Cancer Genomics Consortium, 16th Annual Meeting
August 3-6, 2025
The Royal Sonesta Houston Galleria, Houston, Texas

All session times are in US Central Daylight Time.

SATURDAY, AUGUST 2, 2025

In-Person Unconference
Unconference participation incurs an additional registration fee.

9:00 AM – 5:00 PM   **In-Person Variant Interpretation Unconference**
Presenters TBA

6:30 – 8:30 PM   **Evening Social for Unconference Attendees**
Location TBA

SUNDAY, AUGUST 3, 2025

Pre-Meeting Workshops
Workshop participation incurs an additional registration fee.

8:30 – 10:00 AM   **Navigating Academic vs. Non-academic Clinical Pathways and Achieving Success/Happiness in Academic Medicine**
Presenters:
Rachel Burnside, *University of Florida College of Medicine, FL*
Marilyn Bui, *Moffitt Cancer Center and Research Institute, FL*

10:00 – 10:15 AM   **Coffee Break for Workshop Attendees**

10:15 – 11:45 AM   **Bioinformatics Workshop on Recurrent Biomarkers in Cancer Genomes**
Presenters:
JianJiong Gao, *Memorial Sloan Kettering Cancer Center, NY*
Olena Vaske, *University of California Santa Cruz, CA*
Jinghui Zhang, *St. Jude Children's Research Hospital, TN*

Opening of the 16th Annual Cancer Genomics Consortium

1:00 – 1:05 PM   **Welcome**

Fady Mikhail, *University of Alabama at Birmingham, AL*

1:05 - 1:15 PM   **Presidential Address**
Jane Houldsworth, *Icahn School of Medicine at Mount Sinai, NY*

1:15 – 2:15 PM   **Keynote Presentation**
Clinical application of genomics for childhood cancer patients - an update on two decades of precision oncology
Will Parsons, *Baylor College of Medicine and Texas Children's Hospital, TX*

2:15 – 3:15 PM   **Platform Session 1: Solid Tumors**

Rare oncogenic structural variations in *FGFR* genes in childhood brain tumors provide potential therapeutic targets
Mary Clay Bailey, *Baylor College of Medicine, TX*

Chromothripsis in meningiomas is associated with more aggressive behavior
Ha Nguyen, *Northwestern Medicine, IL*

Clinicopathologic features and outcomes for colorectal carcinomas with *KRAS* codon 146 mutations
Bryan Iorgulescu, *MD Anderson Cancer Center, TX*

Complex copy number variation in atypical melanocytic neoplasms and early melanoma: A focused study of 60 cases
Katherine Geiersbach, *Mayo Clinic, MN*

3:15 – 4:00 PM   **Coffee Break**
Science Café Presentations

4:00 – 4:30 PM   **Diamond Exhibitor Showcase**
(No CME or CEUs available)

4:30 – 4:45 PM   **CGC Annual Award**

4:45 – 5:15 PM   **CGC 2025 Business Meeting**

5:15 – 6:15 PM   **Platform Session 2: Variant Curation, Interpretation, and Standardization**

Advancing gene curation in hereditary cancer: A comprehensive re-curation of breast/ovarian and colon cancer genes
Jasmine Baker, *Baylor College of Medicine, TX*

The landscape of germline and somatic cancer variants in tumor suppressor genes
Suhasini Lulla, *Baylor College of Medicine, TX*

Application of expert panel-derived oncogenicity guidelines in *BCR::ABL1*-like B-lymphoblastic leukemia/lymphoma
Mark Evans, *Caris Life Sciences, UT*

Systematic curation of defining and supportive diagnostic variants to enhance genomic diagnostics in pediatric oncology
Morteza Seifi, *ClinGen, WI*

6:15 – 8:15 PM **Welcome Reception**
CGC Exhibit Hall, Legends Ballroom

MONDAY, AUGUST 4, 2025

8:30 – 9:30 AM **Platform Session 3: Emerging Technologies in Clinical Genomics and Technical Lab Topics**

Clinical utility of optical genome mapping (OGM) for B-cell acute lymphoblastic leukemia (B-ALL)
Angela Lager, *University of Chicago, IL*

Optical genome mapping on pediatric leukemia samples: A single hospital experience
John Herriges, *Children's Mercy Hospital, Kansas City, MO*

Impact of long-term plasma storage on cell free DNA biomarker studies
Zejuan Li, *Houston Methodist Hospital, Weill Cornell Medical College, TX*

Analytical validation and cross-platform analysis of the oncomine TCR pan-clonality assay for T-Cell receptor profiling
Mohamed Maher, *University of Texas MD Anderson Cancer Center, TX*

9:30 – 10:30 AM **Invited Session 1**
Federal regulations affecting molecular diagnostic testing and gene patenting
Donald Karcher*, George Washington University Medical Center*
Roger Klein, *Arizona State University Law School*

10:30 – 11:15 AM **Coffee Break with Exhibitors**
Science Café Presentations

11:15 – 11:30 AM **Platinum Exhibitor Showcase**
(No CME or CEUs available)

11:30 AM – 12:00 PM **CGC Updates**

12:00 – 1:00 PM **Platform Session 4: Hematologic Malignancies**

Diagnostic utility of FISH testing for Ph-like B-ALL: A 5-year institutional experience
Fady Mikhail, *University of Alabama at Birmingham, AL*

Genomic characterization of *CRLF2*-rearranged pediatric B-ALL using transcriptome sequencing (RNA-Seq)
Gordana Raca, *Children's Hospital Los Angeles, CA*

Genomic Proximity Mapping (GPM): Evaluation of a next generation cytogenomic assay for acute myeloid leukemia
Min Fang, *Fred Hutchinson Cancer Center, WA*

Comparative analysis of targeted RNA-Seq and optical genome mapping for detecting clinically significant gene rearrangements
Gokce Toruner, *University of Texas MD Anderson Cancer Center, TX*

1:00 – 2:00 PM   **Buffet Lunch and Networking**
Exhibit Hall and Foyer

2:00 – 3:00 PM   **Invited Session 2**
Genome mapping and sequencing technologies for characterizing structural variants
Lisa Lansdon, *Children's Mercy Hospital, Kansas City and University of Missouri-Kansas City School of Medicine, MO*
Fritz Sedlazeck, *Baylor College of Medicine, TX*

3:00 – 4:00 PM   **Keynote Presentation**
Molecular-genomic findings in leukemias: Diagnostic, prognostic, and therapeutic implications
Hagop Kantarjian, *University of Texas MD Anderson Cancer Center, TX*

4:00 – 4:45 PM   **Coffee Break with Exhibitors**
Science Café Presentations

4:45 – 5:30 PM   **Speed Abstract Session 1: Solid Tumors, Bioinformatics, Artificial Intelligence, Emerging Technologies, and Other Advances in Clinical Genomics**

Tumor mutation burden (TMB) as a biomarker in advanced and metastatic breast cancers - An analysis of clinical NGS data in a 74 cases series
Liu Liu, *Brown University Health, RI*

Multi-modal validation and pan-cancer analysis of 9p21 loss: Diagnostic and prognostic implications
Holly Hill, *University of Texas MD Anderson Cancer Center, TX*

Expanding MAVE data maps for use in human genomics applications
Jeremy Arbesfeld, *The Ohio State University, OH*

New Q-Band artificial intelligence-based chromosome analysis and karyotyping - A pilot evaluation
Cristina Steele, *Applied Spectral Imaging for Laboratorio Clinico Colcan, Columbia*

5-hydroxymethylcytosine as a liquid biopsy biomarker in colorectal cancer
Christopher Maher, *Washington University School of Medicine, MO*

Accurate and reliable detection of clonal hematopoiesis in plasma cell-free DNA
Alyssa Parker, *Vanderbilt University, TN*

5:30 – 6:30 PM   **Poster Session (Odd Numbered Posters), Cash Bar**
CGC Exhibit Hall

7:00 PM   **Early Career Social**
For attendees in training or recently out of training

8:30 – 9:30 AM

Platform Session 5: Bioinformatics, Artificial Intelligence, and Machine-Learning

Prediction of BRAF V600 mutation status in cutaneous melanoma using an explainable deep learning model
Vibha Rao, *Dartmouth Health, NH*

Prediction of gene expression in NSCLC tumors and their microenvironment using an explainable machine learning model
Shrey Sukhadia, *Dartmouth Hitchcock Medical Center, NH*

Improving fusion detection sensitivity in the TruSight Oncology 500 Panel through DNA-based structural variant analysis
Qiliang Ding, *Mayo Clinic, MN*

Improved copy number estimation in central nervous system (CNS) tumors using methylation array
Drew Duckett, *Northwestern University, IL*

9:30 – 10:30 AM

Keynote Presentation
Discovering and defining the telomere biology disorders
Sharon Savage, *National Cancer Institute, National Institutes of Health, MD*

10:30 – 11:15 AM

Coffee Break with Exhibitors
Science Café Presentations

11:15 – 11:30 AM

Platinum Exhibitor Showcase
(No CME or CEUs available)

11:30 – 11:45 AM

Platinum Exhibitor Showcase
(No CME or CEUs available)

11:45 AM – 12:45 PM

Invited Session 3
Cancer genome bioinformatics in a clinical setting
Mark Cowley, *Children's Cancer Institute, Australia*
Sheryl Elkin, *QIAGEN Digital Insights, MA*

12:45 – 2:00 PM

In-Person Round Table Discussions with Lunch
Table topic selection is during conference registration.

2:00 – 2:45 PM

Speed Abstract Session 2: Variant Curation, Interpretation and Standardization, and Equity/Access in Genomic Medicine

Development of standards for the assessment of gene fusion oncogenicity
Karen Tsuchiya, *Nationwide Children's Hospital, OH*

The actionable transcriptome: A framework for incorporating transcriptional profiling into precision oncology
Amber Johnson, *MD Anderson Cancer Center, TX*

Introduction of an online portal for cancer-specific gene list curation
Beth Pitel, *Mayo Clinic, MN*

Enhancing data standardization and structure to improve clinical variant classification
Wesley Goar, *Nationwide Children's Hospital, OH*

Somatic variant classifications in ClinVar: An update after one year
Melissa Landrum, *NCBI/NLM/NIH, MD*

Clinical impact of in-house molecular testing of solid tumors in resource-limited settings: A pilot study in Pakistan
Romena Qazi, *Shaukat Khanum Memorial Cancer Hospital and Research Centre, Pakistan*

2:45 – 3:45 PM	**Poster Session (Even Numbered Posters)** CGC Exhibit Hall
3:45 – 4:30 PM	**Coffee Break with Exhibitors** **Science Café Presentations**
4:30 – 4:45 PM	**Platinum Exhibitor Showcase** *(No CME or CEUs available)*
4:45 – 5:00 PM	**Platinum Exhibitor Showcase** *(No CME or CEUs available)*
5:00 – 6:00 PM	**Panel Discussion on the Integration of Cytogenetics and Molecular Genetics Laboratories** **Panelists:** Yassmine Akkari, *Nationwide Children's Hospital, OH* Shashikant Kulkarni, *MD Anderson Cancer Center, TX* Gordana Raca, *Children's Hospital Los Angeles, CA* Daynna Wolff, *Medical University of South Carolina, SC*
7:00 – 8:30 PM	**Optional After Hours Social Activities** *Register for activities during meeting registration. Participants can pick up tickets at the CGC 2025 Registration Desk.* **Ice at the Galleria** **Museum of Illusion**

WEDNESDAY, AUGUST 6, 2025

9:00 – 10:00 AM	**Platform Session 6: Germline/Constitutional Genomics, Mosaicism, and Equity/Access in Genomic Medicine**

Assessing the efficacy of additional cell analysis in detecting low-level constitutional mosaic karyotypes
Aiko Otsubo, *University of Michigan, MI*

Best practices for testing low-level mosaic variants: Recommendations from CGC somatic overgrowth & vascular anomalies working group
Avinash Dharmadhikari, *Children's Hospital Los Angeles, CA*

Genetic regulation of inflammatory proteomes: Bridging genomic disparities between African and European populations
Caroline Amour, *Kilimanjaro Christian Medical University College, Tanzania*

Current state of molecular cancer testing in resource-limited and underserved communities
Casey Brewer, *Cincinnati Children's Hospital Medical Center, OH*

10:00 – 11:00 AM	**Invited Session 4**

Clinical variant interpretation knowledgebases in cancer genomics
Beth Pitel, *Mayo Clinic and Variant Interpretation for Cancer Consortium (VICC), MN*
Alex Wagner, *Nationwide Children's Hospital and Variant Interpretation for Cancer Consortium (VICC), OH*

11:00 – 11:30 AM	**Coffee Break with Exhibitors**

11:30 AM – 12:30 PM	**Platform Session 7: Diagnostic Challenge Case Studies**

Detection of *IGH::MYC* and a cryptic *IGH::BCL6* rearrangement refines diagnosis in high-grade B-Cell lymphoma
Will Coward IV, *University of North Carolina Healthcare Cytogenetics Laboratory, NC*

Decoding the genetic complexity of B-ALL through long-read and RNA sequencing methods
Jiadi Wen, *Yale School of Medicine, CT*

Rare *TBL1XR1*::*JAK2* fusion in a patient with pediatric T-ALL identified by optical genome mapping and long-read sequencing
Aravindh Nagarajan, *Children's Mercy Hospital, Kansas City, MO*

A rare recurrent 11;19 rearrangement resulting in *KMT2A::MYO1F* fusion in pediatric AML
Manisha Sutariya, *University of Minnesota, MN*