Environmental Mutagenesis and Genomics Society

56th Annual Meeting, September 6-10, 2025

Hyatt Regency Rochester

Saturday, September 6, 2025

3:45 to 5:30 pm	***EMGS Council Meeting***
5:30 to 5:45 pm	***Break***
5:45 to 6:45 pm	**Local Keynote** Vera Gorbanova, PhD (*University of Rochester*) Mechanisms of genome stability and longevity: from bats to whales
6:45 to 8:15 pm	**Student and Early Career investigator Welcome Reception and Poster Presentation**

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Sunday, September 7, 2025

8:00 to 9:00 am **High Profile Keynote**

Andrea Baccarelli, PhD (*Harvard T. H. Chan School of Public Health*)
Precision environmental health: Using omics for identifying risk factors and predicting risk

9:00 to 9:30 am ***Coffee Break***

9:30 to 11:30 am **Symposium 1: Impact of Alternative DNA Structures on Genome Integrity and Cellular Function**

Chairs: Amy Whitaker, PhD (*Fox Chase Center),* Elise Fouquerel, PhD (University of Pittsburgh), and Alexandra Berroyer, PhD (*Harvard T. H. Chan School of Public Health*)

Abstract: Alternative non-B DNA structures form in the genome and play key roles in cells. They can regulate transcription and drive cellular responses to stress and environmental exposures. While non-B DNAs have positive roles in cells, their formation can be mutagenic and block essential DNA transactions like replication and transcription. Thus, non-B DNA structures are a double-edged sword that can be both harmful and helpful to cells and human health. This symposium explores how alternative nucleic acid structures such as G-quadruplexes and R-loops can positively and negatively impact genome integrity and cellular function. Understanding the impact of alternative DNA structures on genome integrity is timely and highly significant for many scientists attending this conference given the recent efforts of targeting non-B DNA structures in cancer therapy and the interplay between alternative DNA structures and DNA repair.

Speakers: Nayun Kim, PhD (*University of Texas*)
G-quadruplex-induced genomic instability and transcriptional regulation in Saccharomyces cerevisiae

Kirill Lobachev, PhD (*Georgia Institute of Technology*)
DNA structures that form from inverted repeats

Catherine Freudenreich, PhD (*Tufts University*)
Structure-capable trinucleotide repeats

9:30 to 11:30 am **Symposium 2: ecNGS: Has the Genotoxicity Revolution Arrived?**

Chairs: Javed Bhalli, PhD (*Frontage Laboratories*), Connie Chen, PhD (*Health and Environmental Sciences Institute*), and Hannah Battaion, PhD (*Health Canada*)

Abstract: Error-corrected Next Generation Sequencing (ecNGS) has the potential to revolutionize genotoxicity testing as it has been shown to be an accurate method for identification and characterization of mutation spectrum and frequency in any cell type, tissue, or organism from which DNA can be isolated. This method has the potential to be used to detect weak mutagens/genotoxicants, and once it has appropriate guidelines, it can be used as part of the safety assessment to support IND-enabling studies. Technology has been around for the past few years now and there is sufficient awareness using ecNGS to determine the DNA damaging compounds. The current symposium will focus more on the ideas of using this technology to support safety assessment in nonclinical drug development processes. Talks will compare the concordance of ecNGS with the in vivo genetic toxicology assays including gene mutation (TGR and Pig-a), chromosomal damage (micronucleus), and DNA damage (Comet) assays. Speakers will be selected from a current multi-lab project on an

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interesting compound from nucleoside analogue class and comparing the data from the standard genetox end points with different techniques of ecNGS.

Speakers: Javed Bhalli, PhD (*Frontage Laboratories*)
TBD

Javier Revollo, PhD (*US FDA/NCTR*)
TBD

David Schuster, PhD (*University of Ottawa*)
TBD

11:30 to 11:45 pm ***Break***

11:45 to 12:45 pm **SIG Meetings**
Applied Genetic Toxicology
Germ Cell and Heritable Effects

12:45 to 2:15 pm ***Student and Early Career Investigator Luncheon (Invitation only)***

2:15 to 4:15 pm **Platform Session 1: DNA Repair**
Selected from abstract submissions.

Chairs: TBD

2:15 to 4:15 pm **Platform Session 2: New Approach Methodologies (NAMs)**
Selected from abstract submissions.

Chairs: Alexandra Long, PhD (*Health Canada*), Steve Bryce, PhD (*Litron Laboratories*)

4:15 to 4:30 pm ***Coffee Break***

4:30 to 5:30 pm **Hollaender Award Lecture** (*to be announced*)

5:30 to 7:00 pm **Poster Session 1**
Odd poster presentations.

7:00 to 9:00 pm **EMGS Networking Lounge**

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8:00 to 9:00 am **Tech Keynote**
Carole Yauk, PhD (*University of Ottawa*)
Genomic insights into PAH-induced mutagenesis across tissues and time

9:00 to 9:30 am ***Coffee Break***

9:30 to 11:30 am **Symposium 3: Deciphering the Developmental Exposome: Epigenetic Mechanisms and Potential Tools to Assess Environmental Exposures**

Chairs: Bambarendage P. Perera, PhD (*University of Michigan School of Public Health*) and Jackie Goodrich, PhD (*University of Michigan School of Public Health*)

Abstract: This symposium highlights the cutting-edge research on the epigenetic consequences of developmental exposure to environmental toxicants. It will delve into the vulnerabilities of the developing organism and how exposures during this time period can lead to persistent epigenetic alterations, potentially resulting in adverse health outcomes, consistent with the developmental origins of health and disease (DOHaD) hypothesis. The symposium will present emerging epigenomics tools and methodologies that provide new insights into the complex mechanisms of epigenetic regulation in response to environmental challenges that occur during pregnancy and early development. The goal of this symposium is to provide an overview of the latest advancements in epigenomics technologies, such as high-throughput sequencing, bioinformatic analyses, and innovative in vitro models, and how they can be applied to DOHaD research. This symposium will also foster discussions on applying this knowledge to bridge the gap between mechanistic epigenomic research and real-world environmental health challenges.

Speakers: Marisa Bartolomei, PhD (*University of Pennsylvania Perelman School of Medicine*)
Mammalian Reprogramming During Development and Under Adverse Environmental Conditions

Rebecca Fry, PhD (*University of North Carolina – Chapel Hill*)
TBD

Dana Dolinoy, PhD (*University of Michigan*)
ToxicoEpigenetics & the Use of piRNA for Developmental Origins of Health and Disease Research

9:30 to 11:30 am **Symposium 4:** Improving Hazard Identification of Nitrosamines: Enhancing the Ames Assay and Mammalian Cell Approaches

Chairs: Alisa Vespa, PhD (*Health Canada*), Anthony Lynch, PhD (*GlaxoSmithKline), and Raechel Puglisi, PhD (Health and Environmental Sciences Institute)*

Abstract: Nitrosamines are a group of mutagenic impurities that vary widely in structure, encompassing both small molecules and complex drug-related nitrosamines, and ranging from Cohort of Concern compounds to weak mutagens or to non-mutagens. Ascertaining the carcinogenic potential and distinguishing between high- and low-potency nitrosamines has been an important focus of researchers in recent years. Hazards Identification (Hazard ID) and genotoxicity risk assessment of nitrosamines have been the subject of intensive research, leading to new insights into this class of mutagenic impurities. In the process, new knowledge about this old class of mutagenic impurities has been developed, leading to adopting the known assay and strategies to the new challenges. However, the predictivity of the Ames protocol has been a topic of debate, and researchers have investigated the inclusion of hamster S9 to enhance the sensitivity and specificity of the assay. In

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addition, researchers have explored the potential of in vitro mammalian cell assays to provide valuable information on the characterization of nitrosamines.

Speakers: Anthony Lynch, PhD (*GlaxoSmithKline*)
Optimizing the Ames Assay for Nitrosamine Testing: Results of a HESI Multi-Sector Ring Trial

Roland Froetschl, PhD (*Federal Institute for Drugs and Medical Devices*)
MutaMind Project: Results and Conclusions of Ames and Mammalian Cell Studies

Wen Sun, PhD (*Pfizer*)
Building the Bridge: Exploring Alternative In vitro Mammalian Cell Models to Support Nitrosamine Testing

11:30 to 11:45 pm ***Break***

11:45 to 12:45 pm **SIG Meetings**
Genotoxicity Risk Assessment and Public Health (GRAPH)
Epigenomics

12:45 to 2:15 pm ***Women in EMGS Luncheon (Invitation only)***

2:15 to 4:15 pm **Platform Session 3: Artificial Intelligence (AI) and Bioinformatic Advances**
Selected from abstract submissions.

Chairs: Kathleen Hill PhD (*The University of Western Ontario*), Matthew Meier *(Health Canada)*, David Schuster *(University of Ottawa)*, and Lila Kari *(University of Waterloo)*

2:15 to 4:15 pm **Platform Session 4: Environmental Justice**
Selected from abstract submissions.

Chairs: Michelle Campbell, PhD (*NIEHS*) and Sarah Park, PhD (*CalEPA*)

4:15 to 4:30 pm ***Coffee Break***

4:30 to 5:30 pm **Young Scientist Award Lecture** (to be announced)

5:30 to 7:00 pm **Poster Session 2**
Even poster presentations.

7:00 to 9:00 pm **EMGS Networking Lounge**

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8:00 to 9:00 am **EMGS Award Lecture** (to be announced)

9:00 to 9:30 am ***Coffee break***

9:30 to 11:30 am **Symposium 5: Using Early Detection of Mutational Signatures to Understand the Etiology of Cancer**

Chairs: Stephanie Smith-Roe, PhD (*NIEHS*), Jesse Salk, PhD (*University of Washington and Fred Hutchinson Cancer Research Center*), and Alper James Alcaraz, PhD, (*University of Ottawa*)

Abstract: Advancements in error-corrected next generation sequencing (ecNGS) and deep-sequencing methodologies have ushered in a new era of unprecedented precision in mutation detection from DNA sequencing data, enabling analysis of both spontaneous and induced mutational events within endogenous loci in any organism. By harnessing the power of ecNGS and related methods, researchers are now able to identify mutational signatures as robust biomarkers of environmental and occupational chemical exposures in animal models and in human populations. Comparison of mutational signatures in tissue lacking pathological changes with those identified in tumors may significantly enhance our understanding of how certain exposures influence the etiology of cancer, and link exposures to cancer outcomes in individuals and populations. Biomonitoring mutational signatures holds the potential to revolutionize intervention strategies to protect and improve health, cancer treatment, and risk assessment paradigms.

Speakers: John Essigmann, PhD (*Massachusetts Institute of Technology*)
Therapeutic mutagenesis: diversify neoantigen arrays as an adjuvant in checkpoint inhibitor cancer immunotherapy and spectral measurement of efficacy by Duplex Sequencing

Jennifer Kay, PhD (Silent Spring Institute)
Measuring Mutation Signatures in Female Firefighters to Uncover Drivers of Occupational Cancer Risk

Advaitha Madireddy, PhD (*Rutgers Cancer Institute*)
Understanding the Mechanisms Driving Somatic Hypermutation in Clonal Hematopoiesis: Influence of Exposure to World Trade Center Fallout

9:30 to 11:30 am **Symposium 6: Single-Cell DNA and Copy Number Variations Analysis: Insights into sources of DNA Damage and Mutations**

Chairs: Matthew Meier, PhD (*Health Canada*), Jun Xia, PhD (*Creighton University*), and David Umbaugh, PhD (*Duke University*)

Abstract: DNA copy number variations, along with single base substitutions/indels, are critical in revealing mechanisms of spontaneous DNA damage, mutation processes, cancer evolution, and environmental exposures. The resolution of cell-to-cell heterogeneity via single-cell DNA methodologies is vital for understanding clonal structures, which can predict disease prognosis, identify early biomarkers, and aid in early disease prevention. In this session, we invited leaders in the single cell DNA analysis field on single-cell DNA copy number, base mutations, and ATAC-seq techniques to discuss both normal and disease mechanisms under spontaneous and disease conditions.

Speakers: Ruli Gao, PhD (*Northwestern University*)

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Tumor genetic evolution models revealed by single cell DNA and RNA sequencing technologies

Jiyeon Choi, PhD (*National Cancer Institute*)
Insights into lung cancer etiology from single-cell multiomics of normal lung tissues in smokers and never-smokers

Yusi Fu, PhD (*Creighton University*)
Tracing the somatic genome evolution with single-cell analysis

11:30 to 11:45 am ***Break***

11:45 to 12:45 pm **SIG Meetings**
In Vivo Mutagenesis
Genomics and Data Sciences

12:45 to 2:15 pm ***EMM Editorial Board Lunch (Invitation only)***

2:15 to 4:15 pm **Symposium 7: Infertility as the Novel Biomarker for Cancer Risks: Current perspective through the lens of Genome Instability**

Chairs: Zachary Nagel, PhD (Harvard T. H. Chan School of Public Health) and Ana Cheong (Harvard T. H. Chan School of Public Health)

Abstract: Infertility is emerging as a risk factor for cancers. Spermatogenetic defect and female infertility are associated with higher levels of DNA damage and increased risks for multiple cancers. Accumulating epidemiological studies also support the protective role of pregnancy and high parity against cancer risks. Yet, how infertility leads to higher cancer risks remains largely unknown. Genomic instability is well recognized as a hallmark of cancer, and some DNA repair proteins also function as tumor-suppressors. Genetic predisposition of DNA repair defects has also been linked to infertility and higher cancer risks. Though mutagens are not necessarily carcinogenic, some environmental toxicants have been shown to reduce fertility and increase cancer risks through epigenetic mechanisms and oxidative stress. In this symposium, we will highlight the effects of environmental exposures on reproduction and disease susceptibility and explore the interplay between fertility status and genomic instability in the context of cancer. Topics will include the impact of occupational and environmental exposures on the epigenome, gene expression, and genome integrity in the male reproductive system. Speakers will also discuss interactions between these exposures and other variables such as nutrition, windows of susceptibility, and the immune system.

Speakers: Aleks Rajkovic, PhD *(University of California, San Francisco)*
TBD

Jorge E. Chavarro, PhD *(Harvard T. H. Chan School of Public Health)*
TBD

Dolores Lamb, PhD *(Weill Cornell Medicine)*
TBD

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2:15 to 4:15 pm **Symposium 8: The Mutagenic and Carcinogenic Hazards of Wildfire Combustion Emissions**

Chairs: Paul White, PhD (*Health Canada*), Aris Polyzos, PhD (*Lawrence Berkeley National Laboratory*), and Linda Reilly, PhD (*Swansea University*)

Abstract: The increasing frequency and severity of wildfires have had a significant negative impact on numerous communities. The 2023 fire season resulted in levels of air pollution that posed a risk to those in proximity to the wildfires; moreover, to those individuals in surrounding regions affected via long-range transport of smoke and other pollutants. The declaration by the International Agency for Research on Cancer (IARC) that outdoor air pollution is a known human carcinogen underscores the serious health risks associated with exposure to air pollutants. However, relatively little is known about the health impacts of wood smoke, which is a significant component of outdoor air impacted by wildfires. Research conducted at the U.S. Environmental Protection Agency has evaluated the mutagenic activity of wood combustion emissions; the presence of complex polycyclic aromatic hydrocarbons (PAH) mixtures in wood smoke highlights its carcinogenic hazard. The acute need to understand the mutagenic and carcinogenic risks associated with wildfire smoke underscores the need for focused research and comprehensive risk assessment. This would not only contribute to better protection and awareness for communities at risk, but also provide guidelines to protect those involved in wildland firefighting. This symposium will provide the EMGS audience with an appreciation of the genotoxic and carcinogenic hazards posed by wildfire combustion emissions. It will include researchers who are assessing the genotoxic properties of wood combustion emissions, as well as researchers using molecular methods to assess the health impacts of complex wildfire combustion emissions.

Speakers: David DeMarini, PhD *(US EPA)*
Genotoxicity and Carcinogenicity of Combustion Emissions and Carcinogenic Risks to Wildfire Firefighter

Julia Rager, PhD (*University of North Carolina*)
Wildfire Health Risks: Identifying Chemical Drivers and Underlying Mechanisms of Highly Variable Smoke Exposure Conditions using Computational Approaches

Yong Ho Kim, PhD (*US EPA*)
Growing New Threat of Wildfire Smoke as Burning Biomass, Households, and Beyond

4:15 to 5:15 pm **Business Meeting**

5:15 to 6:00 pm **EMGS Awards Ceremony**

6:00 to 6:30 pm **Transportation to Radio Social**

6:30 to 10:30 pm **EMGS Banquet at Radio Social**
Included with registration

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8:00 to 9:00 am **Early/Mid-Career Keynote**
Lydia Contreas, PhD (*University of Texas - Austin*)
Molecular marks of susceptibility under environmentally-induced oxidative stress: how do cells manage transcriptional reprogramming to cope?

9:00 to 9:30 am ***Coffee Break***

9:30 to 11:30 am **Symposium 9: Germ cell toxicology in the crosshairs: implications of mutagenesis to offspring health**

Chairs: Mathia Colwell, PhD (*University of Michigan*) and Carole Yauk, PhD (*University of Ottawa)*

Abstract: The protection of our germ cells is of the utmost importance for population health. Sperm and eggs have evolved sophisticated repair mechanisms to guard against mutagenesis and ensure the integrity of the genome that is inherited. Nonetheless, every offspring inherits mutations transmitted via both the paternal and maternal gametes. Thus, understanding the impact of genotoxic agents on the landscape and rates of mutations in germ cells and their profound consequences for offspring health is critical to human and ecological health risk assessment. This symposium will focus on advancing our understanding of germ cell toxicology, shedding light on the implications of mutagenesis on the well-being of future generations. The session will feature cutting-edge genomic and epigenomic technologies applied in human cohorts and novel model systems to elucidate the mechanisms of mutagenesis in germ cells and the transmission of these alterations to offspring. Insights into the identification and characterization of germ cell mutagenic agents will be provided, discussing the importance of environmental factors, lifestyle choices, and occupational exposures. The symposium presentations will also extend to the broader ramifications of germ cell mutagenesis, encompassing discussions on hereditary diseases, developmental disorders, and potential intergenerational effects. Attendees will gain valuable insights into strategies for risk assessment, mitigation, and intervention to safeguard the genetic integrity of future generations.

Speakers: Evan Eichler, PhD (*University of Washington*)
Telomere-to-telomere human genomes and germline mutational processes

Ina Dobrinski, PhD (*University of Calgary*)
Modeling spermatogenesis in testicular organoids

Brandon Pearson, PhD (*Columbia University*)
Gene-level vulnerability to mutagens in pre- and early post-conception cells

9:30 to 11:30 am **Symposium 10: Environmental toxicants and Genome Integrity: The regulation and roles of DNA polymerases**

Chairs: Mark Hedglin, PhD (*Pennsylvania State University*), Zac Pursell, PhD (*Tulane University School of Medicine*), and Tatiana Moiseeva, PhD (*University of Pittsburgh*)

Abstract: Genomic DNA is continuously subjected to damage from exposure to environmental toxicants. Prominent examples are DNA strand breaks that disrupt the continuity of template DNA strands as well as covalent modifications (lesions) to the native template nucleobases that alter or eliminate

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their base pairing capabilities. To counteract DNA damages and restore native genomic sequences, all organisms utilize a diverse array of complex pathways that are strictly regulated. Central to these pathways are DNA polymerases. This symposium will highlight and showcase recent advances on the regulation and functional roles of DNA polymerases in cellular pathways that maintain genome integrity in response to environmental toxicant exposure. Pathways of interest are (but not limited to); Canonical DNA replication, DNA damage tolerance (Translesion DNA synthesis, Homology-dependent recombination, template switching), and DNA damage Repair (Base Excision Repair, Nucleotide Excision Repair, Homologous Recombination, Non-homologous End-joining, etc.).

Speakers: Vanesa Gottifredi, PhD (*Fundación Instituto Leloir*)
The primary function of the cyclin kinase inhibitor p21 is not related to CDK regulation but with the control of PrimPol and Translation DNA Synthesis Polymerases-mediated nascent DNA synthesis

Penny Beuning, PhD (*Northwestern University*)
Characterization of cancer-associated variants of DNA polymerase kappa

Robert Eoff, PhD (*University of Arkansas*)
Insights into the mechanism of replication gap suppression by DNA polymerase kappa

11:30 to 11:45 pm ***Break***

11:45 to 12:45 pm **SIG and Board Meetings**
DNA Repair & Mutagenic Mechanisms
Endowment Board

12:45 to 2:15 pm ***Program Committee Lunch (Invitation only)***

2:15 to 4:15 pm **Symposium 11: Navigating the Non-Coding RNA landscape: Unveiling the Interplay with Environmental Exposures Through Epigenomics Tools**

Chairs: Bambarendage P. Perera, PhD (*University of Michigan School of Public Health*) and
Jackie Goodrich, PhD (*University of Michigan School of Public Health*)

Abstract: This symposium addresses challenges and opportunities of using non-coding RNAs (ncRNAs) in the context of environmental exposure, addressing fundamental questions about their regulatory roles and the consequences of their dysregulation. ncRNAs, including microRNAs (miRNAs), Piwi-interacting RNAs (piRNAs), small nucleolar RNA (snoRNA), transfer RNA (tRNA), long non-coding RNAs (lncRNAs), and circular RNAs (circRNAs), are recognized as key epigenetic mediators that can modulate gene expression in response to environmental cues. Environmental factors such as pollutants in air and water and chemicals in products can lead to aberrant ncRNA expression profiles, which in turn may contribute to a wide array of pathologies. The symposium will address state-of-the-art methodologies such as high-throughput ncRNA sequencing, ncRNA detection, epigenomic mapping, and innovative bioinformatics pipelines to dissect the ncRNA-mediated mechanisms of toxicity. The goal of this symposium is to enhance our knowledge of how researches may interpret ncRNA functions, outline the challenges in deciphering their complex roles, and develop potential ncRNA-based biomarkers or therapeutic strategies for environmental diseases.

Speakers: Isidore Rigoutsos, PhD (Sidney Kimmel Medical College, Thomas Jefferson University)

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TBD

David J. Waxman, PhD (Boston University)
TBD

Brian Chorley, PhD *(US EPA)*
MicroRNA biomarker development for chemical screening and hazard identification

2:15 to 4:15 pm **Symposium 12: Somatic Mosaicism and Clonal Expansion of Cancer Driver Mutants**

Chairs: Barbara Parsons, PhD (*FDA, NCTR*), Kathleen Hill, PhD (*Western University*), and Christina Castellani, PhD (*Western University*)

Abstract: Advanced sequencing technologies have provided new insight into the prevalence of somatic mosaicism and clonal expansion of cells carrying cancer driver mutations. However, the complexity of both the data and the underlying biology creates challenges regarding how such information can be used to identify biomarkers of disease risk and, otherwise, be leveraged to support public health protection. Further, this symposium will provide examples of recent and novel approaches and applications, for which clonal expansion of mutant cells is a central component. From a computational biology perspective, the state of the science regarding identification of cancer driver mutations, mechanisms governing clonal expansion of mutant cells, and obstacles to clinical implementation will be described, with a focus on epigenetic biomarkers. Ongoing efforts to develop a cancer intervention will be presented, including a description of how measurements of clonal expansion of cancer driver mutants as a tool to probe cancer signaling pathways is supporting the research effort. The symposium will include a presentation on associations between post-zygotic somatic mosaicism and disease, with a specific focus on role of clonal expansion in neurological disease development. Finally, evaluation of data analytic approaches for assessing clonal expansion of mutants based on error-corrected mutant fraction measurements and their potential application to carcinogenicity testing will be presented. This symposium aligns well with the interests of multiple EMGS Special Interest Groups (SIGs), including the: Genotoxicity Risk Assessment & Public Health, Genomics & Data Sciences, In Vivo Mutagenesis, Applied Genetic Toxicology, and Epigenetics SIGs.

Speakers: Anna Panchenko, PhD (*Queen's University*)
Discovering Driver Mutations in Cancer: Coming of Age

Eva Turley, PhD (*Western University*)
Host Mechanisms for Preventing Clonal Expansion of UVB-induced Mutant Cells

Kathleen Hill, PhD (*Western University*)
Tissue Specifics of Somatic Mosaicism: A Study of Mouse Families