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MEETING/RENCONTRE

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NOVEMBER 3 – 6 NOVEMBRE, 2022

VANCOUVER, BRITISH COLUMBIA
VANCOUVER, COLOMBIE-BRITANNIQUE

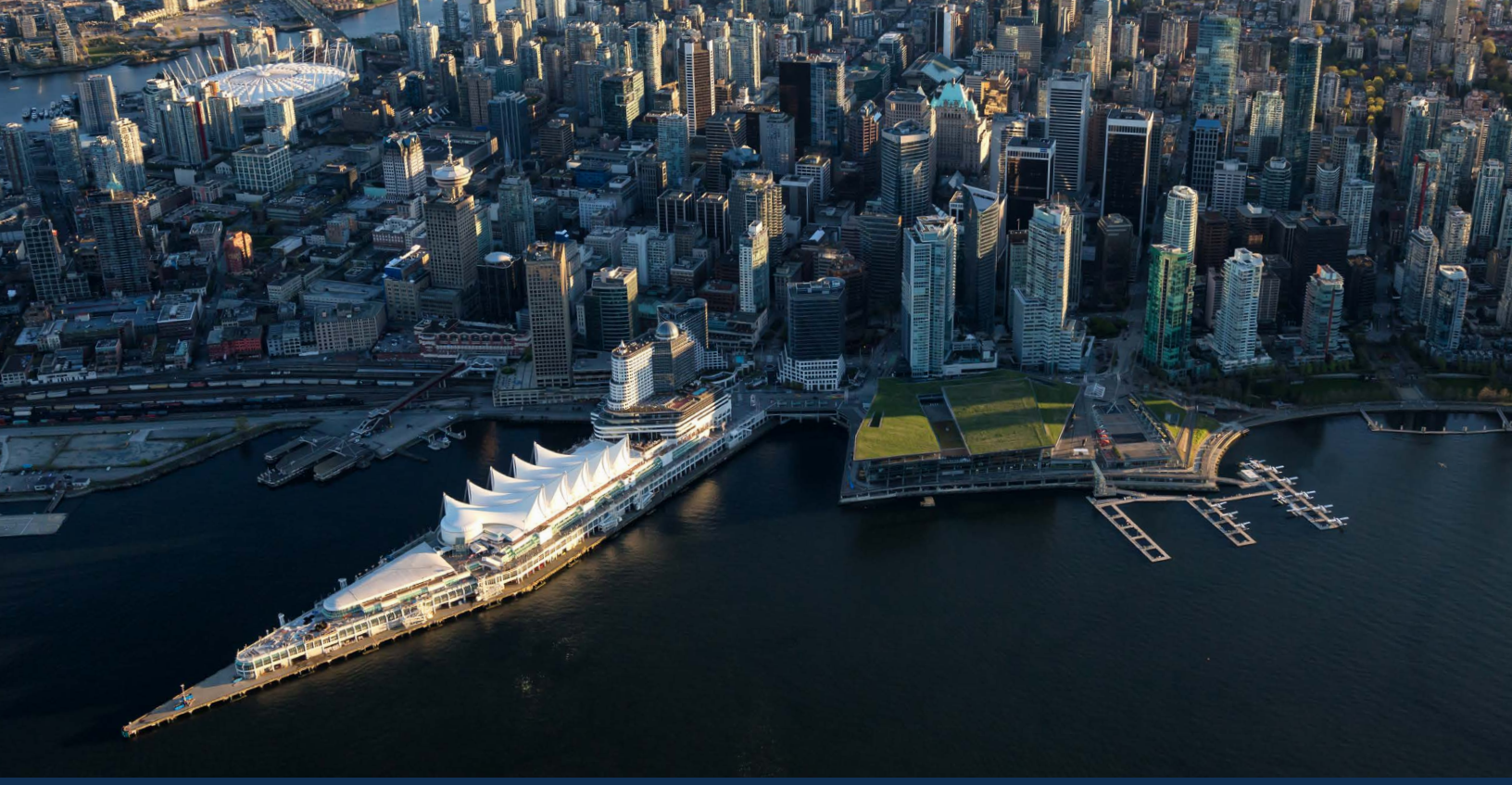
Cancer Research in Canada: Past, Present and Future

La Recherche sur le Cancer au Canada : Passé, Présent et Futur

THE TERRY FOX RESEARCH INSTITUTE
L'INSTITUT DE RECHERCHE TERRY FOX

MARATHON OF HOPE CANCER CENTRES NETWORK

PROGRAM
PROGRAMME



PRESIDENT'S MESSAGE

Welcome Back!

It is such a pleasure to be with you here in Vancouver! This marks our first large in-person, pan-Canadian gathering of our funded teams and research community since the pandemic began. And it is TFRI's first scientific meeting since it's 10th anniversary in 2017. We are thrilled to have our talented, committed and expanding group of funded research teams together under the same roof!

A lot has happened in five years! While the pandemic still challenges us today, it has also shown the importance of science, innovation and collaboration to achieve solutions that have impact. We look forward to reconnecting face to face with longstanding colleagues as well as getting acquainted with those who are new.

There's much to celebrate! Notably, this marks the first scientific meeting of both TFRI and Marathon of Hope Cancer Centres Network (MOHCCN) researchers coming together on a pan-Canadian level since the Government of Canada announced funding for the MOHCCN. It's an exciting time of growth, change and renewal for TFRI, and Terry Fox's mission to end cancer continues to be our heartbeat.

Our scientific organizing committee this year has built a program around the theme of Cancer Research: Past, Present and Future, with plenaries intended for all attendees and breakouts to permit the TFRI and MOH teams to drill down, exchanging knowledge of scientific discoveries and findings, formulating policies and practices around data sharing and privacy, reviewing and modifying core research program funding, and charting our progress. There are a number of new teams and projects you will be hearing from. We hope you will all attend the rapid-fire talks and posters sessions featuring the work of our trainees. Our wine and cheese on Nov. 4 and early morning run on Nov. 5 are great networking opportunities, so please join us!

Importantly, on Nov. 5 we will recognize 14 years of leadership by Dr. Victor Ling at the helm of TFRI with a celebration dinner that evening. We have a great program lined up with talks from Dr. Mona Nemer, Canada's Chief Science Advisor; Dr. Marla Shapiro, well-known media and health personality, cancer survivor and TFRI Board member; and Darrell Fox, Terry's younger brother.

Enjoy our 9th scientific meeting, it's good to be back!

Jim Woodgett,
TFRI President and Scientific Director

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Network name: TFRI Scientific Meeting 2022
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Statement On Respect For Confidentiality Of Unpublished Material

The Institute has invited everyone attending this meeting because of their contribution, or potential for contribution, to the work of our research community. In building our community, we are committed to respecting the confidentiality of ideas and data that is unpublished at this meeting. We request and require that all registrants refrain from recording such confidential information, and do not discuss such information with colleagues outside of this meeting. It is only in this way that we will collectively build the trust and respect that is necessary for effective collaborations. We appreciate your respect of and compliance with this important request.

TFRI 9th Annual Scientific Meeting

Scientific Organizing Committee

Dr. Jim Woodgett,
Dr. André Veillette
Dr. Christopher Paige
Dr. Marco Marra
Dr. Morag Park
Dr. Jennifer Chan
Dr. Robert Rottapel
Dr. Steve Robbins
Dr. Anne-Marie Mes-Masson
Dr. Robin Urquhart
Dr. Russ Watkins
Kelly Curwin
Marina Lefilliatre

Abstract and Poster Committee

Dr. Rob Rottapel
Dr. Vincent Giguere
Dr. Jeanette Boudreau
Dr. Julie St-Pierre
Dr. Marco Marra
Dr. Russ Watkins
Vivian Lee
Peter Mothe

AGENDA: Thursday, November 3

TIME	DURATION	EVENT	LOCATION
6:00 – 9:00 pm	180 min	**EARLY REGISTRATION**	Ocean Foyer
6:00 – 9:00 pm	180 min	**POSTER SET UP**	Ocean Foyer

AGENDA: Friday, November 4

TIME	DURATION	EVENT	LOCATION
7:00 am – 12:00	300 min	**REGISTRATION & POSTER SET UP**	Rooms 215–216, Ocean Foyer
7:00 am		**Breakfast**	Rooms 211–214
8:00 – 9:00 am	60 min	**OPENING REMARKS** **Dr. Jim Woodgett**, TFRI President and Scientific Director: *"TFRI: State of the Union"* **Dr. Andre Veillette**, Executive Director, Marathon of Hope Cancer Centres Network, *"An Update on MOH"* **Mr. Michael Mazza**, Executive Director, Terry Fox Foundation	Rooms 220–222
9:00 – 10:30 am	**90 min** Three talks of 25 min each	**PLENARY I** **Session Chair: Dr. Steve Robbins**, Lady Davis Institute, Jewish General Hospital PRESENTERS: **Dr. John Bell**, Ottawa Health Research Institute, *"Design and application of oncolytic viruses"* **Dr. Jeanette Boudreau**, Dalhousie University, *"The role of natural killer cells in the spatial immunology of tumours"* **BC Cancer Consortium Investigators:** PRESENTERS: **Dr. Laura Hilton** and **Dr. Steve Jones**, Precision Medicine Initiatives at the BC2C	**Rooms 220–222**
10:30 – 11:30 am	60 min	**RAPID FIRE AND POSTER SESSION #1** **Chair: Dr. David Goertz**, University of Toronto RF PRESENTERS: **Shaghayegh Nouruzi** (Zoubeidi), **Zhen Jin** (Vu), **Tariq Bhat** (Lim), **Lan Valerie Tao** (Renouf) (3 min each) *BREAK and poster viewing to follow* This will be a 15-minute rapid-fire session followed by 45 minutes for break and viewing posters	Rooms 220–222, Ocean Foyer
11:30 am – 1:00 pm	**90 min** Three talks of 25 min each	**PLENARY II** **Session Chair: Dr. Morag Park**, McGill University PRESENTERS: **Dr. Ly Vu**, BC Cancer *"Targeting RNA modification pathways in leukemia"* **Dr. Peter Siegel** and **Dr. Julie St-Pierre**, McGill University and University of Ottawa, *"Discovering and targeting metabolic vulnerabilities in cancers"* **Marathon of Hope – Québec Investigators:** PRESENTERS: **Dr. Ian Watson**, **Dr. Philippe Lefrançois**, McGill University; and **Dr. Anne Marie Mes-Masson**, Centre Hospitalier de l'universite de Montreal, *"MOH-Quebec: Investigation of genomic and cellular mechanisms of treatment resistance and aggressive tumour behaviour across skin cancers"*	**Rooms 220–222**
1:00 – 2:00 pm	60 min	**Lunch**	Rooms 211–214

AGENDA: Friday, November 4

TIME	DURATION	EVENT	LOCATION
2:00 – 3:00 pm	60 min	**TFRI AND MOHCCN BREAKOUTS #1** **MOHCCN** *New Approaches to Precision Oncology (Presenters and Discussion)* **Co-Chairs: Dr. André Veillette** and **Dr. Isabel Serrano**, MOHCCN PRESENTERS: **Dr. Ian Watson**, McGill University: *New Approaches to Immune Profiling* **Dr. Ian Watson,** McGill University and **Dr. Hanne Ostergaard**, University of Alberta: *Immune Profiling Sub-Committee Mandate* **Dr. John Stagg**, CHUM: *Comparison of all existing predictive signatures of immunotherapy responses* **TFRI Programs Forum with Q&A** **Forum Chair: Dr. Rob Rottapel**, University Health Network, TFRI-Ontario Node Leader PRESENTERS: **Dr. Jessica McAlpine**, BC Cancer, *"Working to provide precision medicine for all newly diagnosed endometrial cancer patients"* **Dr. Livia Garzia**, McGill University, *"Drivers of therapy resistance in fusion-positive sarcomas"*	**MOHCCN Breakout: Rooms 220–222** **TFRI Breakout: Rooms 217–219**
3:00 – 3:30 pm	30 min	**Break**	
3:30 – 6:00 pm	**90 min**	**RAPID FIRE AND POSTER SESSION #2 AND WINE & CHEESE** **Chair: Dr. Hartland Jackson**, Lunenfeld-Tanenbaum Research Institute, Sinai Health RF PRESENTERS: **Charlotte Girondel** (Siegel), **Aghababazadeh Masoumeh** (Garzia), **Julyanne Brassard** (McAlpine), **Cameron Herberts** (Zoubeidi) (3 min each) This will be a 15-minute rapid-fire session followed by poster viewing and wine and cheese	**Rooms 220–222, 223–224, Ocean Foyer**
		FREE EVENING /DELEGATES DINE ON THEIR OWN	

AGENDA: Saturday, November 5

TIME	DURATION	EVENT	LOCATION
6:15 – 8:00 am	**105 min**	**TERRY FOX EARLY MORNING RUN** Group will depart at 6:30am sharp	Meet in Vancouver Convention Centre East Lobby – by the Totem Pole
7:00 – 9:00 am	120 min	**Breakfast**	Rooms 211–214
8:00 – 9:30 am	**90 min**	**PLENARY III** **Session Chair: Dr. Marco Marra**, Michael Smith Genome Sciences Centre, TFRI BC Node Leader and Member, MOHCCN Steering Committee PRESENTERS: **Dr. Rama Khokha**, Princess Margaret Cancer Centre, UHN *"Lineage vulnerabilities and druggable targets for breast cancer prevention"* **Dr. Jüri Reimand**, OICR, University of Toronto, *"Pan-cancer analyses of whole cancer genomes for finding driver mutations and oncogenes, especially in the non-coding genome"* **Princess Margaret Cancer Consortium Investigators:** **Dr. Lillian Siu** and **Dr. Trevor Pugh**, *"PMCC: Precision Medicine Initiatives"*	**Rooms 220–222**
9:30 – 10:30 am	60 min	**RAPID FIRE AND POSTER SESSION #3** **Chair: Dr. Jeanette Boudreau**, Dalhousie University RF PRESENTERS: **Curtis McCloskey** (Khokha), **Charles Chesnelong** (Dick), **Vallijah Subasri** (Malkin), **Shirin Soleimani** (Pugh) (3 min each) *BREAK and poster viewing to follow* This will be a 15-minute rapid-fire session followed by 45 minutes for break and viewing posters	Rooms 220–222, Ocean Foyer
10:30 – 11:30 am	**60 min**	**KEYNOTE SPEAKER** **Dr. John Dick**, Princess Margaret Cancer Centre, *"What makes a stem cell a stem cell and how does it go bad?"*	**Rooms 220–222**

AGENDA: Saturday, November 5

TIME	DURATION	EVENT	LOCATION
11:30 am – 12:00	**30 min**	**GROUP PHOTOGRAPH**	Hallway outside Room 211 or outdoors (depending on weather)
12:00 – 1:30 pm	90 min	**Lunch**	Rooms 211–214
1:30 – 3:00 pm	**90 min**	**Plenary IV** **Session Chair: Dr.Jennifer Chan**, University of Calgary , Prairie Cancer Research Consortium PRESENTERS: **Dr. Jeff Wrana**, Sinai Health System, Lunenfeld-Tanenbaum Research Institute, *"Taming the Hippo: Signaling pathways controlling cell state dynamics and how to target them"* **Dr. Sachin Katyal**, University of Manitoba and CancerCare Manitoba, *"The cellular base excision repair (BER) pathway mediates temozolomide resistance in recurrent Glioblastoma Multiforme (GBM): opportunities for new interventions?"* **Prairie Cancer Research Consortium Investigators:** PRESENTERS: **Dr. Sorana Morrissy, Dr. Mike Monument, Dr. Jennifer Chan**, *"Prairie Cancer Research Consortium: Precision Medicine Initiatives"*	**Rooms 220–222**
3:00 – 4:00 pm	**60 min**	**RAPID FIRE PLENARY AND POSTER SESSION #4** **Chair: Dr. Lawrence Kazak**, Rosalind and Morris Goodman Cancer Institute, McGill University RF PRESENTERS: **Ali Saleh** (Katyal), **Masroor Bayati** (Reimand), **Khalid Al-Zahrani** (Wrana), **Rajesh Detroja** (Kridel) (3 min each) *BREAK and poster viewing to follow* This will be a 15-minute rapid-fire session followed by 45 minutes for break and viewing posters	Rooms 220–222, Ocean Foyer
4:00 – 5:00 pm	**60 min**	**MOHCCN AND TFRI BREAKOUT #2** **MOHCCN** *Data Ingestion and the Pathfinder Project* **Chairs: Dr. Natalie Szudy** and **Dr. Adrian Thorogood**, TFRI/MOHCCN PRESENTERS: **Dr. Michael Brudno**, CanDIG, University Health Network and Daisie Huang, BC Cancer **TFRI** **Session on TFRI Programs: Q&A** **Chair: Dr. Rob Rottapel**, UHN, TFRI-Ontario Node Leader PARTICIPANTS: **Dr. Jim Woodgett**, **Dr. Russell Watkins**, and **Gordon Schwark** (attending), TFRI General introduction and presentation of TFRI programs, history and changes, followed by discussion and look ahead at future strategic direction	**MOHCCN Breakout: Rooms 223–224** **TFRI Breakout: Rooms 220–222**
6:30 pm		**CELEBRATION DINNER FOR DR. VICTOR LING** **Co-chairs: Dr. Christopher Paige**, UHN, TFRI Board Chair and **Dr. Anne-Marie Mes-Masson**, CRCHUM, TFRI-Quebec Node Leader SPEAKERS: **Dr. Mona Nemer**, Canada's Chief Science Advisor **Dr. Marla Shapiro**, TFRI Board member, physician and media health and medical expert **Mr. Darrell Fox**, Terry's younger brother and TFRI Senior Advisor	Room 305

AGENDA: Sunday, November 6

	EVENT
	HOTEL CHECK OUT AND DEPARTURE Closed Door Meetings for MOHCCN Leadership – Fairmont Vancouver Airport

PLENARY I: Friday, November 4

9:00 – 10:30 am / Rooms 220–222 / **Session Chair: Dr. Steve Robbins**, Lady Davis Institute, Jewish General Hospital

9:00 am

DESIGN AND APPLICATION OF ONCOLYTIC VIRUSES

Dr. John Bell, Ottawa Health Research Institute

Oncolytic Viruses were originally conceived of/designed to, selectively grow in and lyse cancer cells, acting as self-replicating cytolytic agents. Over the last twenty years of pre-clinical and clinical research, our understanding of these agents has completely changed and while "oncolysis" is an important, if not essential component of these agents, it is clear that an oncolytic virus' (OV's) ability to deliver multiple potent payloads to the tumour bed creates a unique biological tool for remodeling the tumour microenvironment (TME) and facilitating therapeutic immune responses. Using a combination of bio-selection, functional genomics and recombineering we created a new virus platform using the Copenhagen strain of vaccinia virus. We strategically deleted 25kb from the viral genome encompassing in excess of 30 viral genes. This new virus backbone (herein referred to as SKV) demonstrates exquisite selectivity for a broad spectrum of human tumor cell lines but unlike both wild type and thymidine kinase deleted vaccinia strains, it does not replicate in any normal tissues of nude or NOD SCID mice following systemic delivery. We view the SKV platform as an "oncolytic chassis" with over 50Kb of transgene coding capacity. We are integrating into this chassis a variety of independently regulated "genetic modules" tailored to augment its efficacy, safety and tumour persistence. Our vision is to create an SKV based virus that acts as a "mobile pharmacy" dispensing therapeutic projects where and when they are needed.

9:30 am

THE ROLE OF NATURAL KILLER CELLS IN THE SPATIAL IMMUNOLOGY OF TUMOURS

Dr. Jeanette Boudreau, Dalhousie University

Natural killer (NK) cells are lymphocytes that weigh incoming signals for activation and inhibition using an array of germline-encoded receptors. Diversity in NK cell function is generated not by antigen-specific receptors, but by variegated co-expression of these receptors among the NK cells comprising an individual's NK cell repertoire. The result is that the NK cells within and between individuals will have different impacts on a putative target cell, including cancer.

Previous studies, especially in hematopoietic malignancies, have revealed a central role for NK cells in immunosurveillance and tumor rejection, but the impact of NK cells in solid tumors is poorly understood. In high-grade serous ovarian cancer, NK cells have been alternately reported as beneficial or detrimental; we think this reflects a lack of resolution to understand how different NK cell subsets interact with the disease. Using the Canadian Ovarial Experimental Unified Resource (COEUR), we assessed the activity of two NK cell subsets in situ, dividing based on CD16a expression, which can be used to dichotomize two broad NK cell subsets. While nearly all tumors (>95%) had some NK cell infiltration, only the CD16a+ NK cell subset associates with beneficial prognosis and co-infiltration of other immune cells known to associate with improved survival, CD8+ T cells and macrophages. In contrast, CD16a- NK cells infiltrated alone, and were not associated with the same beneficial outcome. High-parameter flow cytometry analysis revealed further distinction of these subsets based on expression of CD73, an enxyme involved in adenosine production. CD73+CD16- NK cells were prone to suppression within the tumor microenvironment (but not other subtypes), revealing that interactions between the tumor and NK cells may diminish immune reactivity, with consequences on function. Efforts are ongoing to model these interactions in 3D culture and humanized immune-competent mouse models to test interventions that support ongoing NK cell reactivity.

10:00 am

PRECISION MEDICINE INITIATIVES AT THE BC2C

BC Cancer Consortium Investigators: Drs. Laura Hilton and Steve Jones

This session will discuss precision medicine initiatives being undertaken by the BC Cancer Consortium (BC2C) for the Marathon of Hope Cancer Centres Network. The challenge of precision medicine informed through comprehensive genomic and transcriptomic analysis is the large amount of data that needs to be analysed, interpreted and communicated in a short and clinically relevant timeframe. In his presentation, Dr. Jones will discuss the approaches, including machine learning approaches, that are being used by BC2C teams to address this challenge. Dr. Hilton's portion of the presentation will focus specifically on work being done by the BC2C cohort investigating aggressive diffuse large B-cell lymphoma (DLBCL). She will present a new study from the team, which used whole genome and whole exome sequencing of multiple biopsies from patients with relapsed or refractory DLBCL to make findings that could have implications for optimal management of DLBCL relapse in the era of CAR-T therapy.

PLENARY II: Friday, November 4

11:30 am – 1:00 pm / Rooms 220–222 / **Session Chair: Dr. Morag Park**, McGill University

11:30 am

TARGETING RNA MODIFICATION PATHWAYS IN LEUKEMIA

Dr. Ly Vu,BC Cancer

Dysregulation of normal gene expression programs and cellular identities drive cancer development. While somatic alterations in genetic and epigenetic mechanisms have been studied extensively, how processes that affect post-transcriptional and translational regulation impact tumorigenesis is much less well understood. RNA modifications comprise all chemical alternations on an RNA molecule, ranging from classical 5′ cap, 3′ poly(A) to modifications on nucleotides such as m6A methylation. RNA modifications have recently emerged as critical mediators of gene expression control in development and disease. In the seminar, Dr. Vu will discuss her laboratory's effort toward understanding the role of RNA modifications in myeloid leukemia and developing strategy to exploit these pathways as therapeutic targets for Acute Myeloid Leukemia, a genetically complex and heterogeneous set of diseases with poor survival and morbidity.

12:00 pm

DISCOVERING AND TARGETING METABOLIC VULNERABILITIES IN CANCERS

Drs. Peter Siegel and Julie St-Pierre, McGill University and University of Ottawa

Cancer cells must adapt their metabolism to meet the energetic and biosynthetic demands that accompany rapid growth of the primary tumor and colonization of distinct metastatic sites. Cancer cells must manage metabolic stress that 1) results from changing conditions within the primary tumor, 2) is encountered during distinct steps of the metastatic cascade and 3) manifests following exposure to therapeutic agents. Other understudied modulators of metabolic stress include systemic/whole organism changes, such as obesity, that can impact cancer cell metabolism. In the context of the current Terry Fox New Frontiers Program Project Grant in targeting metabolic vulnerabilities in cancer, we are focused on delineating the signaling pathways and metabolic networks engaged within cancer cells in response to local changes in the primary tumor or metastatic microenvironments, whole organism changes (obesity) and therapy-induced stresses. Delineating metabolic adaptations that occur during the emergence of drug resistance is one area of interest for our Terry Fox Program Project Grant. Drug concentrations decrease with distance from blood vessels within solid tumors, but cellular adaptations accompanying the gradated exposure of cancer cells to drugs is largely unknown. In this study, we investigated the spatiotemporal changes promoting chemotherapy resistance. Using pairwise competition assays at each step during chemoresistance acquisition, we revealed an important priming phase that is necessary for acquired resistance in cancer cells previously exposed to sub-lethal drug concentrations. Therapy resistant cells throughout the concentration gradient displayed higher expression of the solute carriers SLC38A7 and SLC46A1 and elevated intracellular concentrations of their associated metabolites. Therapy resistant cells with reduced expression of SLC38A7 and SLC46A1 displayed diminished proliferative potential, and elevated expression of these SLCs in patient tumors is associated with reduced survival. Our work provides mechanistic evidence to support dose-intensive treatment modalities for patients with solid tumors and reveals two members of the SLC family as potential actionable targets.

12:30 pm

MOH-QUEBEC: INVESTIGATION OF GENOMIC AND CELLULAR MECHANISMS OF TREATMENT RESISTANCE AND AGGRESSIVE TUMOUR BEHAVIOUR ACROSS SKIN CANCERS

Dr. Ian Watson, Philippe Lefrançois and Dr. Anne Marie Mes-Masson, McGill University and Centre Hospitalier de l'universite de Montreal

With the advances in multi-omics technology, we now have the ability to ascertain the full complement of cancer aberrations and integrate precision medicine into the health care system. However, the scientific community is still in the early stages of interpreting and implementing this knowledge in clinical practice. The Marathon of Hope Cancer Centres Network (MOHCCN) is building a high-quality data commons of tumor signatures and clinical information to advance our understanding, diagnosis and treatment of cancer patients to significantly impact patient outcomes. The creation of the Montreal Cancer Consortium (MCC) Pilot Project for the MOHCCN and the subsequent establishment of the Marathon of Hope consortium in Quebec (MOH-Q) has allowed Quebec-based institutions to come together to accelerate this vision. This session will focus on work being done by MOH-Q researchers specializing in skin cancers. Dr. Ian Watson, who successfully co-led the MCC pilot project, will present work focusing on understanding the variable immune therapy responses in melanoma patients through multi-omic profiling. Dr. Philippe Lefrançois, a recipient of the MOHCCN Clinician-Scientist Award, will present preliminary work being done to identify novel actionable pathways/targets and microenvironment features in Basal Cell Carcinoma, and the MOH-Q's plan to characterize the molecular and cellular landscape of advanced BCC and early high-risk BCC tumors.

TFRI AND MOHCCN BREAKOUTS: Friday, November 4

2:00 – 3:00 pm / **MOHCCN** Breakout in Rooms 220-222 / **TFRI** Breakout in Rooms 217–219

MOHCCN

MOHCCN NEW APPROACHES TO PRECISION ONCOLOGY

Co-Chairs: *André Veillette and Isabel Serrano*

Presenters: *Dr. Ian Watson, McGill University: New Approaches to Immune Profiling, Dr. Ian Watson and Dr. Hanne Ostergaard, University of Alberta: Immune Profiling Sub-Committee Mandate, Dr. John Stagg, CHUM: Comparison of all existing predictive signatures of immunotherapy responses*

This session aims to initiate a discussion about the outcomes and development of Network wide strategies supported by two MOHCCN working groups that are currently in the early stages of their development. The Canadian Spectrum working group goal is to give voice to the under-represented populations, which includes rare cancers, rural and remote, indigenous, immigrants, refugees, etc. The Immune Profiling group will work on the harmonization of new profiling technologies that will further enrich the MOHCCN dataset. This session will include an overview of the working groups and will provide an opportunity to discuss their strategies moving forward.

TFRI

TFRI PROGRAMS FORUM WITH Q&A

Forum Chair: Dr. Rob Rottapel, University Health Network, TFRI-Ontario Node Leader

Presenters:

WORKING TO PROVIDE PRECISION MEDICINE FOR ALL NEWLY DIAGNOSED ENDOMETRIAL CANCER PATIENTS

Dr. Jessica McAlpine, BC Cancer

Endometrial cancer is the most common gynecologic cancer and increasing globally in both incidence and mortality. Histomorphologic pathological classification is poorly reproducible and has hindered clinical and research advancements. Our team has developed a novel molecular classification tool in endometrial cancer that provides prognostic and predictive information to direct endometrial cancer care and can be applied at first diagnostic biopsy. Within this new framework we aim to provide new systems for equitable and resource-conscious triage, characterize the less common and difficult to treat endometrial cancers, and develop new thereputic strategies for the most aggressive molecular subtype of endometrial cancer.

DRIVERS OF THERAPY RESISTANCE IN FUSION-POSITIVE SARCOMAS

Dr. Livia Garzia, McGill University

Fusion driven sarcomas affect mostly children and adolescents, and have a relatively good prognosis when localized and responding to chemotherapy. Failure to respond to therapies or presence of metastasis are the major causes of adverse outcomes in sarcoma patients. Fusion-driven sarcomas have relatively simple somatic genomes, with very few mutations beyond the pathognomonic gene fusions. However, the differential response to treatment of primary disease vs metastasis vs recurrent disease suggests an underappreciated complexity where other players potentially have a role in driving advanced disease. To investigate cooperating pathways that may synergize with the fusions and contribute to chemoresistance and metastasis we developed in vivo functional genomics screenings with transposons. Gain of function and loss of function mutations patterns showed that different tumor entities, characterized by different fusions, follow separate paths to resistance and metastasis. Stemness features are enriched in resistant CIC-DUX4 tumors while activation of the Hippo pathway potentially cooperates with the EWS-Fli1 fusion in Ewing sarcomas at recurrence.

PLENARY III: Saturday, November 5

8:00 – 9:30 am / Rooms 220–222 / **Session Chair: Dr. Marco Marra**, Michael Smith Genome Sciences Centre, TFRI BC Node Leader & Member, MOHCCN Steering Committee

8:00 am

LINEAGE VULNERABILITIES AND DRUGGABLE TARGETS FOR BREAST CANCER PREVENTION

Dr. Rama Khokha, Princess Margaret Cancer Centre, UHN

Much remains to be understood about what makes the high-risk breast uniquely predisposed to breast cancer and more likely to develop highly aggressive subtypes of disease. It is increasingly appreciated that progenitors underlie cancer development, yet therapeutic strategies targeting them are lacking. It is imperative to understand the composition, activity, and vulnerabilities of these cancer precursors in the high-risk breast to advance breast cancer prevention. We recently have identified fundamental molecular programs that govern mammary stem cell biology and features unique to distinct breast cell types, including progenitors. The current goals of our TFRI MOMICs-PPG Team are to apply a multi-OMICs approach to profiling mammary cells from a variety of clinically well-defined high-risk tissues at successive levels of biology (epigenome, transcriptome, proteome, and metabolome). Leveraging these insights our overarching aim is to advance breast cancer interception and develop novel precision-based primary prevention options.

PLENARY III: Saturday, November 5

8:30 am

PAN-CANCER ANALYSES OF WHOLE CANCER GENOMES FOR FINDING DRIVER MUTATIONS AND ONCOGENES, ESPECIALLY IN THE NON-CODING GENOME

Dr. Jüri Reimand, OICR, University of Toronto

Cancer is driven by somatic mutations that deregulate hallmark pathways of cancer. Most currently known driver mutations are found through signals of positive selection and affect the protein-coding genome, while the entire cancer genome contains many more mutations that are thought to be inactive passengers induced by endogenous and extrinsic mutational processes through tumor evolution. However, the dichotomy of driver and passenger mutations is only a limited representation of the genetic origins of cancer. Our recent pan-cancer studies of thousands of whole genomes of primary and metastatic cancers reveal non-coding regulatory elements with frequent simple mutations and structural rearrangement hotspots as candidate cancer drivers. On the other hand, endogenous and carcinogen-related mutational processes contribute to tumor heterogeneity by systematically inducing functional mutations. Pan-cancer analyses also reveal non-coding RNAs as novel oncogenes and prognostic markers. Therefore, integrative analyses of whole cancer genomes have the potential for new fundamental and translational insights.

9:00 am

PRINCESS MARGARET CANCER CONSORTIUM: PRECISION INITIATIVES

Princess Margaret Cancer Consortium Investigators: Drs. Lillian Siu and Trevor Pugh

Since its inception within MOHCCN, PM2C has enrolled 580 patients in FY22 and the planned additional accrual for FY23 is 638. In total, 8 cohorts were included in FY22 and 20 cohorts are to be included in FY23. In partnership with the Ontario Institute for Cancer Research (OICR) Genomics Program, PM2C has built a custom workflow to systematically perform quality control and harmonize external/legacy and newly generated MOHCCN whole genome and transcriptome sequencing (WGTS) datasets. Additionally, some of the key achievements from PM2C to date include: collaborative development of laboratory manuals and tissue selection, processing, and sequencing best practices guidelines for MOHCCN cases; approval by the Ontario Cancer Research Ethics Board for a PM2C-specific MOHCCN study protocol (MOHCCN-O) and consent to enable prospective patient recruitment; and on-boarding of Kingston Health Sciences Centre as a member of PM2C, and this site will begin to contribute to PM2C in FY23. Current activities with PM2C include creation of a RedCap database for clinical annotation of prospectively enrolled patients within the Consortium and upload of clinical and genomic data to cBioPortal.ca, both of which will contain all the required fields proposed by the MOHCCN Clinical Data Standards Team. To illustrate the utility of this precision medicine initiative, demonstration scientific projects are being developed from some of the PM2C cohorts (e.g. BIOCAN comprising resected head and neck cancers who developed disease recurrence; OCTANE comprising patients who have had previous next generation panel sequencing without actionable alterations; HCC, a liver transplantation cohort with detailed clinical relapse and longitudinal cell-free DNA data; and IRIS comprising patients with primary versus acquired resistance to immune therapy). Once this step is accomplished, the goal is to reach out to other MOHCCN partners across Canada to identify similar cases that are ready for data and samples sharing.

KEYNOTE SPEAKER: Saturday, November 5

Keynote Speaker

10:30 – 11:30 am / Rooms 220–222 / **Dr. John Dick**, Princess Margaret Cancer Centre

10:30 am

WHAT MAKES A STEM CELL A STEM CELL AND HOW DOES IT GO BAD IN AML

John E. Dick, Andy G.X. Zeng, Murtaza S. Nagre, Alex Murison, Stephanie Z. Xie
Princess Margaret Cancer Centre, University Health Network, Toronto, ON, Canada

Long-term hematopoietic stem cells (LT-HSC) are responsible for life-long blood production and show functional erosion due to aging or inflammatory dysregulation. However, the molecular programs underlying aging or LT-HSC responsiveness to emergency hematopoiesis as triggered by stress stimuli, notably inflammation, are poorly understood. We previously identified transcriptional, epigenetic, and functional heterogeneity in human LT-HSC in the transition from quiescence to cellular activation, with inflammatory pathways implicated (Garcia-Prat et al, 2021, Takayama et al, 2021, Kaufmann et al, 2021 and Xie et al, 2021). We now have examined how inflammation-naive CB HSC respond to and recover from inflammatory stress using a xenotransplantation model challenged either with human TNFα or lipopolysaccarides (LPS). We find that there are long-term effects of acute inflammatory stress that persist in a subset of human HSCs following a 2.5 month recovery period. Multiome analysis revealed two transcriptionally and epigenetically distinct HSC subsets: homeostatic HSC (HSC-H) and memory HSC (HSC-M). Only HSC-M cells experienced dramatic changes between PBS and TNFα treatment pertaining to gene expression, chromatin accessibility, and enrichment for transcription factor (TF) binding sites; determinants that represent candidates for encoding memory at the HSC level. Overall, these studies point to the discovery of a novel memory HSC pool that may be linked to human aging.

The discovery of distinct HSC subsets raises important considerations for leukemic origins. A key step in understanding cellular origins of leukemia comes from our new approach to classify AML based on hierarchy composition. Cancer is a caricature of normal tissue development and the defining feature of a tissue is the hierarchical structure. Cellular hierarchies in AML can be distorted in different ways, depending on genetic alterations and cell of origin. Thus, interrogation of leukemic hierarchies may provide an opportunity to potentially integrate features of the genetic and stem cell models of AML. We characterized the cellular hierarchies of >1000 AML patients through gene expression deconvolution on bulk AML transcriptomes using single-cell reference profiles of distinct AML stem, progenitor, and mature types. This approach to characterizing AML heterogeneity enabled integration of both the genomic and functional models of AML resulting in a novel framework for understanding disease biology and predicting drug response.

PLENARY IV: Saturday, November 5

1:30 – 3:00 pm / Room 220–222 / **Session Chair: Dr.Jennifer Chan**, University of Calgary, Prairie Cancer Research Consortium

1:30 pm

TAMING THE HIPPO: SIGNALING PATHWAYS CONTROLLING CELL STATE DYNAMICS AND HOW TO TARGET THEM

Dr. Jeff Wrana, Sinai Health System, Lunenfeld-Tanenbaum Research Institute

Morphogen signalling pathways assemble into higher order networks that play a central role in orchestrating tissue morphogenesis throughout development and homeostatic functions in the adult. Hippo is a central regulator of tissue size in animals that integrates multiple pathways with tissue stiffness to control stem cell dynamics and cell fate. The intestinal epithelium turns over at a tremendous rate, and we showed previously that while Hippo in the epithelium is not important for homeostatic turnover, it is critically required for regeneration in response to injury. Hippo is also a key regulator of mesenchymal biology where it integrates mechanotransduction with TGFβ via the Nuak signalling axis to drive myofibroblast activation and fibrotic responses in inflammatory environments. Furthermore, single cell profiling has now revealed that fibroblasts, once thought to be relatively homogeneous populations of cells providing structural support, display a variety of cell states. Indeed, distinct subtypes of intestinal fibroblast-like cells (IFLCs) called Trophocytes, Telocytes, and Interstitial Stroma are organized along the crypt-lumen axis to provide critical morphogen gradients that pattern the overlying epithelium. We performed single cell profiling of IFLCs in the mouse colon to further show that Trophocytes reflect a diverse network of spatially arranged substates. Moreover, analysis of Ulcerative Colitis, pediatric Crohn's disease, familial adenomatous polyposis polyps and colorectal cancers showed that Trophocytes are highly dynamic, and display both conserved and disease-specific states. Finally, we show that the Hippo transcriptional regulators Yap and Taz are required for Trophocyte function, maintenance of the homeostatic intestinal stem cell niche, and recovery from damage. These studies suggest that Trophocyte cell state plasticity plays a key role in supporting homeostatic and disease states and point to the Nuak-Hippo- TGFβ axis as a key target in cancer-associated stroma.

2:00 pm

THE CELLULAR BASE EXCISION REPAIR (BER) PATHWAY MEDIATES TEMOZOLOMIDE RESISTANCE IN RECURRENT GLIOBLASTOMA MULTIFORME (GBM): OPPORTUNITIES FOR NEW INTERVENTIONS?

Dr. Sachin Katyal, University of Manitoba and CancerCare Manitoba

Glioblastoma multiforme (GBM) is a highly aggressive form of brain cancer that can afflict individuals of all ages. While rare, these tumours are responsible for a significant amount of malignancy-related morbidity and mortality. GBM treatment usually involves surgical resection of the tumour followed by radiation and chemotherapy (typically Temozolomide, TMZ); however, GBM prognoses are generally poor and rarely curable due to tumour recurrence and a lack of effective treatments and surgical options. As such, there is a critical requirement to improve upon current anti-GBM therapeutic strategies.

Chemotherapeutic agents have multiple mechanisms of action, but primarily exert their anti- tumour activities via pervasive DNA damage that overwhelms the cellular DNA repair capacity resulting in cell death. We have developed novel TMZ-resistant cell models and an innovative high-throughput DNA damage analysis platform; combined these led to the discovery that persistent TMZ treatment stabilizes XRCC1 (an essential gene) and enhances PARP/XRCC1-dependent DNA base excision repair (BER). Our findings have been confirmed in a cohort of patient-derived recurrent GBM (rGBM) brain tumour initiating cells (BTICs); thus implicating XRCC1 as a TMZ drug-resistance factor underpinning recurrent GBM. Furthermore, our data suggests that hyperactive XRCC1-mediated DNA repair capacity promotes cross-resistance to second line DNA damaging chemotherapeutics, including radiation and Topoisomerase poisons. We hypothesize that XRCC1 is a novel targetable biomarker for the resensitization of subsets of rGBM to TMZ treatment.

2:30 pm

PRAIRIE CANCER RESEARCH CONSORTIUM: PRECISION MEDICINE INITIATIVES

Prairie Cancer Research Consortium Investigators: Dr. Sorana Morrissy, Dr. Mike Monument, Dr. Jennifer Chan

In this session, we will provide a brief overview of the Prairie Cancer Consortium (PR2) followed by presentations from two of our initial cohorts. The PR2C glioblastoma and sarcoma cohorts are focused on proteogenomic and spatial deconvolution of tumour and tumour microenvironment states and crosstalk, aimed to improve understanding of these poor-outcome malignancies. We are using multi-regional and temporal sampling of tumours to chart key molecular states and their evolution during the course of standard treatment regimes. Coupling these comprehensive profiles with a novel data-integration approach, we aim to ultimately uncover molecular targets for rational and/or immune-based therapies.

TFRI AND MOHCCN BREAKOUTS: Saturday, November 5

4:00 – 5:00 pm / **MOHCCN** Breakout in Rooms 223–224 / **TFRI** Breakout in Rooms 220–222

MOHCCN

ROUNDTABLE: DATA INGESTION AND THE PATHFINDER PROJECT

Chairs: *Dr. Natalie Szudy and Dr. Adrian Thorogood, TFRI/MOHCCN*

Presenters: *Dr. Michael Brudno, CanDIG, University Health Network and Daisie Huang, BC Cancer*

The MOHCCN Pathfinder Project is a network-level effort, connecting and validating data sharing frameworks and data preparation across sites. The data sharing demonstration will serve as a testbed for MOHCCN policies, procedures, and requirements and extend the technical capabilities of CanDIG to support the range of 'omic analyses required by the Network. This session will include an overview of the Pathfinder project and key learnings from the data ingestion activities. Building on these learnings this session will include a discussion on the development and implementation of a Network-wide strategy for data ingestion and development of data sharing use cases.

TFRI

SESSION ON TFRI PROGRAMS: Q&A

Chair: *Dr. Rob Rottapel, UHN, TFRI-Ontario Node Leader*

Presenters:

Dr. Jim Woodgett, Dr. Russell Watkins, and Gordon Schwark (attending), TFRI

This session will facilitate a discussion about the future strategic priorities of TFRI's two legacy funding programs, the Program Project Grants and the New Investigator Grants. The Program Project Grants have a long history within the Canadian cancer research community and have funded many projects which delivered breakthrough research with global impact. The New Investigator Program has supported a stellar array of upcoming leaders in the Canadian cancer research space, a great many of whom have gone on receive TFRI funding as leaders of PPGs as well as many additional national and international awards. Looking forward, it is time to reconsider both the priorities and the processes which could be updated to ensure that these programs remain responsive to the changing funding environment and the needs of the community. This session will encourage open discussion of the strengths and weaknesses of the current programs as well as possible new strategic funding initiatives.

DINNER CELEBRATION: Saturday, November 5

Celebration Dinner for Dr. Victor Ling, O.C. O.B.C, PhD

6:30 pm / Room 305

Co-chairs: **Drs. Christopher Paige**, *UHN, TFRI Board Chair and* **Dr. Anne-Marie Mes-Masson**, *CRCHUM, TFRI-Quebec Node Leader*

Speakers:

Dr. Mona Nemer, Canada's Chief Science Advisor

Dr. Marla Shapiro, TFRI Board member, physician and media health and medical expert

Mr. Darrell Fox, Terry's younger brother and TFRI Senior Advisor

John Bell

Dr. John Bell received his PhD from McMaster University in 1982. In the three years that followed, he trained as a post-doctoral fellow at the University of Ottawa and then at the Medical Research Council in London, England. Dr. Bell began his independent research career at McGill University in 1986 and moved to the University of Ottawa, Department of Medicine, in 1989. He is a member of the Center for Cancer Therapeutics at The Ottawa Hospital Cancer Center, a Senior Scientist with the Ottawa Hospital Research Institute and Professor of Medicine at the University of Ottawa. He is the Director of the Canadian Oncolytic Virus Consortium supported by a Terry Fox Program Project Grant and is the Scientific Director of BioCanRx, a Network of Centres of Excellence that aims to bring novel immune stimulating therapies to cancer patients across Canada. His research program has focused on the development of novel viral and cell-based therapeutics for the treatment of cancer.

Jeanette Boudreau

Dr.Jeanette Boudreau is an Associate professor in the departments of Pathology and Microbiology & Immunology at Dalhousie University. She is the Dalhousie Medical Research Foundation Cameron Cancer scientist and a Senior Scientist with the Beatrice Hunter Cancer Research Institute. Dr. Boudreau received her PhD from McMaster University in Hamilton, Ontario, with mentorship from Dr. Yonghong Wan. Dr. Boudreau completed post-doctoral training at Memorial Sloan Kettering Cancer Center in New York, under the mentorship of Dr. Katharine Hsu*, studying the impacts of human natural killer cell immunogenetics on NK cell function and outcomes of hematopoietic stem cell transplantation. The Boudreau laboratory now focuses on NK cells in cancer, with a goal of developing NK cell-based immunotherapeutic approaches. They use techniques in spatial biology, humanized animals and primary tumors and NK cells to understand how NK cells interact with tumors, and the impacts of this on patients with cancer.

**Hsu is pronounced "Shoe"*

Michael Brudno

Michael Brudno is a Professor in the Department of Computer Science at the University of Toronto, as well the Chief Data Scientist at the University Health Network (UHN). He is also a faculty member at the Vector Institute for Artificial Intelligence and the Scientific Director of HPC4Health, a private computing cloud for Ontario hospitals. After receiving a BA in Computer Science and History at UC Berkley, Michael continued his studies and completed his PhD from the Computer Science Department of Stanford University. His main research interest is in the development of computational methods for the analysis of clinical and genomic datasets, in particular the capture of precise clinical data from clinicians using effective user interfaces, and its utilization in the automated analysis of genomes. His work focuses on the capture of structured phenotypic data from clinical encounters, using both refined User Interfaces, and mining of unstructured data (based on Machine Learning methodology), and the analysis of omics data (genome, transcriptome, epigenome) in the context of the structured patient phenotypes, mostly for rare diseases.

Jennifer Chan

Dr. Jennifer Chan is the Consortium Lead for the MOH's Prairie Cancer Consortium (PR2C) and the Director of the Arnie Charbonneau Cancer Institute, bringing leadership to the cancer research enterprise in Calgary and beyond. As a pathologist and scientist, Jennifer's ability to traverse between the lab and the clinic has enabled her to bring together investigators from across the cancer research continuum. Prior to her appointment as Charbonneau's director, Jennifer served as its deputy director, lead for space and infrastructure, and program leader for the Childhood Cancer Research Program. Previously, she was also the Pathology Leader at the Broad Institute, where she oversaw the tissue and biospecimen support for its cancer studies in its early years. Jennifer's research focuses on brain tumour biology, pediatric cancers, and molecular oncologic pathology. She contributes to several large-scale projects to discover new genes and therapeutic targets in a variety of cancers through her expertise in biobanking and patient-derived model generation. Jennifer earned a bachelor's degree in Biochemistry and Molecular Biology from Dartmouth College, an MD from McGill University.

John Dick

John Dick is a Senior Scientist and Canada Research Chair in Stem Cell Biology at the Princess Margaret Cancer Centre, Professor of Molecular Genetics and University Professor at the University of Toronto.

He is recognized for identifying and characterizing normal and leukemic human hematopoietic stem cells. His lab provided direct evidence for the cancer stem cell hypothesis, transforming our views of the origin and nature of cancer and laying the foundation for new approaches to cancer therapy. Similarly, his work on normal human hematopoiesis involving new methods for isolation and characterization of human HSC and downstream progenitors at single cell resolution has changed the textbook view of the human blood hierarchy.

Livia Garzia

Dr. Garzia graduated on a joint PhD program from the Telethon Institute of Genetics and Medicine, Naples (Italy) and The Open University, Cambridge (UK). Her thesis work investigated the role of miRNAs in brain tumors development. She trained as a post-doctoral fellow at the Hospital for Children in Toronto in the lab of Dr. Michael Taylor, where her work contributed to delineates the genetic mechanisms of relapse and metastasis in medulloblastoma. In 2017, she joined McGill as an assistant professor in the Department of Surgery and a principal investigator in the Cancer Research Program of the Research Institute of the McGill University Health Centre. She holds the Nicole et Francois Angers Sarcoma Research Chair for Basic and Translational Sarcoma research. Her research program focuses on pediatric sarcomas such as Ewing Sarcoma and Osteosarcoma. Dr. Garzia's lab uses genetic and molecular techniques approaches to understand mechanisms of therapy resistance and metastasis.

Laura Hilton

Laura Hilton completed her PhD in 2013, using classical genetics to understand the structure and regulation of cilia in the single-celled green alga Chlamydomonas reinhardtii. She joined the world of lymphoma genomics as a postdoctoral fellow in the lab of Dr. Ryan Morin at Simon Fraser University in 2018, working on gene expression-based biomarkers and reconstructing structural variants in whole genome sequencing data. As a Staff Scientist in the lab of Dr. David Scott at the BC Cancer Centre for Lymphoid Cancer, she has spearheaded efforts to standardize the analysis of lymphoma omics data through our "Genomic Analysis of Mature B-cell Lymphomas" (GAMBL) project.

Daisie Huang

Daisie Huang brings both bioinformatics knowledge and software engineering expertise to their role at CanDIG. They have worked as a researcher in phylogenomics as well as a software developer for data repositories and API workflows, all of which inform their understanding of the challenges for creating a distributed system that works to facilitate research and discovery for clinical and genomics researchers in Canada.

Steven Jones

Dr.Jones gained his PhD at the Sanger Institute, Cambridge, UK in 1999, where he was involved in the C. elegans genome project. Currently, he is Head of Bioinformatics and Co-Director of the Genome Sciences Centre at BC Cancer in Vancouver. Dr.Jones has played a role in numerous other genome projects, including that of the human, mouse, rat, bovine, fruitfly and the SARS coronavirus.

Dr.Jones's research focus is the computational analysis of DNA sequence and the analysis of genomic and transcriptomic data. He has applied next-generation DNA sequencing technology to determine the mutations and rearrangements driving many tumour types. A key goal is to develop bioinformatic approaches to predict the most efficacious therapies from the genetic analysis of patient tumour samples to help guide clinical decision-making.

Sachin Katyal

Dr. Katyal is a CIHR- and TFRI-funded Associate Professor within the Department of Pharmacology and Therapeutics (D-PT), a Senior Scientist within CCMR and Director of the Manitoba Tumour Bank. He was the recipient of the CIHR Institute of Cancer Research 2014 Early Career Award in Cancer Research and a CIHR New Investigator award. He has also established industrial partnerships, which have facilitated the development of innovative methodological platforms to accelerate his DNA damage repair research program. These were instrumental in obtaining a CFI JELF award to develop an innovative high-throughput genotoxicity and drug screening facility to interrogate DNA repair biology and to identify new therapies against neurological and lymphoproliferative malignancy.With this platform in-hand and his research program maturing, he was awarded a TFRI Terry Fox New Investigator Award to study deficiency/hyperactivity of DNA damage repair pathways underpinning resistant/recurrent disease.

Rama Khokha

Dr. Rama Khokha is a senior scientist at the Princess Margaret Cancer Centre, and a Professor in the Department of Medical Biophysics, at the University of Toronto. She obtained her PhD at University of Western Ontario, followed by postdoctoral training in London, Ontario, and at European Molecular Biology Labs, Germany. Her laboratory studies cell microenvironment in homeostasis and disease, and adult stem cell niches. Her program is also active in developing genetically engineered mouse models for human cancers, as well as novel tools for cancer gene discovery.

Philippe Lefrançois

Dr. Phillippe Lefrançois is an assistant professor at McGill University, dermatologist at the Jewish General Hospital, and an investigator at the Lady Davis Institute since summer 2021. His lab studies skin cancers, in particular basal cell carcinoma, using genomics and computational biology approaches on patient-derived tumors. His research program is supported by TFRI-MOHCCN and by FRQS. He obtained his Ph.D. from Yale University in 2012 under the supervision of Drs. Mike Snyder and Shirleen Roeder. He completed his MD from Université de Montréal in 2016 and his dermatology residency from McGill University in 2021. During residency, he performed postdoctoral work on translational cancer genomics of melanoma with Dr. Ian Watson, and of cutaneous lymphoma with Dr. Ivan Litvinov, work for which he obtained the highest research awards from the Canadian Dermatology Association and the American Academy of Dermatology.

Jessica McAlpine

Dr. McAlpine is a surgeon-scientist at the University of British Columbia and BC Cancer. She was born and raised in Vancouver. She did her medical training in the US; medical school at Johns Hopkins, residency at Stanford in Obstetrics and Gynecology, and Fellowship at Yale in Gynecologic Oncology. In 2006 she returned to Vancouver to take a position at UBC and BC Cancer. She currently splits her time equally between clinical/surgical duties and translational research. She has been appointed the Dr. Chew Wei Memorial Chair in Gynecologic Oncology at the University of British Columbia and BC Cancer, Vancouver Canada. She is co-Division Head, Tumor Bank Director, and part of the OVCARE and GCI research teams and recipient of a CIHR New Investigator Award (2013-2018) and BC Cancer Foundations Clinician Scientist Award (2016-2021). Her research focuses on molecular subtypes of endometrial, ovarian and vulvar cancers, and prevention of ovarian cancers.

Anne-Marie Mes-Masson

Dr. Mes-Masson trained as a molecular oncologist and obtained her Ph.D. from the Department of Microbiology and Immunology at McGill University in 1984. From 1984-1986, she completed post-doctoral studies at the Molecular Biology Institute, University of California Los Angeles. After a short period as a research associate at the Biotechnology Research Institute, Dr.Mes-Masson joined the Institut du cancer de Montréal and the Department of Medicine at the Université de Montréal in 1989. A full professor since 2001, Dr. Mes-Masson was the scientific director of the Institut du cancer de Montréal and Director of cancer research at the Centre de recherche du Centre hospitalier de l'université de Montréal (CRCHUM) from 2003-2018 and in 2017 accepted the position of Associate Director, Basic and Translational Research, at the CRCHUM. In 2003 Dr. Mes-Masson was named the Director of the Réseau de recherche sur le cancer du Fonds de recherche du Québec - Santé (FRQS), a provincial cancer network of over 200 scientists focused on translational and clinical cancer research (www.rrcancer.ca). She will complete her mandate in 2023.

Mike Monument

Dr. Monument is a mid-career surgeon scientist from the University of Calgary, Canada. He is an MSK oncology surgeon who treats adult and paediatric patients with sarcoma. He leads a translational sarcoma lab using mouse models to study sarcoma immunology and novel immunotherapies. In collaboration with UCalgary sarcoma team and scientists from the Charbonneau Cancer Research Institute, he leads a clinical sarcoma research program, iSARP, focussed on clinical databases, tumour banking and developing precision oncology tools for high-risk sarcomas.

Sorana Morrissy

Dr. Sorana Morrissy completed her PhD in Medical Genetics at the University of British Columbia, and a postdoctoral fellowship at the Hospital of Sick Children in Toronto, Canada. Her work is collaborative and translational, focusing on understanding genetic and functional heterogeneity in cancer, with particular emphasis on identification of novel targetable vulnerabilities in recurrent disease. At the University of Calgary her research program brings together an interdisciplinary team of bioinformaticians, computer scientists, and biologists to investigate the clinical implications of intra-tumoral heterogeneity, to measure and model tumor evolution, and seek therapeutic strategies that incorporate this key aspect of tumor biology.

Hanne Ostergaard

Dr. Ostergaard completed both her B.Sc. in Cellular and Molecular Biology and PhD in Immunology at the University of California, Los Angeles (UCLA). Following completion of her PhD she undertook postdoctoral studies at The Salk Institute during which time she was supported by a Damon-Runyon Walter Winchell Cancer Research Fund Fellowship and then a Leukemia Society of America Fellowship. She then moved to the University of Alberta as an Assistant Professor and is currently a Professor in the Department of Medical Microbiology & Immunology. She was director for seven years of the Immunology Network, and Associate Dean, Research (Graduate Programs) for the Faculty of Medicine and Dentistry from 2012-2020. She has served on numerous peer review committees locally, nationally and internationally and was a member of the Advisory Committee on Research for the Canadian Cancer Society for eight years. She has been the President of the Canadian Society for Immunology and organized a number of its annual meetings. She has been an Associate Editor of the Journal of Immunology and served on the Editorial Board for the Journal of Biological Chemistry. She is currently the Director of the Cancer Research Institute of Northern Alberta at the University of Alberta. Her research centers on cytotoxic T lymphocytes of the immune system and how they recognize and kill cancer cells. She is focused on mechanistic studies that examine the cell biology of how these cytotoxic cells migrate and function and how different populations of CD8 T cells suppress tumor grown.

Trevor Pugh

Dr. Trevor Pugh PhD, FACMG is a cancer genomics researcher, board-certified molecular geneticist, and holder of the Canada Research Chair in Translational Genomics. He is Director of the Joint Genomics Program of the University Health Network and Ontario Institute for Cancer Research which delivers basic, translational, and clinically-accredited genomics services. He is also appointed as Associate Professor in the University of Toronto Department of Medical Biophysics, Senior Scientist at the Princess Margaret Cancer Centre, and Senior Investigator at the Ontario Institute for Cancer Research. His research lab is focused on understanding clinical implications of clonal shifts in cancer and non-cancerous cell populations during treatment, most recently using cell-free DNA, immune repertoire, and single cell RNA-seq sequencing. Most recently, he was recognized by Canada's Top 40 Under 40, the Canadian Cancer Society Bernard and Francine Dorval Prize, a Terry Fox New Investigator Award, and inclusion on the Web of Science Highly Cited Researchers List (top 1% of citations by field internationally).

Jüri Reimand

Jüri Reimand is a principal investigator at the Ontario Institute for Cancer Research and associate professor at the University of Toronto. His lab focuses on computational biology, cancer genomics, and development of statistical and machine-learning methods. Areas of interest include the non-coding cancer genome, multi-omics data integration, and cancer biomarker discovery. He received his PhD in computer science at the University of Tartu, Estonia, and completed post-doctoral training at the Donnelly Centre of the University of Toronto.

Peter Siegel

Dr. Peter Siegel received his Ph.D. degree from McMaster University and pursued his post-doctoral training at the Memorial Sloan-Kettering Cancer Center. He is currently a Professor in the Department of Medicine at McGill University and a member of the Goodman Cancer Institute. Since beginning his independent academic career at McGill, Dr. Siegel has held career awards from the CCS (Harold Johns Award), FRQS (Junior II research scholar) and is currently a McGill University William Dawson Scholar. Dr. Siegel's research focuses on the fundamental mechanisms that control organ-selective breast cancer metastasis and employs pre-clinical animal models and clinical material to identify molecular mediators and cellular process that promote breast cancer metastasis to distinct sites such as the bone, lung, liver and brain. He has expanded his research program to investigate colorectal cancer metastasis to the liver and solid cancer metastasis to the brain (lung, breast, melanoma).

Lillian Siu

Dr. Siu is a senior medical oncologist at Princess Margaret Cancer Centre since 1998, and has been a Professor of Medicine at the University of Toronto since 2009. She is the Director of the Phase I Program and Co-Director of the Bras and Family Drug Development Program at Princess Margaret Cancer Centre, and holds the BMO Chair in Precision Genomics (2016-2026). She is also the Clinical Lead for the Tumor Immunotherapy Program at Princess Margaret Cancer Centre. Dr. Siu served on the Board of Directors for the American Society of Clinical Oncology (ASCO) for a four-year term (2012-2016); she also served on the American Association for Cancer Research (AACR) Board of Directors for a three-year term (2017-2020). Dr. Siu's major research focus is in the area of new anticancer drug development, particularly with respect to phase I trials and head and neck malignancies.

Julie St-Pierre

The central research focus of the St-Pierre laboratory is the understanding of metabolic adaptations in cancer. During the last decade, her team contributed to understanding the role of the metabolic regulators PGC-1s in cancer, with a particular focus on poor outcome breast cancers. They showed that PGC-1alpha plays a key role in setting the metabolic state of poor outcome breast cancers, and that it promotes breast cancer growth and metastasis. Recently, they are pursuing research projects on metabolic adaptations fueling metastasis and therapeutic resistance.

Dr. St-Pierre received her PhD at the University of Cambridge and was Postdoctoral Fellow at the University of Cambridge, Harvard Medical School, and University of Montréal. From 2008-2017, she was Assistant and Associate Professor at McGill University. Currently, she is a Full Professor at the University of Ottawa and the Director of the metabolomics core facility. She holds a CRC tier 1 in Cancer Metabolism and she is co-leading a Terry Fox team grant on oncometabolism.

John Stagg

Dr.John Stagg is Associate Professor at the Faculty of Pharmacy of University of Montreal and Lab Head at the CHUM Hospital Research Center since 2010. An established cancer immunologist, Dr. Stagg cumulates over 100 research publications. Dr. Stagg is known for having identified the adenosine-producing enzyme CD73 as a novel target in immuno-oncology and for contributing to the development of therapeutic agents now in phase 2-3 clinical trials. Dr. Stagg is scientific co-founder and Scientific Advisory Board member of SURFACE ONCOLOGY, co-director of the Montreal Cancer Consortium, part of Marathon of Hope Cancer Centers, and Board member of BioCanRx.

Dr. Stagg's work is supported by several agencies, including FRQS, CIHR, IVADO, Genome Quebec, and the Jean-Guy Sabourin Research Chair in Pharmacology from the Université de Montréal Faculty of Pharmacy.

Ly Vu

Dr. Vu is a scientist at the Terry Fox Laboratory, British Columbia Cancer Center (BC Cancer) and an Assistant Professor at Faculty of Pharmaceutical Sciences at University of British Columbia (UBC). Dr. Vu is originally from Vietnam with a Bachelor of Science in Biology from Vietnam National University. Dr. Vu completed both her PhD and post-doctoral training at Memorial Sloan Kettering Cancer Center, NYC, US, where she uncovered the critical roles of RNA binding proteins and RNA methylation in pathogenesis of myeloid leukemia. At BC Cancer and UBC, Dr. Vu's laboratory aims to understand molecular mechanisms underlying control of stem cells and pathogenesis of hematological malignancies with a focus on post-transcriptional and translational gene regulation pathways. The ultimate goal is to develop innovative therapeutic approaches for treatment of leukemia and other cancers.

Ian Watson

Dr. Ian Watson is a member of the Goodman Cancer Institute (GCI), an investigator at the Research Institute of the McGill University Health Centre (RI-MUHC), and an Associate Professor in the Department of Biochemistry at McGill University. He is a Canadian Research Chair II in functional genomics of melanoma, the Co-Chair for the melanoma disease working group for the Canadian Cancer Trials Group (CCTG) and the former Co-Chair for the melanoma Cancer Genome Atlas (TCGA) project. Dr. Watson's research program focuses on understanding the intersection of targeted and immune therapy resistance in melanoma utilizing an inter-disciplinary approach combining unbiased molecular characterization of melanomas, rapid development of preclinical models using genome-editing technology, and bioinformatic approaches.

Jeff Wrana

Jeff Wrana, PhD, FRSC received his PhD in Biochemistry from the University of Toronto. After completing a postdoctoral fellowship at Memorial Sloan Kettering, in NY, he returned to Toronto where he is now a Senior Investigator at the Lunenfeld-Tanenbaum Research Institute (LTRI) at Sinai Health Systems and Professor of Molecular Genetics at the University of Toronto. His work uncovered the Transforming Growth Factorb-Smad signalling pathway. He is currently co-director of the Network Biology Collaborative Centre at the LTRI and his research interests encompass the generation and analysis of large diverse biological datasets to define molecular networks of importance in cell fate determination, tissue regeneration and cancer. He has received numerous awards that include the Gertrude B. Elion prize from the American Association of Cancer Research, the Paul Marks prize from Memorial Sloan Kettering (NY), the Ontario Premier Summit award and most recently the McLaughlin Medal from the Royal Society of Canada.

RAPID-FIRE TALKS (RF) / ATTENDED POSTER SESSIONS

Rapid Fire Talks to be held in the Main Plenary Rooms 220-222 and the Poster Sessions take place in the Ocean Foyer.

The following posters will be presented at TFRI's 9th Scientific Meeting. Poster winners will be announced at the end of the Wine and Cheese session on the evening of Nov. 4th. Rapid Fire winners will be announced at the end of the last poster session on the evening of Nov. 5th.

All abstracts appear in our online Abstracts Book (located on our web site). See the corresponding page and poster number within this book to view the full submissions. **Not all posters are eligible for awards.**

RAPID FIRE JUDGES

Laura Hopkins, Amber Simpson, Robyn Urquhart

POSTER JUDGES

Tommy Alain, Mark Basik, Sid Croul, Steven Jones, Lawrence Kazak, Rama Khokha, Marianne Koritzinsky, Dan Renouf, Amber Simpson, Julie St-Pierre, Daniel Schramek, Jeff Wrana, George Zogopoulos

Friday, November 4

RAPID FIRE AND POSTER SESSION #1 / 10:30 – 11:30am

This will be a 15-minute rapid-fire session followed by 45 minutes for break and viewing posters

Shaghayegh Nouruzi, Zhen Jin, Tariq Bhat, Lan Valerie Tao

RAPID FIRE AND POSTER SESSION #2 / 3:30 – 6:00pm

This will be a 15-minute rapid-fire session followed by poster viewing and wine and cheese. Poster winners will be announced during the wine and cheese session.

Charlotte Girondel, Aghababazadeh Masoumeh, Julyanne Brassard, Cameron Herberts

Saturday, November 5

RAPID FIRE AND POSTER SESSION #3 / 9:30 – 10:30am

This will be a 15-minute rapid-fire session followed by 45 minutes for break and viewing posters

Curtis McCloskey, Charles Chesnelong, Vallijah Subasri, Shirin Soleimani

RAPID FIRE AND POSTER SESSION #4 / 3:00 – 4:00pm

This will be a 15-minute rapid-fire session followed by 45 minutes for break and viewing posters. Rapid Fire winners will be announced at the end of this session.

Ali Saleh, Masroor Bayati, Khalid Al-Zahrani, Rajesh Detroja

PAGE & POSTER		PRESENTER	TITLE
1	RF2	MASOUMEH AGHABABAZADEH	DECIPHERING METASTASIS MAINTENANCE AND CHEMO RESISTANCE EVENTS IN CIC-DUX4 SARCOMA
2		SHARON TZELNICK	NANOPARTICLE PHOTOSENSITIZER IN HEAD AND NECK CANCER: FROM PRECLINICAL DATA TO FIRST-IN-HUMAN CLINICAL TRIAL
3		FELIPE ELTIT	PROSTATE CANCER METASTASIS INDUCES IRREGULAR BONE FORMATION ASSOCIATED TO SPECIFIC ANDROGEN-DEPENDENT PHENOTYPES
4	RF2	CAMERON HERBERTS	CLONAL ARCHITECTURE AND EVOLUTION OF TREATMENT-RESISTANT PROSTATE CANCER VIA DEEP WHOLE-GENOME CTDNA SEQUENCING
5		CELINE LAUMONT	SINGLE-CELL PROFILES AND PROGNOSTIC IMPACT OF TUMOR-INFILTRATING LYMPHOCYTES COEXPRESSING CD39, CD103, AND PD-1 IN OVARIAN CANCER
6	RF1	VAL TAO	ELUCIDATING THE ROLE OF THE INSULIN RECEPTOR ISOFORM EXPRESSION IN METASTATIC PANCREATIC DUCTAL ADENOCARCINOMA
7		YANNICK AUDET-DELAGE	SPATIOTEMPORAL MODELING OF CHEMORESISTANCE EVOLUTION IN BREAST TUMORS UNCOVERS KEY DEPENDENCIES ON SLC38A7 AND SLC46A1
8		EDWARD CHEN	IMMUNE MODULATION IN HIPPO PATHWAY REGULATED BREAST TUMOUR MICROENVIRONMENTS
9		IVAN KOSIK	A PHOTOTHERMAL THERAPY GUIDANCE PLATFORM BASED ON PHOTOACOUSTIC IMAGING, DIFFUSE OPTICAL TOMOGRAPHY AND PORPHYSOME NANOTECHNOLOGY
10		MICHAEL VALIC	OPTIMISATION STRATEGY FOR NANOPARTICLE-BASED PHOTODYNAMIC THERAPY USING CLINICAL VETERINARY MODELS OF THYROID CANCER
11	RF1	ZHEN JIN	UNCOVERING THE FUNCTION AND REGULATION OF LONG NON-CODING RNA LNC-35682/PAN3-AS1 IN ACUTE MYELOID LEUKEMIA
12	RF4	KHALID AL-ZAHRANI	FUNCTIONAL GENOMIC CHARACTERIZATION OF COPY-NUMBER ALTERATIONS IN BASAL-LIKE BREAST CANCER

RAPID-FIRE TALKS (RF) / ATTENDED POSTER SESSIONS

Rapid Fire Talks to be held in the Main Plenary Rooms 220-222 and the Poster Sessions take place in the Ocean Foyer.

PAGE & POSTER		PRESENTER	TITLE
13		DEREK WONG	INTEGRATED ANALYSIS OF CELL-FREE DNA FOR THE EARLY DETECTION OF CANCER IN LI-FRAUMENI SYNDROME PATIENTS
14	RF1	SHAGHAYEGH NOURUZI	ASCL1 ACTIVATES NEURONAL STEM CELL-LIKE LINEAGE PROGRAMMING THROUGH THE REMODELING OF THE CHROMATIN LANDSCAPE IN PROSTATE CANCER
15		ARASH NABBI	TRANSCRIPTIONAL IMMUNOGENOMIC ANALYSIS TO IDENTIFY INFLAMED IMMUNE MICROENVIRONMENT ACROSS PEDIATRIC SOLID TUMORS
16		DAVID PAPADOPOLI	DECIPHERING THE ROLE OF ETFDH ON CANCER BIOLOGY
17	RF3	CHARLES CHESNELONG	POLYAMINE METABOLISM AND INFLAMMATORY STATE CONTROL A VIRAL MIMICRY-DRIVEN QUIESCENT PHENOTYPE IN GSC
18	RF4	RAJESH DETROJA	DNA-METHYLATION ANALYSIS IN FOLLICULAR LYMPHOMAS IDENTIFIES DIFFERENTIALLY METHYLATED REGIONS ASSOCIATED WITH CLINICAL STAGE
19		AHMAD MALIK	IDENTIFICATION OF THERAPEUTIC TARGETS FOR HEAD AND NECK SQUAMOUS CELL CARCINOMA (HNSCC)
20		HUY-DUNG HOANG	ADAPTATION OF TRANSGENE MRNA TRANSLATION BOOSTS THE ANTICANCER EFFICACY OF ONCOLYTIC HSV1
21		YOTA OHASHI	OPTIMIZATION OF ANTI-MESOTHELIN CAR-T CELLS THROUGH SCFV ENGINEERING
22		GEORGINA BARNABAS	PRIORITIZING TREATMENT TARGETS FOR A RARE PEDIATRIC MALIGNANCY USING PROTEOMICS AND XENOGRAFT MODELS WITHIN AN ACTIONABLE TIMEFRAME
23		HOSSEIN HAGHI	THE ROLE OF INTERBUBBLE INTERACTIONS ON THE RESONANCE FREQUENCY OF ULTRASONICALLY EXCITED MICROBUBBLES
24		YIFAN YIN	DYNAMIC CHANGES IN THE CLASSIC HODGKIN LYMPHOMA TUMOR MICROENVIRONMENT USING SINGLE CELL TRANSCRIPTOME SEQUENCING
25		NILOUFAR SHIRAZI	OPTIMIZING IMAGING PARAMETERS OF CONTRAST-ENHANCED ULTRASOUND USING NANOBUBBLES TO QUANTIFY KIDNEY INJURY
26	RF2	CHARLOTTE GIRONDEL	DELINEATING METABOLIC PROGRAMS IN COLORECTAL CANCER LIVER METASTASES
27		MARCO BIONDINI	REDOX METABOLIC ADAPTATIONS PROMOTE LIVER METASTASIS OF BREAST CANCER
28	RF3	SHIRIN SOLEIMANI	PAN-CANCER ASSESSEMENT OF TUMOUR AND PERIPHERAL T-CELL RECEPTOR REPERTOIRE DYNAMICS IN PATIENTS TREATED WITH PEMBROLIZUMAB
29		PAIGE SMITH	IMPROVING INTRATHECALLY ADMINISTERED METHOTREXATE PENETRATION TO THE SPINAL CORD USING FOCUSED ULTRASOUND
30		ALEC BAHCHELI	INVESTIGATING THE ROLES OF PROGNOSTIC ION CHANNEL GENES IN GLIOBLASTOMA
31	RF4	MASROOR BAYATI	SYSTEMATIC PAN-CANCER ANALYSIS TO REVEAL THE PROGNOSTIC SIGNIFICANCE OF DRIVER MUTATIONS AND THE TUMOR IMMUNE MICROENVIRONMENT
32	RF3	CURTIS MCCLOSKEY	A NOVEL MAMMARY PROGENITOR POPULATION REGULATED BY FATTY ACID METABOLISM
33		RIFAT SAJID	EXPLORING THE ROLE & THERAPEUTIC POTENTIAL OF HYPOXIA-DRIVEN AKAP12 EXPRESSION IN GLIOBLASTOMA
34		PIRASHAANTHY THARMAPALAN	PROGESTERONE RECEPTOR (PR) LINEAGE TRACING REVEALS EARLY PR-PRIMED PROGENITOR IN MAMMARY EPITHELIAL HIERARCHY
35		ALEX MURISON	SINGLE-CELL CHROMATIN AND TRANSCRIPTIONAL PROFILING REVEALS DISTINCT CHARACTERISTICS OF FETAL LIVER HSPC SUBPOPULATIONS ACROSS ONTOGENY

RAPID-FIRE TALKS (RF) / ATTENDED POSTER SESSIONS

Rapid Fire Talks to be held in the Main Plenary Rooms 220-222 and the Poster Sessions take place in the Ocean Foyer.

PAGE & POSTER		PRESENTER	TITLE
36		HAYA SHA'ALAN	GENOME-WIDE METHYLATION AND HAPLOTYPE-RESOLVED ABERRANT SOMATIC HYPERMUTATION PATTERNS IN DIFFUSE LARGE B-CELL LYMPHOMA
37	RF4	ALI SALEH	COUNTERACTING TEMOZOLAMIDE (TMZ)-RESISTANT GLIOBLASTOMA MULITFORME (GBM) VIA INHIBITION OF THE CELLULAR BASE EXCISION REPAIR (BER) PATHWAY
38	RF2	JULYANNE BRASSARD	TURNING IMMUNE-COLD TUMORS INTO HOT TUMORS USING AN ANTIBODY-DRUG CONJUGATE TARGETING A TUMOR-SPECIFIC GLYCOEPITOPE OF PODOCALYXIN
39		LUKE NEUFELD	HYPOXIA CONTROLS TUMOUR ASSOCIATED MACROPHAGE PHENOTYPE VIA HIF1*A*N PANCREATIC DUCTAL ADENOCARCINOMA
40		MARYAM ASADI	THE USE OF ARTIFICIAL INTELLIGENCE-BASED HISTOPATHOLOGY IMAGE ANALYSIS TO IDENTIFY A NOVEL SUBTYPE OF ENDOMETRIAL CANCER WITH UNFAVORABLE OUTCOME
41		MODELINE LONGJOHN	A SMALL RNA SIGNATURE IN PLASMA EXTRACELLULAR VESICLES THAT IDENTIFIES B-ACUTE LYMPHOBLASTIC LEUKEMIA
42		YANA MOSCOVITZ	DICER1 SYNDROME-ASSOCIATED CANCERS MOLECULAR CHARACTERIZATION AND THERAPEUTIC TESTING USING A NOVEL MURINE MODEL
43	RF1	TARIQ AHMAD BHAT	EVALUATING TARGETED DRUG THERAPIES FOR PEDIATRIC TUMOURS USING THE CHICK CHORIOALLANTOIC MEMBRANE (CAM) XENOGRAFT MODEL
44		DEOK JANG	PRE-TREATMENT PREDICTION OF BREAST CANCER RESPONSE TO NEOADJUVANT CHEMOTHERAPY USING MR RADIOMICS WITH HIGHER-ORDER TEXTURE FEATURES
45		ALLYSON BANVILLE	SEEING IS B-LIEVING: DISCOVERING THE ANTIGEN REACTIVITY OF TUMOR-INFILTRATING B CELLS
46		DORY ABELMAN	MONITORING MULTIPLE MYELOMA WITH CELL-FREE DNA
47		THEO HUSBY	MEASUREMENT OF PORPHYSOME NANOPARTICLE CONCENTRATION IN TURBID PHANTOMS AND EX VIVO USING DIFFUSE REFLECTANCE AND FLUORESCENCE SPECTROSCOPY
48		JOSHUA SCURLL	PRELIMINARY DATA FROM THE GENOMIC UMBRELLA NEOADJUVANT STUDY (GUNS), A PHASE-II TRIAL OF TARGETED COMBINATION THERAPIES FOR PROSTATE CANCER
49		DAMEHAN TCHELOUGOU	DEFINING MELANOMA COMBINATION THERAPIES THAT PROVIDE SENOLYTIC SENSITIVTY IN HUMAN MELANOMA CELLS
50		SHAMINI AYYADHURY	UTILIZING PIXEL-DERIVATIVES FOR PATTERN RECOGNITION, IN UNDERSTANDING THE FUNCTIONAL RELEVANCE OF 2D CELL ORGANIZATION IN GBM
51		FOROUH KALANTARI	HUMAN ENDOMETRIUM ORGANOIDS, A NEW MODEL TO STUDY CLEAR CELL OVARIAN CARCINOMA
52		SHAOCHENG WU	INTEGRATED SINGLE CELL ANALYSIS REVEALS CO-EVOLUTION OF MALIGNANT B CELLS AND THE TUMOR MICROENVIRONMENT IN TRANSFORMED FOLLICULAR LYMPHOMA
53	RF3	VALLI SUBASRI	DNA METHYLATION PREDICTS EARLY ONSET OF PRIMARY TUMOR IN PATIENTS WITH LI-FRAUMENI SYNDROME
54		NAKISA TABRIZIAN	ASCL1 IS ACTIVATED DOWNSTREAM OF ROR2/CREB SIGNALING PATHWAY TO SUPPORT LINEAGE PLASTICITY
55		RYAN GHORAYEB	AN EX VIVO ORGANOID MODEL TO STUDY MAMMARY ALVEOLOGENESIS
56		FANGWU WANG	CHARACTERIZATION OF THE HUMAN B LYMPHOID AND NEUTROPHIL/MONOCYTE LINEAGE RESTRICTION PROCESS
57		MARISSA FOO	DNMT3A LIMITS MYELOID SIGNALING RESPONSES IN COMMITTED T CELLS DURING NORMAL AND LEUKEMIC DEVELOPMENT
58		HAYLE KINCROSS	LOSS OF FBXO11 FUNCTION ESTABLISHES A STEM CELL PROGRAM IN ACUTE MYLEOID LEUKEMIA THROUGH DYSREGULATION OF THE MITOCHONDRIAL PROTEASE LONP1

Posters 56-58 not judged.

RAPID-FIRE TALKS (RF) / ATTENDED POSTER SESSIONS

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These posters are provided by MOHCCN participants to share information about their projects and will not be judged.

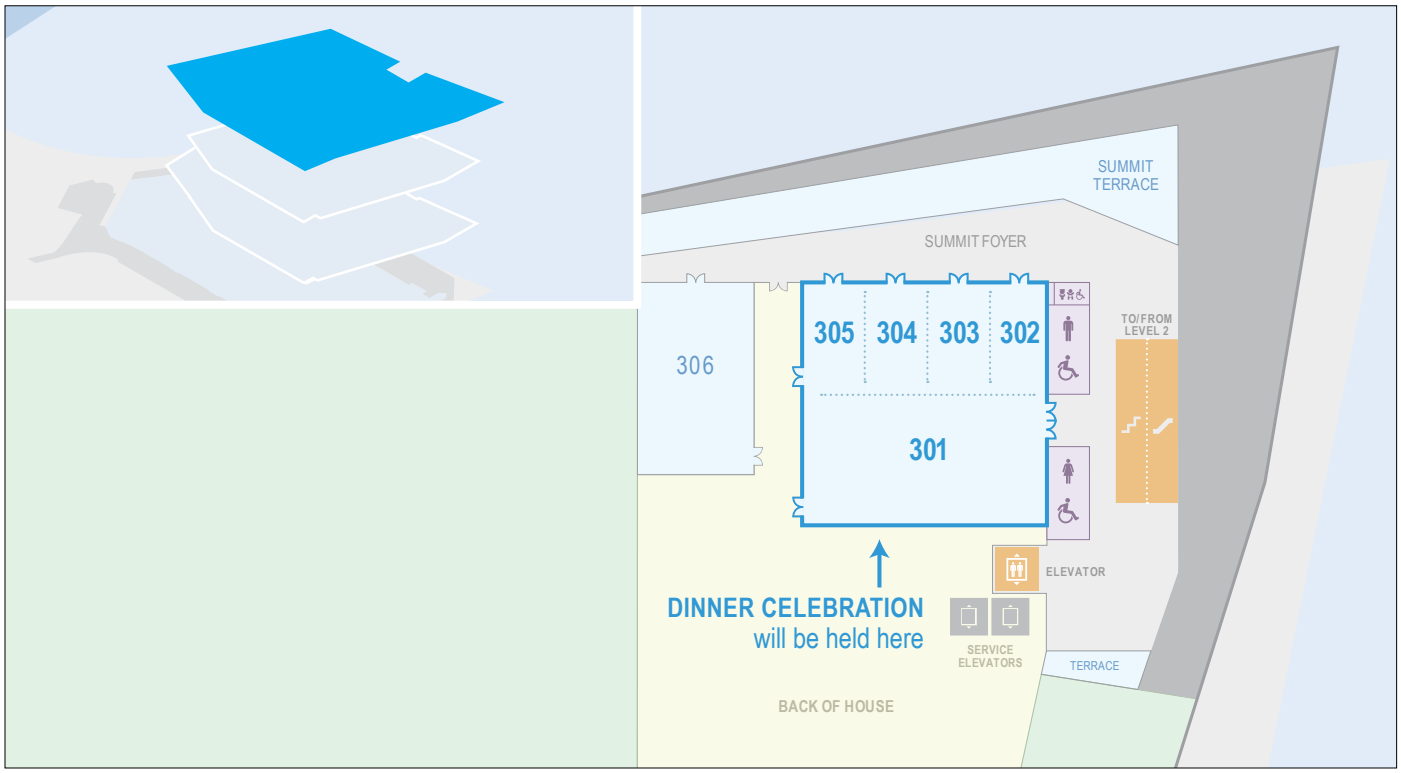
PAGE & POSTER	PRESENTER	TITLE
MOHCCN 1	**DANIEL GASTON**	EVALUATION OF HIGH DEPTH SOMATIC VARIANT CALLING METHODS USING TUMOR-ONLY APPROACH
MOHCCN 2	**MARTIN HIRST**	HETEROGENEITY IN BIVALENT CHROMATIN STATES DEFINES A DISEASE SPECTRUM IN SYNOVIAL SARCOMA
MOHCCN 3	**ALY KARSAN**	GENOMIC SEQUENCING TO UNRAVEL RESISTANCE AND RELAPSE IN ACUTE MYELOID LEUKEMIA
MOHCCN 4	**ESTHER KONG**	DETECTING EARLY STAGE RESIDUAL DISEASE IN TNBC WITH WHOLE GENOME PLASMA SEQUENCING
MOHCCN 5	**JANESSA LASKIN**	PERSONALIZED ONCOGENOMICS (POG) PROGRAM
MOHCCN 6	**DAN MOLDOVEANU**	SPATIALLY MAPPING THE IMMUNE LANDSCAPE OF MELANOMA USING IMAGING MASS CYTOMETRY
MOHCCN 7	**SOPHIE COOKE, SEVAN HAKGOR, EMILY VAN DE LAAR**	EXPLORING A PATIENT'S JOURNEY INTO THE MARATHON OF HOPE CANCER CENTRES NETWORK
MOHCCN 8	**AMBER SIMPSON**	THE KINGSTON SITE: CONTRIBUTING BLADDER AND BRAIN COHORTS TO THE MARATHON OF HOPE
MOHCCN 9	**STEPHANIE GROVER**	THE PRECISION ONCOLOGY FOR YOUNG PEOPLE (PROFYLE) PROGRAM: A NATIONAL PRECISION ONCOLOGY PROGRAM FOR CHILDREN, ADOLESCENTS AND YOUNG ADULTS WITH HARD-TO-CURE CANCER IN CANADA
MOHCCN 10	**TREVOR PUGH**	SINGLE CELL SEQUENCING SERVICES AT THE PRINCESS MARGARET CANCER CENTRE

GLOSSARY

BCCA	BC Cancer Agency
BCCRC	BC Cancer Research Centre
CBCF	Canadian Breast Cancer Foundation
CCS	Canadian Cancer Society
CCSRI	Canadian Cancer Society Research Institute
CFI	Canadian Foundation for Innovation
CHUM	Centre hospitalier de l'Université de Montréal
CHUQ	Centre hospitalier de l'Université de Quebéc
CIHR	Canadian Institutes of Health Research
CPAC	Canadian Partnership Against Cancer
CRCHUM	Centre de recherche du Centre hospitalier de l'Université de Montréal
ICGC	International Cancer Genome Consortium
IWK	Izaak Walton Killam
MSFHR	Michael Smith Foundation for Health Research
MSGSC	Michael Smith Genome Sciences Centre
NIH	National Institutes of Health
NSERC	Natural Sciences and Engineering Research Council
OCI	Ontario Cancer Institute
OHRI	Ottawa Hospital Research Institute
OICR	Ontario Institute for Cancer Research
PMCC	Princess Margaret Cancer Centre
SFU	Simon Fraser University
TBCC	Tom Baker Cancer Centre, Calgary
UBC	University of British Columbia
UdeM	Université de Montréal
UHN	University Health Network
UofC	University of Calgary
UofM	University of Manitoba
UofT	University of Toronto
VGH	Vancouver General Hospital
VPC	Vancouver Prostate Centre

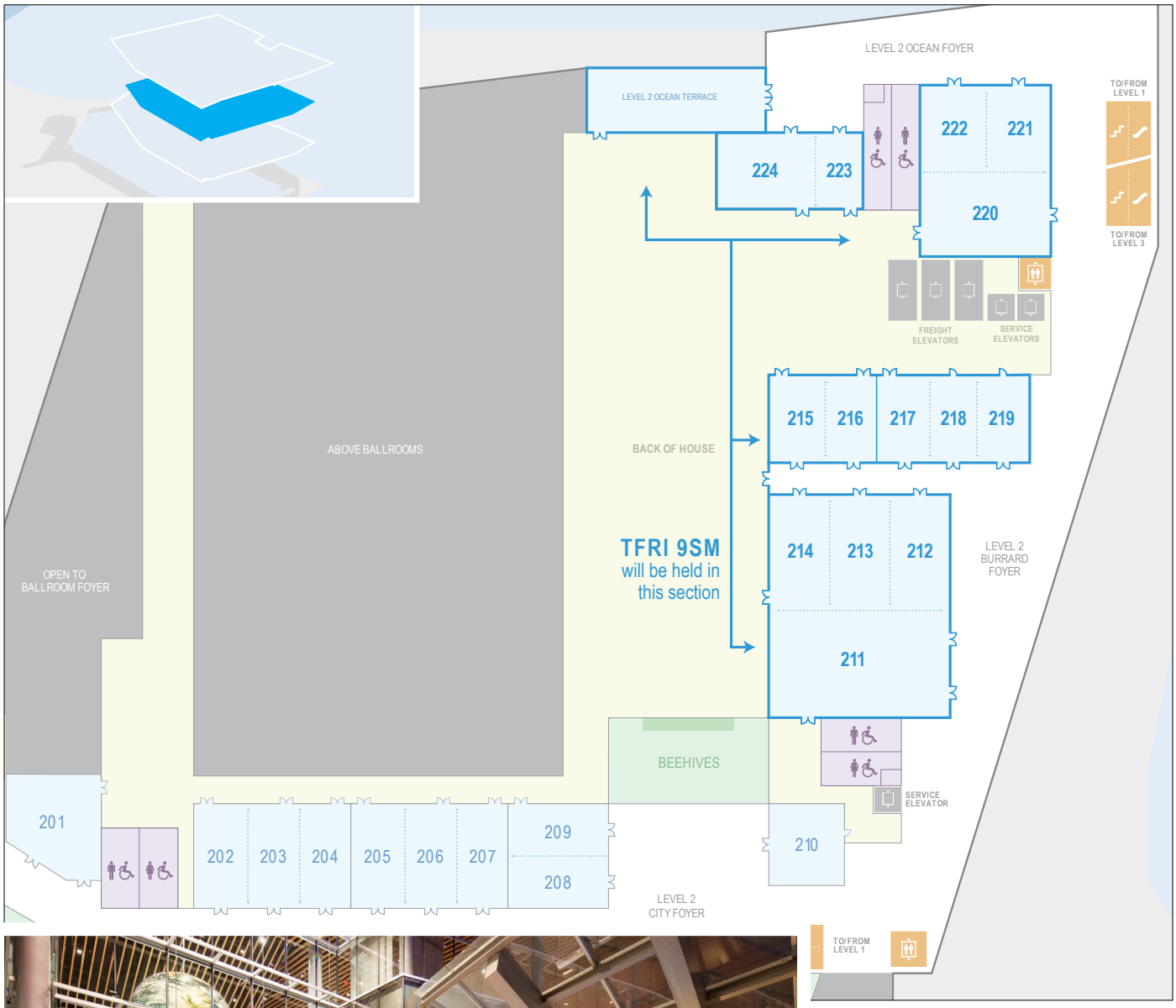
RUN MAP & HOTEL FLOOR PLANS

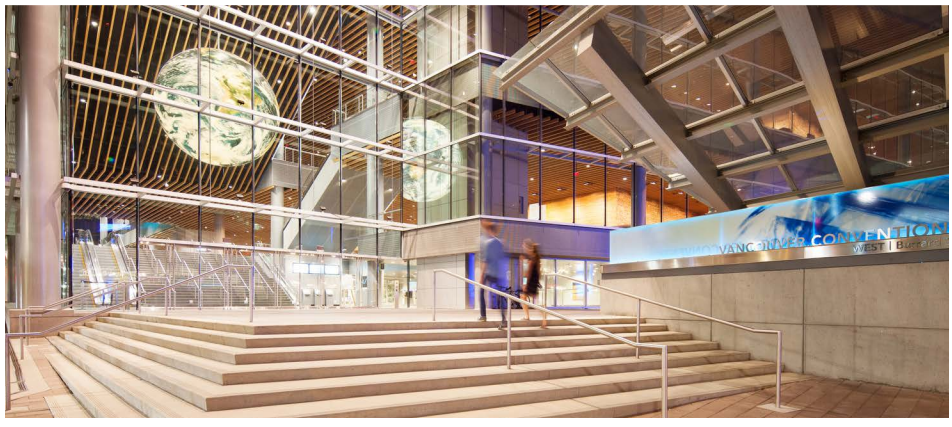
OUR CELEBRATION DINNER WILL BE HELD IN ROOMS 301 – 305



HOTEL FLOOR PLANS

TFRI 9SM WILL BE HELD IN ROOMS 211 – 224 AND OCEAN FOYER





The entrance to the Vancouver Convention Center

The Terry Fox Research Institute from coast to coast

TFRI is an Institute without walls linking the capabilities of 93 leading cancer care and cancer research institutes and universities organized through six regional "nodes".

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The Terry Fox Foundation

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MARATHON OF HOPE CANCER CENTRES NETWORK