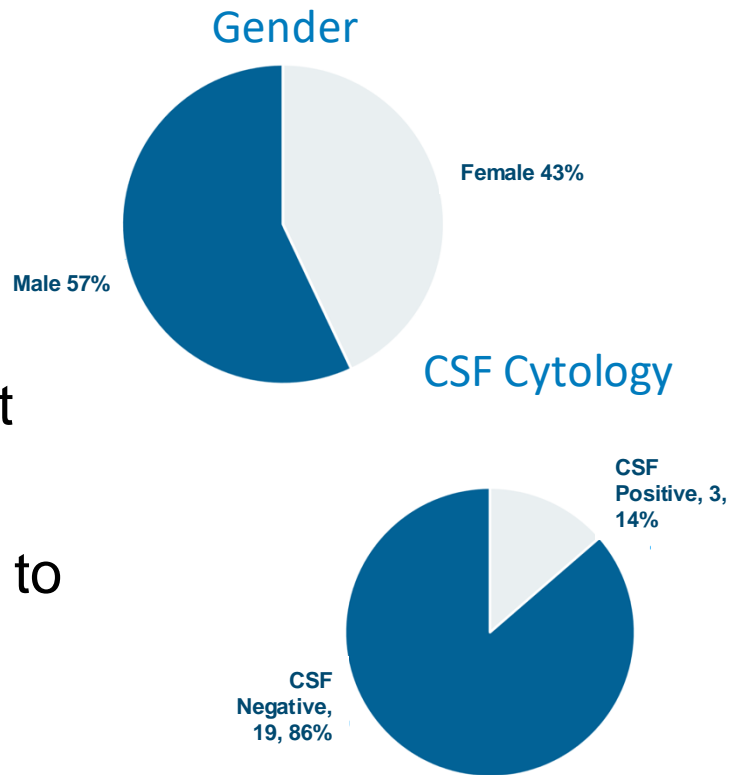
NF1

**No
NF1**

**No NF1
RELAPSE**

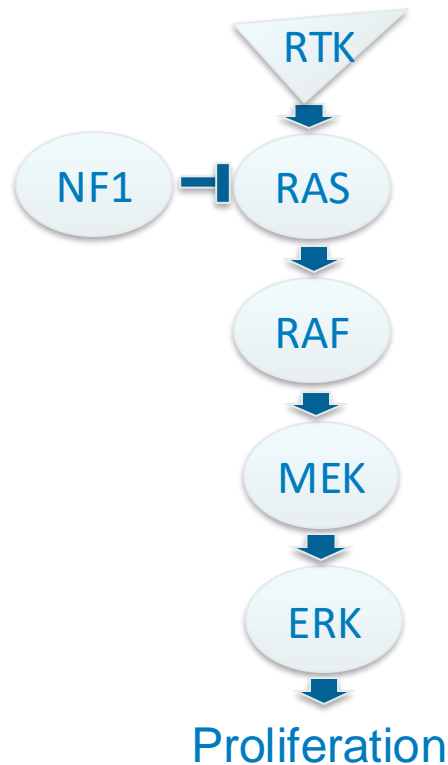
MCI CNS Diagnosis: Diffuse Midline Glioma, H3K27 Altered (n=86)

- Median Age: 9 years (range 3-20)
- Gender: 57% male:43% female
- Stage: 3/22 (14%) positive CSF cytology (most not tested)
- One Year Follow-Up available for first 14 patients: 43% survival
- All tumors with alterations in addition to H3K27



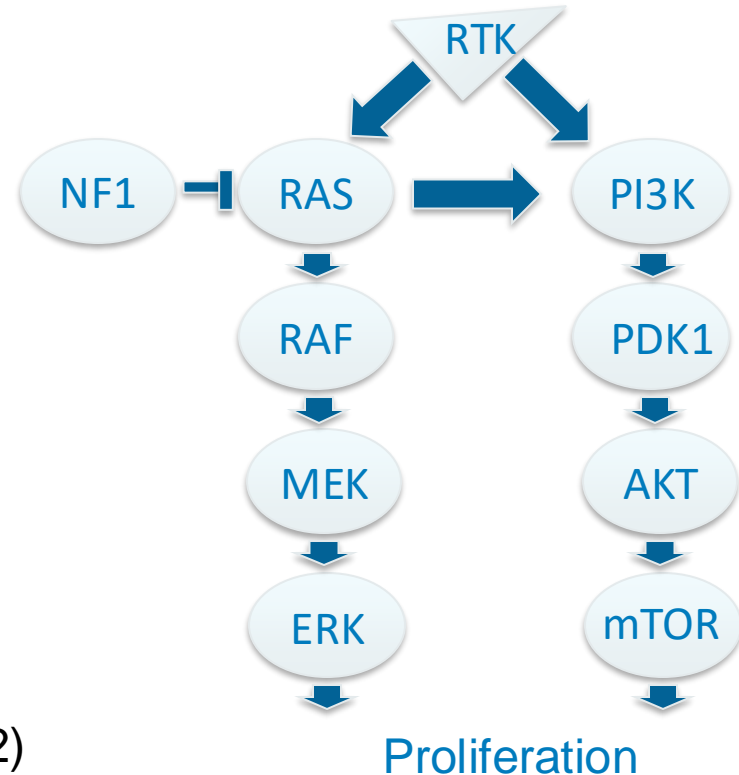
Potentially Targetable Pathway Alterations in Diffuse Midline Glioma, H3K27 Altered (n=86)

- MAPK pathway alterations
 - BRAF*: 7 mutations
(4 V600E, 4 other, 1 fusion)
 - RAS: 3 mutations
(2 *NRAS*, 1 *KRAS*)
 - RAF: 1 mutation (*RAF1* germline)
 - NF1*: 15 mutations (1 germline)



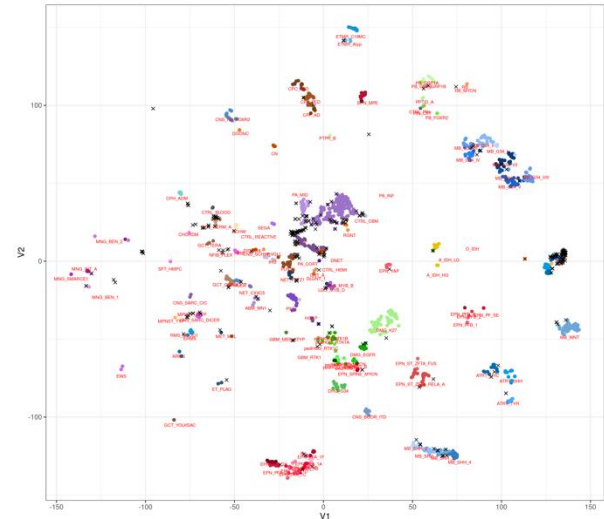
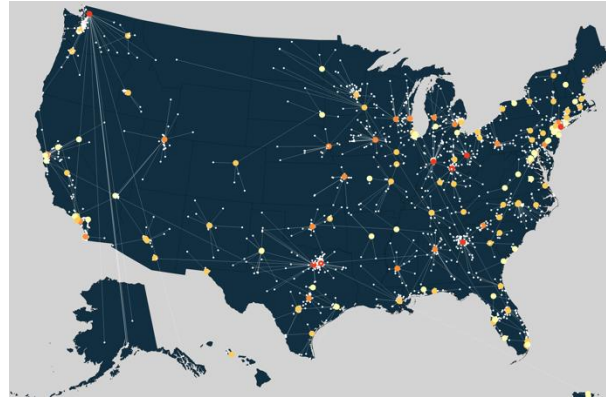
Potentially Targetable Pathway Alterations in Diffuse Midline Glioma, H3K27 Altered (n=86)

- Selected other targetable alterations
 - PGFR1: 9 mutations
 - PDGFRA: 11 mutations
 - PI3K: 15 mutations
(10 *PIK3CA*, 5 *PIK3R1*)
 - 7 Fusions:
(4 *MET*, 1 *BRAF*, 1 *NRG1*, 1 *NTRK*)
 - Germline: 5 alterations
(*CHEK2*, *TP53*, *MUTYH*, *NF1*, *PMS2*)



Building on the MCI

- Cancer predisposition
- Collection to other clinical data sources
- Genomic discovery
- Clinical research in ultra rare tumor populations



NCI/CCDI/COG/BPC/IGM Teams

COG Leadership/APEC14B1

- Doug Hawkins
- Mary Beth Sullivan
- Thalia Beeles
- Michael Thomas, Kelly Gissy

NIH CTEP

- Malcolm Smith

NCI CCDI

- Greg Reaman
- Subhashini Jagu
- Malcolm Smith
- Sean Burke
- Patrick Dunn

Biopathology Center

- Nilsa Ramirez
- Shoun tea Stover
- Natalie Bir
- Lisa Beaverson
- Yvonne Moyer

IGM

- Elaine Mardis
- Cathy Cottrell
- **Greg Wheeler**
- **Ke Qin**
- Katie Schieffer
- Grant Lammi

COG/CNS Operations Team

- Linda Springer
- Natasha Mirt, Melina Chanthanouvong
- Dalia Ortega, Shu-Lin Shen

COG CNS Statisticians

- **Yu Wang**
- Arzu Onar-Thomas

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- Maryam Fouladi (Columbus, Ohio)
- Nick Gottardo (Perth, Australia)
- Sarah Leary (Seattle, Washington)
- Diana Thomas (Columbus, Ohio)

Q&A

Join Us at Our Next Event

Comparing Proton and Photon Therapy: Insights from an NCI Pediatric Study

Tuesday, October 8, 2024, from 1:00–2:00 p.m. ET

Learn about a CCDI-supported study, the NCI Pediatric Proton and Photon Therapy Comparison Cohort. This webinar explores the study's design, current enrollment status, and state-of-the-art methods—developed specifically for this cohort—to determine a participant's amount of radiation exposure.

Learn more and register at events.cancer.gov/ccdi/webinar

How You Can Engage with CCDI



Learn about CCDI and subscribe to our monthly newsletter:
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Access CCDI data and resources:
ccdi.cancer.gov



Questions? Email us at:
NCIChildhoodCancerDataInitiative@mail.nih.gov

Thank you for attending!



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