CURRICULUM VITAE

Marco Antonio Marra

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AREAS OF EXPERTISE:

genomics, bioinformatics, genetics, epigenomics, cancer biology

EDUCATION:

Start Date	End Date	Institution	Degree	**Supervisor**
09/1989	09/1994	Simon Fraser University	PhD (Genetics)	Dr. David Baillie
09/1984	05/1989	Simon Fraser University	BSc (Molecular & Cell Biology)	

PhD Thesis Title: Genome analysis in *Caenorhabditis elegans*: Genetic and molecular identification of genes tightly linked to *unc-22*(IV).

ACADEMIC EMPLOYMENT HISTORY:

04/2023	Present	Member, Michael Smith Laboratories, University of British Columbia
07/2007	Present	Professor, Department of Medical Genetics, University of British Columbia
04/2009	Present	Distinguished Scientist, BC Cancer Research Institute, BC Cancer
04/2002	11/2022	Director, Canada's Michael Smith Genome Sciences Centre, BC Cancer
06/2000	04/2023	Associate Member, Michael Smith Laboratories, University of British Columbia
01/2015	08/2020	Head, Department of Medical Genetics, Faculty of Medicine, University of British Columbia
01/2011	06/2018	Co-Founder & Co-Director, Genome Science and Technology Graduate Program, University of British Columbia
07/2002	06/2007	Associate Professor, Department of Medical Genetics, University of British Columbia
01/2001	12/2015	Adjunct Professor, Department of Molecular Biology and Biochemistry, Simon Fraser University
10/2000	04/2002	Co-Director (Scientific), Genome Sequence Centre, BC Cancer Agency
02/2000	06/2002	Adjunct Professor, Department of Medical Genetics, University of British Columbia
10/1999	03/2009	Senior Scientist, BC Cancer Research Centre, BC Cancer Agency
10/1999	09/2000	Associate Director, Genome Sequence Centre, BC Cancer Agency
10/1999	09/2000	Head, Mapping and Sequencing, Genome Sequence Centre, BC Cancer Agency
09/1998	09/1999	Research Faculty Instructor, Washington University School of Medicine (St. Louis, MO)
09/1996	09/1999	Group Leader, Genome Fingerprinting and Mapping Teams, Genome Sequencing Center (St. Louis, MO)
09/1994	09/1999	Group Leader, EST Sequencing Team, Genome Sequencing Center (St. Louis, MO)
12/1994	09/1998	Postdoctoral Research Associate, Washington University School of Medicine (St. Louis, MO)

HONORS, AWARDS, SCHOLARSHIPS, AND FELLOWSHIPS:

10/01/2023 to 09/30/2028	Terry Fox Leader in Cancer Genome Science Award	Terry Fox Research Institute
2022	Research Partnership Award: HostSeq & CanCOGen	Canadian Association of Research Administrators
11/2021	Highly Cited Researcher and named as one of the 2021 World's Most Influential Scientific Minds	Clarivate Analytics
11/2020	Highly Cited Researcher and named as one of the 2020 World's Most Influential Scientific Minds	Clarivate Analytics
06/2020	2020 Team Science Award	American Association for Cancer Research
04/2020	Canadian Medical Hall of Fame	Canadian Medical Association
11/2019	Highly Cited Researcher and named as one of the 2019 World's Most Influential Scientific Minds	
02/2019	Dr. Don Rix Lifetime Achievement Award	LifeSciences BC
11/2018	Highly Cited Researcher for 2018 and named as one of the 2018 World's Most Influential Scientific Minds	Clarivate Analytics
11/2017	Highly Cited Researcher and named as one of the 2017 World's Most Influential Scientific Minds	Clarivate Analytics
07/2017	Outstanding Achievements in Cancer Research Award	Canadian Cancer Research Alliance
12/2016	Highly Cited Researcher and named as one of the 2016 World's Most Influential Scientific Minds	Thomson Reuters
06/2016	2016 BC Health Care Award of Merit for Collaborative Solutions (for BC Cancer Agency's Personalized Onco-Genomics Project, co-led with Dr. Janessa Laskin)	Health Employers Association of British Columbia
12/2015	Highly Cited Researcher and named as one of the 2015 World's Most Influential Scientific Minds	Thomson Reuters
09/2015	Dr. Chew Wei Memorial Prize in Cancer Research	University of British Columbia
06/2014	Highly Cited Researcher and named as one of the 2014 World's Most Influential Scientific Minds	Thomson Reuters
01/2014	2013 Killam Research Prize	University of British Columbia
11/2012	Medal of Merit Award	The International Association of Lions Clubs
05/2012	Distinguished Achievement Award	Faculty of Medicine, University of British Columbia
11/2010	Terry Fox Medal	British Columbia Medical Association
10/2010	Order of British Columbia	Province of British Columbia
07/2010 to 06/2024	UBC Canada Research Chair in Genome Science	Canadian Institutes of Health Research
04/2010	Genome BC Award for Scientific Excellence	LifeSciences BC
09/2009	Fellow	Canadian Academy of Health Sciences
09/2008	Frontiers in Research Award	British Columbia Innovation Council
07/2007	Distinguished Achievement Award (Excellence in Basic Science Research)	Faculty of Medicine, University of British Columbia

06/2007	Fellow	Medical Sciences Division, Royal Society of Canada
04/2007	Merck Frosst Prize	Canadian Society of Biochemistry and Molecular & Cellular Biology
10/2006 to 09/2011	Career Investigator Award (Senior Scholar level)	Michael Smith Foundation for Health Research
07/2006	Faculty Merit Award	Department of Medical Genetics, University of British Columbia
06/2006	President's 40th Anniversary Award	Simon Fraser University
06/2005	Honorary Degree, Doctor of Laws	University of Calgary
05/2005	The Best of the Best of Canada's Top 40 Under 40	The Caldwell Partners International
06/2004	Terry Fox Young Investigator Award	National Cancer Institute of Canada
06/2004	Honorary Degree, Doctor of Science	Simon Fraser University
03/2004	Innovation and Achievement Award (awarded to entire GSC staff)	LifeSciences BC (formerly BC Biotech)
10/2001 to 09/2006	Career Investigator Award (Scholar level)	Michael Smith Foundation for Health Research
09/2001	Top 40 Under 40 Award	Business in Vancouver
07/2000	Notable Canadian 35 and Under	The Globe and Mail
03/2000	Canada's Top 40 Under 40 Award	The Caldwell Partners International
12/1999	Outstanding Alumni Award for Academic Achievement	Simon Fraser University
09/1994	University Graduate Fellowship	Simon Fraser University
12/1993	President's PhD Research Stipend	Simon Fraser University
12/1989	Pre-doctoral Scholarship	Natural Sciences and Engineering Research Council of Canada
12/1989	Special Graduate Research Fellowship	Simon Fraser University

Named Lectures

1.	The Beatrice Hunter Cancer Research Institute's Picchione Seminar Series. (Virtual). Halifax, NS. Mar 2, 2021. "Towards a Canadian national program for comprehensive genomic profiling of treatment resistant cancer."
2.	Arthur and Sonia Labatt Brain Tumour Research Centre Annual Lectureship. (Virtual). University of Toronto. Toronto, ON. Jan 20, 2021. "Towards a Canadian national program for comprehensive genomic profiling of treatment resistant cancer."
3.	University of Alberta, Department of Oncology. Dr. Carol Cass Lecture in Translational Research in Oncology, Edmonton, AB. May 24, 2013. "Decoding cancers".
4.	University of Toronto, Faculty of Medicine. DSR Sarma Lectureship in Oncologic Pathology, Toronto, ON. Sep 24, 2012. "Decoding cancers".

BRIEF BIOSKETCH:

Dr. Marra is the UBC Canada Research Chair in Genome Science, and a member of the Order of British Columbia. He is a Canadian Medical Hall of Fame awardee and a recipient of: the 2019 Don Rix Lifetime Achievement Award, the 2017 Canadian Cancer Research Alliance's Outstanding Achievements in Cancer Research Award, the 2015 Dr. Chew Wei Memorial Prize in Cancer Research, a 2013 UBC Killam Research Prize, a 2012 UBC Faculty of Medicine Distinguished Achievement Award, and the Medal of Merit Award from the International Association of Lions Clubs. He was elected to the Canadian Academy of Health Sciences in 2009; received the Frontiers in Research Award from the BC Innovation Council in 2008; and was appointed a Fellow of the Royal Society of Canada in 2007. He was a recipient of a Genome BC Award for Scientific Excellence, a MSFHR Career Investigator Senior

Scholar Award, and Simon Fraser University President's 40th Anniversary Award. In 2004, he received a Terry Fox Young Investigator Award and BC Biotech's Innovation and Achievement Award (together with the entire GSC staff) for sequencing the SARS coronavirus genome.

Dr. Marra's contributions to genome science led to an honorary Doctor of Science degree from Simon Fraser University in 2004 and an honorary Doctor of Laws degree from the University of Calgary in 2005.

COMMITTEE INVOLVEMENT:

2023 – Present	Co-Chair, IT Committee, Michael Smith Laboratories, University of British Columbia
05/2023 – Present	Member, TFRI Marathon of Hope Cancer Centre Network Canadian Spectrum Working Group
03/2023 – Present	Co-Chair, Council of Expert Advisors (CEA), Government of Canada
02/2023 – Present	Member, TFRI Marathon of Hope Cancer Centre Network Council
11/2022 – Present	Member, Department of Medical Genetics Graduate Awards Committee, University of British Columbia
04/2022 – Present	Member, Genome BC Jurisdictional Health Framework Working Group
06/2021 – Present	Co-Lead, TFRI Marathon of Hope Cancer Centre Network BC2C Consortium
04/2020 – Present	Member, GSC@ MSL Scientific Steering Committee, University of British Columbia
09/2019 – Present	Co-Chair, TFRI Marathon of Hope Cancer Centre Network Technology Working Group
10/2017 – Present	Member, Northern Biobanking Scientific Advisory Committee, The University of Northern British Columbia
01/2011 – Present	Member, Steering Committee, Genome Science and Technology Graduate Program, University of British Columbia
01/2011 – Present	Member, Admissions Committee, Genome Science and Technology Graduate Program, University of British Columbia
11/2010 – Present	Member, Executive Committee, and BC Node Leader, Terry Fox Research Institute
10/2023 – 04/2024	Member, Faculty Search Committee, Michael Smith Laboratories, University of British Columbia
01/2023 – 05/2024	Member, Leukemia and Lymphoma Society (USA) PedAL Biomarker Discovery Leadership team
01/12/2023	Participant, Department of Medical Genetics Canada Research Chair Adjudication Committee, University of British Columbia
06/2021 – 02/2023	Member, TFRI Marathon of Hope Cancer Centre Network Steering Committee
04/2021 – 03/2023	Member, Provincial Genomics Discipline Committee, Provincial Laboratory Medicine Services, Provincial Health Services Authority
04/2020 – 2022	Member, COVID-19 Clinical Operations and Research Task Force, and COVID Research Coordination Executive Governance Group, University of British Columbia
09/2018 – 2022	Member, Healthy Aging Chair Search Committee, Faculty of Medicine, University of British Columbia
09/2017 – 2022	Member, Research Executive Committee, BC Cancer Research Institute, BC Cancer
08/2019 – 2020	Member, Precision Health Program Advisory Council, Digital Technology Supercluster
12/2018 – 12/2019	Member, Genetic Services Priorities and Impact Assessment Sub-Committee (PIA-G), BC's Agency for Pathology and Laboratory Medicine, Provincial Health Services Authority
05/2018 – 09/2018	Member, Biochemistry and Molecular Biology Search Committee, Faculty of Medicine, University of British Columbia
10/2017 – 04/2021	Member, Search Committee, UBC President's Chair in Precision Oncology, University of British Columbia
09/2017 – 06/2019	Member, Search Committee for Provincial Medical Genetics Program Medical Director, BC Women's Hospital and Health Centre, Provincial Health Services Authority
09/2017	Member, Nomination Committee, Cancer Control Research Department, BC Cancer Research Centre, BC Cancer

06/2017 – 12/2018	Member, BC Cancer Research Strategic Planning Committee, BC Cancer
03/2017 – 10/2019	Member, Health Sector Advisory Council, Genome British Columbia
12/2015 – 07/2016	Member, VP Research Search Advisory Committee, BC Cancer Agency
11/2015 – 10/2016	Member, Interim Research Operations Committee, BC Cancer Research Centre, BC Cancer Agency
10/2015 – 12/2017	Member, Genomics England-Genome British Columbia Steering Committee
09/2015 – 06/2016	Member, MD Undergraduate Education Committee, University of British Columbia
08/2015 – 11/2016	Member, Health Innovation Strategic Advisory Board, Business Council of British Columbia
07/2015 – 12/2016	Member, Research Seminar Series Committee, BC Cancer Research Centre
05/2015 – 06/2016	Member, Dr. Chew Wei Prize Advisory Selection Committee, University of British Columbia
02/2015 – 05/2016	Member, Scientific Advisory Board, Cancer Genome Collaboratory Project, Ontario Institute for Cancer Research
01/2015 – 08/2020	Member, Medical Genetics Graduate Program Advisory Committee, University of British Columbia
01/2015 – 08/2020	Member, Genetics Counselling Program Advisory Committee, University of British Columbia
12/2014 – 05/2015	Member, Selection Committee, BC Cancer Agency President Search, Provincial Health Services Authority
11/2014 – 09/2022	Member, Scientific Advisory Board, Foundation for Burkitt Lymphoma Research
11/2014 –12/2015	Member, Genome BC Health Strategy Task Force
02/2014 – 09/2016	Member, Board of Directors, Michael Smith Foundation for Health Research
01/2013 – 11/2015	Member, BC Cancer Agency Research Advisory Council
01/2012 – 06/2013	Member, Provincial Health Services Authority Research Advisory Council
09/2012 – 01/2013	Member, Search Committee for New TFL Scientist, Terry Fox Laboratory, BC Cancer Agency
2010 – 11/30/2011	Member, Scientific Program Committee, The Canadian Cancer Research Conference, Toronto, ON
2011	Member, Research Seminar Series Committee, BC Cancer Research Centre
2011	Member, Planning Committee, TCGA 1st Inaugural Scientific Symposium
2009 – 06/2016	Member, TCGA Steering Committee, The Cancer Genome Atlas, National Cancer Institute/National Human Genome Research Institute, National Institutes of Health
2009 – 06/2016	Co-Chair, The Cancer Genome Atlas (TCGA) Lymphoma Disease Working Group, National Cancer Institute, National Institutes of Health
08/2009 – 07/2011	Member, Faculty Awards Committee, University of British Columbia
2009 – 2010	Member, NHGRI Informatics and Analysis Planning Committee, National Institutes of Health
2008	Member, Organizing Committee, ICGC, Canadian Cancer Genome Workshop
2008	Member, Genome Canada SIAC 1000 Genomes Working Group
2007 – 06/2016	Member, International Scientific Steering Committee, International Cancer Genome Consortium (ICGC)
2007 – 2011	Member, Scientific Planning Committee (Genome Analyses), ICGC
2007 – 2009	Member, Scientific Advisory Committee, Joint Genome Institute, US Department of Energy
2007	Member, Scientific Advisory Board, Heflin Center for Human Genetics, The University of Alabama at Birmingham
2006 – 11/2013	Member, Board of Directors, Advances in Genome Biology and Technology Conference, Marco Island, FL
2006 – 2009	Member, Discovery Council, British Columbia Cancer Research Centre, BC Cancer Agency
2006 – 2007	Member, Local Organizing Committee, HUGO's 12th Human Genome Annual Meeting, Montreal, QC

2005 – 2009	Member, Genome Canada Scientific Advisory Board (for vervet monkey physical mapping project)
2005 – 2008	Member, External Advisory Board, National Stem Cell Bank, National Institutes of Health
2005 – 2006	Member, Organizing Committee, 7th Annual Advances in Genome Biology and Technology Conference, Marco Island, FL
2005	Member, Genome British Columbia Education Advisory Committee
07/2005	Chair, National Human Genome Research Institute Review Panel ZHGI HGR-P(02) for BAC Library Production RFA, National Institutes of Health
2004 – 2008	Member, Oncology Advisory Council, BC Cancer Agency
2004	Member, Strategic Plan Implementation Council, BC Cancer Agency
2004	Member, Strategic Plan Steering Committee: Leader of Clinical/Functional/Translational Oncology Task Force; Member of Institutes Process Task Force, BC Cancer Agency
2003 – 2006	Member, Genome Research Review Committee, National Human Genome Research Institute (NHGRI), National Institutes of Health
2003 – 2005	Member, Biomedical Research Trainee Evaluation Committee (Junior Graduate Studentship Sub-Committee), Michael Smith Foundation for Health Research
2003	Member, Cancer Control Research Unit, Inaugural Research Unit, Michael Smith Foundation for Health Research
2002 – 2006	Member, Steering Committee, CIHR/MSFHR Bioinformatics Training Program, University of British Columbia
2002 – 2003	Canadian Scientific Representative, NHGRI International Sequencing Consortium, National Institutes of Health
08/2003	Member, Scientific Committee, 10th World Conference on Lung Cancer, Vancouver, BC
2002 – 2003	Chair, Genome British Columbia, President's Scientific Advisory Committee (PSAC)
2002	Genome Canada Search Committee: Director, Science and Technology platforms
2001 – 2004	Member, Joint Animal Facility Management Committee, BC Cancer Agency
2001	Member, Planning Committee, Genomics in Health and Disease Conference
2000 – 2005	Member, Research Executive, British Columbia Cancer Research Centre, BC Cancer Agency
2000 – 2002	Member, Biotechnology Facilities Planning Committee, University of British Columbia
2000	Co-Chair, Genome British Columbia Genotyping Planning Committee
2000	Chair, Genome British Columbia DNA Sequencing Planning Committee
2000	Member, Program Development Team, Strategy Committee, Genome Canada
1999 – 2003	Member, Genomics Projects Selection Panel, Natural Sciences and Engineering Research Council of Canada
1999 – 2001	Member, Orion Genomics L.L.C. Scientific Advisory Board
1999	Member, Advisory Board, Advances in Genome Biology and Technology Conference, Marco Island, FL
1997 – 2000	Member, Cancer Genome Anatomy Project (CGAP) Steering Committee, National Cancer Institute, National Institutes of Health

REVIEWER ACTIVITIES

12/2024 – Present	Co-Chair, Ontario Institute for Cancer Research External Review, Ontario Ministry of Colleges and Universities
09/2020 – Present	Reviewer, Canada Research Chairs Program, Government of Canada
06/2015 – Present	Member, College of Reviewers, Canadian Institutes of Health Research
12/2023 – 01/2024	Reviewer, NCI Intramural Cancer Data Science Innovation Laboratory
11/2023 – 03/2024	Member, AACR Basic Cancer Research Grants Scientific Review Committee
08/2020, 02/2019, 05/2018, 02/2015,	Reviewer, The Alvin J. Siteman Cancer Research Fund, Washington University School of Medicine

02/2014, 01/2013, 03/2011	
01/2017	Reviewer, John R. Evans Leaders Fund, Canada Foundation for Innovation
11/07/2014	Reviewer, KiKA Program Application 181 (Stichting Kinderen Kankervrij' (Foundation Children Cancerfree), The Netherlands
02/2013 & 03/2014	Reviewer, The Royal Society
2007 – 2008	Member, College of Reviewers, Canadian Institutes of Health Research

CONFERENCE PARTICIPATION (as chair / panelist / moderator / organizer)

11/2022	Chair, Plenary Session, 9th TFRI Annual Scientific Meeting, Vancouver, BC
11/2022	Member, 9th TFRI Annual Scientific Meeting Organizing Committee, Vancouver, BC
11/2022	Member, 9th TFRI Annual Scientific Meeting Abstract and Poster Committee, Vancouver, BC
01/15/2021	Co-Chair, Bioinformatics on Cancer Session, 1st International Symposium of CCII - Bioinformatics and its application to cancer and other diseases. (Virtual) Kyoto, Japan.
11/03/2020	Panelist, Data Science: How do you use it in health research? Data Science & Health 2020 Conference. (Virtual). University of British Columbia, Vancouver, BC.
06/24/2019	Panelist, Personalized Medicine and Oncology Session, 19th Annual International Healthcare Summit, The Future of Personalized Medicine, Genomics and Innovation, Kelowna, BC
11/04/2017	Co-Chair, Plenary I: Cancer Biology, TFRI's 8th Annual Scientific Meeting, Vancouver, BC
04/2015 – 07/2016	Member, International Scientific Advisory Committee, 2016 IUBMB Conference, Vancouver, BC
10/2015 – 05/2016	Chair, Scientific Organizing Committee, TFRI's 7th Annual Scientific Meeting, Vancouver, BC
06/2015 – 11/2015	Member, Program Committee, 2015 Canada Gairdner Symposium, Vancouver, BC
2011-2016; 2018-2019; 2021-2022	Organizer, TFRI Research Day, Vancouver, BC
11/30/2011	Session Chair, The Optics of 'Omics, The Canadian Cancer Research Conference, Toronto, ON
06/22/2011	Symposium Chair, Keystone Symposia: Changing Landscape of the Cancer Genome, Boston, MA
04/19/2010	Session Chair, High Throughput Genomic and Computational Biology, 3rd Annual Canadian Human Genetics Conference, Montreal, QC
03/14/2009	Industry Panelist, 4th Canadian Student Conference in Biomedical Computing, Vancouver, BC
10/22/2008	Session Chair - Human Genetic Variation, Genome Canada International Conference, Vancouver, BC
10/01/2007	Moderator, Tumor Characterization Technologies Session; International Cancer Genomics Consortium Meeting, Toronto, ON
05/2007	Co-Chair, Large-Scale Genomics Workshop, HUGO's 12th Human Genome Annual Meeting, Montreal, QC
04/13/2007	Chair, Technology Discussion, Genome BC Genomics Forum, Vancouver, BC
11/2006	Member of the Lymphoma Panel Discussion, Knowledge Translation, 2006 BC Cancer Agency Annual Cancer Conference, Vancouver, BC
02/2002	Session Chair, Mammalian Genetics, 3rd Annual Advances in Genome Biology and Technology Conference, Marco Island, FL
11/2002	Scientist Chair, Translating our science into cancer care, Session on Genomics, 2002 BC Cancer Agency Annual Cancer Conference, Vancouver, BC

PUBLIC OUTREACH / SERVICE:

03/11/2024	Interview with Susie Brown from Let's Talk Science (in partnership with the Royal Society of Canada) on their project nvolves content review for a program they are developing called *DNA Biotechnology Workshop*. Reviewed/edited the Biotech Manual in July 2024.
08/21/2023	Co-hosted the Honourable Brenda Bailey (BC Minister of Jobs, Economic Development and Innovation and Member of the Legislative Assembly for Vancouver-False Creek) during her visit to Canada's Michael Smith Genome Sciences Centre.
01/27/2023	Interview with Stuart McNish, Conversations that Matter. *Personalized Cancer Genomics*. https://youtu.be/xeOL_w3eZ0E https://vancouversun.com/health/conversations-that-matter-personalizing-cancer-treatment
12/09/2022	Personalized OncoGenomics (POG) 10th Anniversary Panel Discussion: The Future of Cancer Genomic Medicine. Moderator: Stuart McNish, Host of *Conversations That Matter* and *Conversations Live*.
11/07/2022	Recorded interview, Terry Fox Research Institute Marathon of Hope Cancer Centres Network: The Roadmap to Cure Cancer
07/28/2022	Canada Foundation for Innovation. *A Promising Future Now*. https://www.youtube.com/watch?v=Te4EITQxjPY
04/2022	Participant, Data Effect – Digital Roundtable, CityAge / Genome BC
11/11/2020	Live phone interview with Gloria Macarenko, CBC Radio's On the Coast, *Preparing for the Next Wave: Technology to Detect and Analyze SARS-CoV-2* https://www.cbc.ca/listen/live-radio/1-46-on-the-coast
04/2020	Featured in the ICGC ARGO News – ICGC Impact Makers Series (https://www.icgc-argo.org/news/11/icgc-impact-makers-series-marco-marra-canada-)
09/20/2019	Hosted the Honourable John Horgan, Premier of British Columbia, during his visit to Canada's Michael Smith Genome Sciences Centre
03/14/2019	Hosted Honorable Jody Wilson-Raybould's visit to Genome Sciences Centre, following a successful funding provided to Dr. Inanc Birol and team, from Genome Canada.
11/30/2018	Interview with Stuart McNish, *Conversations That Matter: The Legacy of Nobel Laureate Michael Smith*. https://www.youtube.com/watch?v=2eLeBvwhz3M https://vancouversun.com/news/local-news/conversations-that-matter-the-legacy-of-a-b-c-nobel-winner
09/20/2018	Interview with Randy Shore, Vancouver Sun, *How Michael Smith put B.C.'s life sciences community on the map with a Nobel Prize 25 years ago.* https://vancouversun.com/news/local-news/how-michael-smith-put-b-c-s-life-sciences-community-on-the-map-with-a-nobel-prize-25-years-ago
07/10/2018	Participated in a documentary about Dr. Nadine Caron & the Northern Biobank initiative https://www.youtube.com/watch?v=BI6Kc8zPw6c
06/2018	Featured in the *Faces of the Genome* book published by Cold Spring Harbor Laboratory Press. This book celebrates scientists who are explorers of the vast arrays of genes ("genomes") that underpin the biology of humans and every other organism. This book portrays 62 outstanding scientists, who have had an extraordinary influence on our current understanding of biology, evolution, and medical science. https://www.cshlpress.com/image.tpl?img=FacesGenome_f.jpg
04/05/2017	The Personalized OncoGenomics Project (POG) featured by Canadian Institutes of Health Research: *Researcher Profiles, Cancer Awareness Month. Is it possible to create personalized cancer treatments?* http://cihr-irsc.gc.ca/e/50284.html#s1
04/04/2017	Participated in a panel discussion at YPO Gold Event (POG Research Update at the BC Cancer Research Centre)
02/23/2017	POG featured on CBC Nature of Things with Dr. David Suzuki, *Cracking Cancer* http://www.cbc.ca/natureofthings/episodes/cracking-cancer

12/07/2016	Interview with Deborah Grainger, Journal of Precision Medicine, *Revolutionizing health care in British Columbia with precision medicine.* http://www.thejournalofprecisionmedicine.com/archive-manager/revolutionizing-healthcare-in-british-columbia-with-precision-medicine/
12/2016	Profiled by BC Cancer, *BC Cancer Agency scientists among World's Most Influential Scientific Minds* http://www.bccancer.bc.ca/about/news-stories/stories/bc-cancer-agency-scientists-listed-among-world%E2%80%99s-most-influential-scientific-minds
11/04/2016	Interview with Theral Timpson of Mendel's Pod on how to scale cancer genomics http://mendelspod.com/podcasts/cancer-genomics-canada-marco-marra-ubc/
09/06/2016	Interview with Matt Hoekstra with Peace Arch News re. Terry Fox Run http://www.peacearchnews.com/news/393311821.html#.V92SSNfGXMY.email
07/19/2016	Member of the Treehouse Childhood Cancer Initiative, a group that advocates and is committed to sharing patient genomic information in real time, to benefit children with cancer.
03/08/2016, 05/26/2015, & 11/03/2014	Organizer of the 2nd, 3rd, & 4th TFRI BC Node-MLA Dinner Events to dialogue with MLAs on the role of research on health and cancer control in British Columbia
04/15/2015	Interview with Brendan McAleer, Vancouver Sun, *Iconic Terry Fox van endures long after Marathon of Hope.* http://driving.ca/ford/auto-news/news/iconic-terry-fox-van-endures-long-after-marathon-of-hope
11/07/2014	Panelist at the Second Annual BC Business Summit "Building BC for the 21st Century - Innovation in Infrastructure", Vancouver, BC
11/03/2014	Interview with Sher-e-Punjab Radio with Kiran Aulakh re: POG
10/02/2014	Interview with Tamara Taggart of CTV re. POG
07/09/2014	Interview with Amanda Smith, The Peak, *SFU scientists recognized as "World's Most Influential Scientific Minds".* http://newspapers.lib.sfu.ca/peak-2091/peak
06/23/2014 & 05/01/2014	Participated in the planning exercise being conducted by research partnership between Northern Health, UNBC, and PHSA to enhance the way health research contributes to better health care and better health outcomes in Northern BC.
06/20/2014	Interview with Ivan Semeniuk, Globe and Mail, *World's Most Influential Scientific Minds*
06/18/2014	Meeting with Minister Andrew Wilkinson and Deputy Minister John Jacobson of the Ministry of Technology, Innovation and Citizens' Services, Province of British Columbia.
04/22/2014	Iinterview with Randy Shore, Vancouver Sun, *Tumour cell genome studies give rise to individualized therapy.* http://www.vancouversun.com/health/tumour+cell+genome+studies+give+rise+individualized+therapy/9802620/story.html
03/31/2014	Participated in Genome BC's Lunch and Learn Event for BC Legislature Members
12/05/2013	Panelist, Data and Discovery: How Technology and Analytics Are Driving Innovation session, The Data Effect.
11/2013	Profiled in International Innovation Magazine, *Dr. Marco Marra, Director of Canada's Michael Smith Genome Sciences Centre* (North America issue; Nov 2013). http://www.research-europe.com/index.php/2013/11/dr-marco-marra-director-canadas-michael-smith-genome-sciences-centre/
10/24/2013	Profiled in Vancouver Sun, Special Report: *Medical research is injecting life back into health sciences* (topic: personalized medicine; Nov 2, 2013).
10/2013	Profiled in National Cancer Institute's Office of Cancer Genomics, *Dr. Marco Marra: Pioneer and Visionary in Cancer Genomics Research.* https://ocg.cancer.gov/news-publications/e-newsletter-issue/issue-10
03/13/2013	Interview for the Guide Outfitters Association of British Columbia's DNA project.
02/21/2013	Interview with CBC Radio Early Edition, *10th Anniversary of SARS* (aired on Mar 7th, 2013).

02/05/2013	Invited attendee at the Genome BC meeting with Minister of Health, Dr. Margaret MacDiarmid.
12/04/2012	Provided testimony and took questions from the House of Commons Standing Committee on Health (Topic: A study of technological innovation, including best practices, in health care in Canada. Sub-topic: Genomics).
07/25/2012	Interviews for CKWX News 1130 and Vancouver Sun re. medulloblastoma article published in *Nature*.
09/2009	Participated in BC's Ministry of Small Business, Technology & Development's Research and Innovation Roundtable Discussion.
03/2009	Featured in *Nature*'s article about personalized genomics/medicine.
11/2006	Participated in Genome Canada's Genomics on the Hill Exhibition, Parliament Hill, Ottawa.
09/2006	Participated in the Premier's Technology Council Roundtable that discussed how British Columbia can realize the optimum economic and social benefit of technology commercialization.
08/14/2006	Interview with CBC Radio French Program re. Bovine genome press release.
05/2006	On the air telephone interview with CBC Radio's On the Coast with Priya Ramu re. potential patient benefits of the Science & Technology Platform funding from Industry Canada.
02/2004	Featured in Vancouver Sun, *People who give us hope for the world* (Feb 5, 2004 issue)
2003–2004	Profiled in The GEEE! In GENOME Exhibit, as one of 20 Canadian experts.

AWARD NOMINATIONS

Year	Name of Award	Role
2024	Health Research Foundation Medal of Honour	Co-nominator
2024	Canadian Medical Hall of Fame	Provided a reference letter
2023	Royal Society of Canada	Primary Nominator
2023	Canadian Cancer Society Robert L. Noble Award	Primary Nominator
2023	Canadian Cancer Research Alliance Outstanding Achievements in Cancer Research Award	Primary Nominator
2022	Royal Society of Canada	Primary Nominator
2022	University of British Columbia Faculty of Applied Science Dean's Medal of Distinction	Primary Nominator
2022	Canadian Medical Hall of Fame	Primary Nominator
2021	YWCA Women of Distinction Award	Primary Nominator
2021	Canadian Cancer Society Bernard and Francine Dorval Prize	Primary Nominator
2021	Doctors of BC Terry Fox Medal	Primary Nominator
2021	Order of British Columbia	Nominator
2020	Canadian Cancer Society Inclusive Excellence Prize	Nominator
2020	Canadian Cancer Society Bernard and Francine Dorval Prize	Nominator
2020	Royal of Society of Canada Fellowship	Primary nominator
2020	Canadian Cancer Society Bernard and Francine Dorval Prize	Provided a reference letter
2020	Canada Research Chair Tier 2 renewal	Provided a reference letter
2020	Royal of Society of Canada Fellowship	Provided a reference letter
2020	Genome BC Award for Scientific Excellence	Nominator
2020	Japan Prize	Provided a reference letter
2020	McGill University Principal's Prize for Outstanding Emerging Researcher	Provided a reference letter
2019	Royal Society of Canada, College of New Scholars, Artists and Scientists	Provided a reference letter
2019	Canadian Cancer Society Robert L. Noble Prize	Provided a reference letter
2019	Royal of Society of Canada	Co-nominator
2018	Canada Research Chair Tier 2 application	Provided a reference letter
2018	Canadian Cancer Society Bernard and Francine Dorval Prize	Provided a reference letter

2018	Royal Society of Canada, College of New Scholars, Artists and Scientists	Provided a reference letter
2018	Terry Fox Medal Award	Co-nominator
2018	Royal of Society of Canada Fellowship	Primary nominator
2018	Royal of Society of Canada Fellowship	Co-nominator
2017	Canada Research Chair Tier 2 application	Provided a reference letter
2017	University of British Columbia Killam Mentoring Award	Nominator
2017	Ontario Ministry of Research, Innovation and Science Early Researcher Award	Provided a reference letter
2016	Research Canada Leadership Award	Nominator
2016	Bill and Marilyn Webber Lifetime Achievement Award	Nominator
2016	Royal of Society of Canada Fellowship	Primary nominator
2015	University of British Columbia Killam Research Prize	Co-nominator
2014	Dan David Prize	Nominator
2014	Canadian Academy of Health Sciences Fellowship	Primary nominator
2013	Canadian Cancer Society Robert L. Noble Prize	Nominator
2012	University of British Columbia Killam Teaching Prize	Nominator
2012	Simon Fraser University Distinguished Community Leadership Award	Nominator
2011	Simon Fraser University Outstanding Alumni Award	Nominator
2011	Royal of Society of Canada Fellowship	Co-nominator
2011	Order of BC	Provided a reference letter
2011	Simon Fraser University Distinguished Community Leadership Award	Nominator
2011	Royal of Society of Canada Fellowship	Primary nominator
2011	University of British Columbia Killam Research Prize	Co-nominator
2010	International Society for Computational Biology Overton Prize	Nominator
2010	Royal of Society of Canada Fellowship	Co-nominator
2010	Eric Jenett Project Management Excellence Award	Nominator
2009	Simon Fraser University Outstanding Alumni Award	Nominator
2008	Terry Fox Young Investigator Award	Nominator
2007	Genome BC Award for Scientific Excellence	Nominator
2006	Canada's Top 40 Under 40	Nominator
2004	Simon Fraser University Outstanding Alumni Award	Nominator

EDITORIAL RESPONSIBILITIES:

2004 – 2009	Member, Editorial Committee, ***Annual Review of Genomics and Human Genetics***
2000 – 2003	Associate Editor, Editorial Board, ***Physiological Genomics***
1999 – 2005	Member, Editorial Board, ***Genome Research***

SOCIETY MEMBERSHIPS:

2015 – Present	Canadian Hematology Society
2006 – Present	American Society of Hematology
2005 – Present	The American Society of Human Genetics
2005 – Present	American Association for Cancer Research
2004 – Present	The American Association for the Advancement of Science
2008 – 2009	Human Genome Variation Society

TEACHING (Lectures):

Date	Program / Course number	Hours taught	Class size
02/09/2024	MEDG 505 (Genome Analysis)	3.0	15
04/04/2023	STAT540 (Statistical Methods for High Dimensional Biology	1.5	
03/31/2023	MEDD 448 Transition into Postgraduate Education and Medical Practice	1.0	295
03/25/2023	MEDG 595 – Emerging Genomics Topics	1.0	~10
02/17/2023 (2022W2)	MEDG 505 (Genome Analysis)	3.0	18
12/07/2022	MEDG 595 Learning Lounge	1.0	25
10/24/2022 (2021W1)	MEDG 420 (Human Genomics & Medical Genetics)	2.0	~17
04/08/2022 (2021W2)	MEDD 448 Transition into Postgraduate Education and Medical Practice	1.0	~288
02/18/2022 (2021W2)	MEDG 505 (Genome Analysis)	3.0	18
12/07/2021 (2021W1)	MEDG 595 (Emerging Genomics Topics Certificate Program)	1.0	14
04/15/2021 & 04/22/2021 (2020W2)	GSAT 502 (Advanced Concepts in Genome Science and Technology)	3.0	14
04/13/2021 (2020W2)	MEDG 595 (Emerging Genomics Topics Certificate Program)	1.0	43
03/05/2021 (2020W1)	MEDG 505 (Genome Analysis)	3.0	17
11/16/2020 (2020W1)	MEDG 420 (Human Genomics and Medical Genetics)	2.0	17
11/03/2020	Data Science & Health 2020 Conference (Data Science: How to Use it in Health Research, Topic: Applications in Personalized Oncogenomics)	20 min	N/A
03/13/2020 (2019W2)	MEDG 505 (Genome Analysis)	3.0	22
11/06/2019 (2019W1)	MEDG 420 (Human Genomics & Medical Genetics)	1.5	22
04/02/2019 (2018W2)	Science One	1.0	66
01/31/2019 & 01/24/2019 (2018W2)	GSAT 502 (Advanced Concepts in Genome Science and Technology)	3.0	7
11/07/2018 (2018W1)	MEDG 420 (Human Genomics & Medical Genetics)	1.5	16
03/16/2018 (2017W2)	MEDG5 05 (Genome Analysis)	3.0	12
03/08/2018 & 03/01/2018 (2017W2)	GSAT 502 (Advanced Concepts in Genome Science and Technology)	2.5	14
10/23/2017 (2017W1)	MEDG 420 (Human Genomics & Medical Genetics)	1.5	12
03/09/2017 & 03/02/2017 (2016W2)	GSAT 502 (Advanced Concepts in Genome Science and Technology)	2.5	10

02/03/2017 (2016W2)	MEDG 505 (Genome Analysis)	3.0	18
11/09/2016 (2016W1)	MEDG 420 (Human Genomics & Medical Genetics)	1.5	12
03/03/2016 & 02/25/2016 (2015W2)	GSAT 502 (Advanced Concepts in Genome Science and Technology)	2.5	10
01/29/2016 (2015W2)	MEDG 505 (Genome Analysis)	3.0	14
12/02/2015 (2015W1)	MBB 801 interview (featured faculty for this seminar course focused on career development) Simon Fraser University	1.0	9
11/04/2015 (2015W1)	MEDG 420 (Human Genomics & Medical Genetics)	1.5	18
03/27/2015 (2014W2)	MEDG 505 (Genome Analysis)	3.0	12
04/02/2015 & 03/26/2015 (2014W2)	GSAT 502 (Advanced Concepts in Genome Science and Technology)	3.0	11
11/05/2014 (2014W1)	MEDG 420 (Human Genomics & Medical Genetics)	1.5	16
04/03/2014 & 03/27/2014 (2013W2)	GSAT 502 (Advanced Concepts in Genome Science and Technology)	3.0	14
01/31/2014 (2013W2)	MEDG 505 (Genome Analysis)	3.0	19
10/30/2013 (2013W2)	MEDG 420 (Human Genomics & Medical Genetics)	1.5	14
03/28/2013 & 03/21/2013 (2012W2)	GSAT 502 (Advanced Concepts in Genome Science and Technology)	3.0	18
03/08/2013 (2012W2)	MEDG 505 (Genome Analysis)	3.0	18
10/03/2012 (2012W1)	MEDG 420 (Human Genomics & Medical Genetics)	1.5	18
03/30/2012 (2011W2)	MBB 446/746 (Cancer Genetics and Cell Death/Survival) Simon Fraser University	2.0	50
03/20/2012 (2011W2)	GSAT 502 (Advanced Concepts in Genome Science and Technology)	2.5	15
01/27/2012 (2011W2)	MEDG 505 (Genome Analysis)	3.0	21
01/25/2012 (2011W2)	MEDG 420 (Human Genomics & Medical Genetics)	1.0	17
03/21/2011 (2010W2)	GSAT 502 (Advanced Concepts in Genome Science and Technology)	2.5	6
03/04/2011 (2010W2)	MEDG 505 (Genome Analysis)	3.0	19
02/28/2011 (2010W2)	MEDG 420 (Human Biochemical & Molecular Genetics)	2.0	16
03/25/2010 (2009W2)	Science One	1.0	63
03/12/2010	MEDG 505 (Genome Analysis)	3.0	22

(2009W2)			
02/10/2010 (2009W2)	MEDG 420 (Human Biochemical & Molecular Genetics)	2.0	14
12/07/2009 & 11/30/2009 (2009W1)	GENE 502 (Genetics)	1.5	10
04/02/2009 (2008W2)	MEDG 421 (Genetics & Cell Biology of Cancer)	1.5	32
03/23/2009 (2008W2	MEDG 420 (Human Biochemical & Molecular Genetics)	1.5	18
02/26/2009 (2008W2)	Science One	1.0	73
02/13/2009 (2008W2)	MEDG 505 (Genome Analysis)	3.0	21
11/13/2008 (2008W1)	MBB 440/839 (Special Topics in Molecular Biology & Biochemistry – Cell Death & Cell Survival) Simon Fraser University	2.0	35
04/10/2008 (2007W2)	Science One (Title: Personal Genomics)	1.0	73
03/26/2008 (2007W2)	MEDG 420 (Human Biochemical & Molecular Genetics)	1.0	16
02/01/2008 (2007W2)	MEDG 505 (Genome Analysis)	3.0	17
03/23/2007 (2006W2)	MEDG 505 (Genome Analysis)	3.0	18
03/12/2007 (2006W2)	MEDG 521 (Molecular & Cell Biology of Cancer)	1.5	24
01/17/2007 (2006W2)	MEDG 420 (Human Biochemical & Molecular Genetics	2.0	22
03/16/2006 (2005W2)	MEDG 505 (Genome Analysis)	3.0	24
03/06/2006 (2005W2)	MEDG 521 (Molecular & Cell Biology of Cancer)	1.5	20
01/09/2006 (2005W2)	MEDG 420 (Human Biochemical & Molecular Genetics)	2.0	20
02/2005 (2004W2)	MEDG 505 (Genome Analysis)	3.0	20
01/2005 (2004W2)	MEDG 420 (Human Biochemical & Molecular Genetics)	4.0	20
02/26/2004 (2003W2)	ISCI 4481 (Medical Innovation & Healthcare Politics)	2.0	-
2003 (2003W2)	MEDG 505 (Genome Analysis)	3.0	-
2002 (2001W2)	MEDG 505 (Genome Analysis)	3.0	-
03/30/2000 (1999W2)	GENE 502 (Genetics)	1.5	16
1992	Biology 302 and Biology 401 (Biochemistry) Simon Fraser University	-	-
1990	Biology 302 (Genetic Analysis) Simon Fraser University	-	-

1988	Biology 302 (Genetic Analysis) Simon Fraser University	-	-

CONTRIBUTIONS TO THE TRAINING OF HIGHLY QUALIFIED PERSONNEL:

ROTATION STUDENTS

From	To	Student	Role	Program
03/07/2016	05/06/2016	Emma Titmuss	Rotation supervisor	MSc (Genome Science and Technology Program), UBC
01/05/2015	04/30/2015	James Topham	Rotation supervisor	MSc (CIHR Bioinformatics Program), UBC
09/01/2013	07/31/2014	Rebecca Johnson	Temporary supervisor	MSc (CIHR Bioinformatics Program), UBC
03/04/2013	05/03/2013	Adi Steif	Rotation supervisor	MSc (Genome Science and Technology), UBC
03/2012	05/2012	Marlo Firme	Rotation supervisor	MSc (Genome Science and Technology), UBC
03/2012	05/2012	Tejomayee Singh	Rotation supervisor	MSc (Genome Science and Technology), UBC
01/2011	04/2011	Emilia Lim	Rotation supervisor	Rotation Student (CIHR Bioinformatics Program), UBC
09/2009	08/2010	Yaojie Chen	Rotation supervisor	MSc (CIHR Bioinformatics Program), UBC
05/2009	08/2009	Rodrigo Goya	Rotation supervisor	Rotation Student (CIHR Bioinformatics Program), UBC
01/2009	04/2009	Bora Uyar	Rotation supervisor	Rotation Student (CIHR Bioinformatics Program), SFU
10/2009	12/2010	Mark Okada	Rotation supervisor	Rotation Student (CIHR Bioinformatics Program), SFU
09/2008	12/2008	Andrew McPherson	Rotation supervisor	Rotation Student (CIHR Bioinformatics Program), SFU
09/2007	12/2006	Olena Morozova	Rotation supervisor	Rotation Supervisor (CIHR Bioinformatics Program), UBC
01/2006	04/2006	Ryan Morin	Rotation supervisor	Rotation Supervisor (CIHR Bioinformatics Program), UBC

GRADUATE STUDENTS

Years	Student / Research area	Program
09/07/2021 – Present	Xiao Yu (Cathy) Yan **Research area:** Single-cell analysis of metastatic non-small cell lung cancer	PhD (Genome Science and Technology Program)
09/07/2021 – Present	Signe MacLennan **Research area:** ecDNAs in HPV+ and HPV- cervical and head and neck cancers	PhD (Medical Genetics Graduate Program)
01/02/2019 – 03/15/2024	Yuka Takemon **Research area**: *In silico* discovery of cancer cell vulnerabilities	PhD (Genome Science and Technology Program)

	Current position: Research Associate, Genome Sciences Centre, Michael Smith Laboratories, University of British Columbia	
02/13/2018 – 02/20/2024	Vanessa Porter **Research area**: Discovery of HPV-Associated Genomic Alterations in Cervical Cancer **Current position:** Postdoctoral Fellow, Genome Sciences Centre, BC Cancer	PhD (Medical Genetics Graduate Program)
10/03/2016 – 01/30/2023	Su min (Lisa) Wei **Research area**: Characterizing gene expression patterns associated with heterogeneity and relapse in pediatric acute myeloid leukemia **Current position:** Computational Biologist, Dana-Farber Cancer Institute, Boston, MA	MSc (Bioinformatics Graduate Program)
09/02/2014 – 09/12/2021	Veronique LeBlanc **Research area:** Genomic Characterization of Inter- and Intra-Tumour Heterogeneity in Primary Adult Diffuse Gliomas and Associated Disease Models **Current position:** Network Program Manager and Scientific Writer, Terry Fox Research Institute	PhD (Genome Science & Technology Program
09/01/2012 – 12/17/2020	Hye-Jung (Elizabeth) Chun **Research area**: Molecular Characterization of Rhabdoid Tumours from Multiple Anatomical Sites **Current position**: Research Associate, Peter Park Lab, Harvard Medical School	PhD (Bioinformatics Graduate Program)
09/06/2016 – 06/02/2020	Stephen Dongsoo Lee **Research area:** Characterization of the Effects of CIC Loss and Neomorphic IDH1 Mutation on the Transcriptome and Epigenome **Current position**: Informatics Analyst, Zymeworks Inc	MSc (Genome Science & Technology Program)
09/06/2016 – 04/06/2018 (Withdrawn)	Anna Cavalla **Research area:** Characterizing Cancer Transcriptomes at the Single Cell Level	MSc (Bioinformatics Graduate Program)
05/09/2016 – 07/13/2018	Emma Titmuss **Research area:** A case study of apparent immune activation following treatment of a colorectal cancer patient with an angiotensin receptor blocker	MSc (Genome Science and Technology Program)

	Current position: Bioinformatician, Medical Oncology, BC Cancer	
09/2009 – 12/2017	Rodrigo Goya *(co-supervised with Dr. Irmtraud Meyer)* **Research area:** Bioinformatic Approaches for Identifying Single Nucleotide Variants and Profiling Alternative Expression in Cancer Transcriptomes **Current position**: Bioinformatics Engineer, AbCellera	PhD (Bioinformatics Graduate Program)
09/2015 – 08/2017	James Topham **Research area:** Comprehensive and Integrative Analysis of the KMT2D Regulome **Current position**: Head of Bioinformatics, Pancreas Centre BC	MSc (Bioinformatics Graduate Program)
05/2012 – 12/2014	Marlo Firme **Research area**: The Regulatory Landscape of the Glioma-associated Transcription Factor Capicua. **Current position**: Vancouver lead for the Citizens' Climate Lobby (volunteer work)	MSc (Genome Science & Technology Program)
09/2011 – 03/31/2016	Emilia Lim **Research area**: miRNA Sequence Analysis Reveals Cancer Subtypes That Correlate With Tumour Characteristics and Patient Outcomes **Current position**: Assistant Professor, Biochemistry and Molecular Biology, University of British Columbia	PhD (Bioinformatics Graduate Program)
09/2011 – 04/30/2015	Ryan Huff **Research area**: Generation and Characterization of a Lysine (K)-Specific Methyltranferase 2D Knockout Human Cell Line **Current position:** PhD student, University of British Columbia	MSc (Medical Genetics Graduate Program)
09/2010 – 06/26/2015	Julia (Pon) Naso **Research area**: The MEF2B Regulatory Network **Current position**: Anatomic Pathologist, Rochester, MN	MD/ PhD Program
09/2008 – 01/2012	Ryan Morin **Research area**: Mutation Discovery and Characterization in Lymphoid Neoplasms using Massively Parallel RNA and DNA Sequencing **Current position**: Professor, Molecular Biology and Biochemistry, Simon Fraser University; Distinguished Scientist, Genome Sciences Centre, BC Cancer	PhD (Bioinformatics Graduate Program)

09/2006 – 06/2012	Olena Morozova **Research area**: Genomic studies of the normal and malignant neural crest **Current position:** Associate Professor, Molecular, Cell, & Development Biology, University of California, Santa Cruz	PhD (Bioinformatics Graduate Program)
09/2005 – 12/2007	Jaswinder Khattra **Research area**: Cloning and annotation of novel transcripts from human ES cells **Current position**: Clinical Molecular Diagnostics Scientist, Molecular Diagnostics, Vancouver, Canada	MSc (Genetics Graduate Program)
09/2005 – 10/2007	Ryan Morin **Research area**: Methods for microRNA profiling and discovery using massively parallel sequencing **Current position**: Professor, Molecular Biology and Biochemistry, Simon Fraser University; Distinguished Scientist, Genome Sciences Centre, BC Cancer	MSc (Bioinformatics Graduate Program)
09/2004 – 12/2010	Sorana Morrissy (formerly Anca Petrescu) **Research area**: Bioinformatic Analysis of Cis-Encoded Antisense Transcription **Current position**: Assistant Professor, Biochemistry and Molecular Biology, University of Calgary	PhD (Genetics Graduate Program)
09/2004 – 01/2010	Malachi Griffith **Research area**: Methods for transcript variant discovery and alternative expression analysis – application to the study of fluorouracil resistance in colorectal cancer **Current position:** Associate Professor, Washington University School of Medicine in St. Louis; and Assistant Director, The Elizabeth H. and James S. McDonell Genome Institute	PhD (Medical Genetics Graduate Program)
09/2004 – 12/2009	Trevor Pugh **Research area**: Analysis of primary human cancers: from single genes to whole transcriptomes **Current position**: Associate Professor, University of Toronto; Senior Scientist, Princess Margaret Cancer Centre; Senior Investigator & Director, Genomics, Ontario Institute for Cancer Research	PhD (Medical Genetics Graduate Program)
09/2003 – 07/2012	Noushin Farnoud **Research area**: Computational Tools for CNV Detection Using Probe-level Analysis of Affymetrix SNP Arrays - Application to the Study of CNVs in Follicular Lymphoma	PhD (Genetics Graduate Program)

	Current position: Senior Bioinformatics Engineer II, Memorial Sloan-Kettering Cancer Center	
09/2003 – 08/2008	Ying-Chen (Claire) Hou *(co-supervised with Dr. Sharon Gorski)* **Research area**: Molecular mechanisms underlying the crosstalk between autophagy and apoptosis **Current position**: ABMGG Fellow, Laboratory Genetics and Genomics at Washington University School of Medicine in St. Louis	PhD (Genetics Graduate Program)
01/2002 – 05/2008	Suganthi Chittaranjan *(co-supervised with Dr. Sharon Gorski)* **Research area**: A functional genomics approach identifies novel genes involved in steroid hormone-induced programmed cell death in *Drosophila*. **Current position**: Staff Scientist, Genome Sciences Centre, BC Cancer	PhD (Genetics Graduate Program)
09/2001 – 07/2008	Ian Bosdet *(co-supervised with Dr. Sharon Gorski)* **Research area**: Identification of echinus and characterization of its role in Drosophila eye development **Current position:** Clinical Assistant Professor, UBC; Molecular Geneticist, BC Cancer	PhD (Genetics Graduate Program)
09/2001 – 12/2005	Angelique Schnerch *(co-supervised with Dr. Steven Jones*) **Research area**: Analysis of Undifferentiated Human Embryonic Stem Cell Lines using Serial Analysis of Gene Expression **Current position:** Works at Arcadis (formerly IBI Group Architects)	MSc (Medical Genetics Graduate Program)

POSTDOCTORAL FELLOWS

Dates	**Fellow / Current Position**	**Research Topic**
02/21/2024 – Present	Vanessa Porter	Discovery of HPV-Associated Genomic Alterations in Cervical Cancer
01/04/2022 – Present	Michelle Ng	3D Genome Architecture in cervical cancer
09/13/2021 – 09/13/2022	Veronique LeBlanc **Current position**: Network Program Manager and Scientific Writer, Terry Fox Research Institute	Multi-omic characterization of glioblastoma multiforme
09/01/2020 – 07/31/2023	Sander Lambo	Single cell genomics of primary, remission and relapsed pediatric AML

	Current position: Postdoctoral Fellow, Dana-Farber Cancer Institute, Boston, MA	
10/31/2016 – 09/30/2023	Dan Jin **Current position**: Research Associate, Marra lab, Michael Smith Laboratories, University of British Columbia	The regulomes and transcriptomes of malignant rhabdoid tumpurs
03/01/2021 – 10/15/2021	Hye-Jung (Elizabeth) Chun **Current position**: Research Associate, Peter Park Lab, Harvard Medical School, Boston, MA	Rhabdoid tumour genomics
12/02/2013 – 11/27/2018	Alessia Gagliardi	Genomic heterogeneity of cervical cancer
04/01/2016 – 03/31/2017	Emilia Lim **Current position**: Assistant Professor, Biochemistry and Molecular Biology, UBC	Comprehensive Sequence Analysis of Pediatric Acute Myeloid Leukemia
02/11/2014 – 02/10/2017	Isabel Serrano-Martinez **Current position**: Managing Director, Marathon of Hope Cancer Centres Network, Terry Fox Research Institute	FOXO1 mutations are associated with inferior survival in DLBCL
07/2012 – 02/28/2013	Noushin Farnoud **Current position:** Senior Bioinformatics Engineer II, Memorial Sloan-Kettering Cancer Center	Software development for copy number analysis
01/2012 – 07/2012	Ryan Morin **Research title:** Genomic characterization of Diffuse Large B Cell Lymphoma patients and cell lines **Current position**: Professor, Molecular Biology and Biochemistry, Simon Fraser University; Distinguished Scientist, Genome Sciences Centre, BC Cancer	Diffuse large B-cell lymphoma
11/2011 – 03/31/2016	Farah Zahir **Research title**: Massively Parallel Genomic Sequencing for Clinical Identification of Mutations That Cause Intellectual Disability (co-supervised with Jan Friedman) **Current position**: Honorary Associate Member, Department of Medical Genetics, University of British Columbia	Genomic diagnostics
01/2011 – 09/2011	Sorana Morrissy **Research title**: Bioinformatic analysis of the relationship between natural antisense transcription and alternative splicing in cancer	Antisense transcription and alternative splicing

	Current position: Assistant Professor, Biochemistry and Molecular Biology, University of Calgary	
03/2010 – 02/2011	Malachi Griffith **Research title**: Alternative transcript diversity in models of cancer progression **Current position:** Associate Professor, Washington University School of Medicine in St. Louis; and Assistant Director, The Elizabeth H. and James S. McDonell Genome Institute	Alternative splicing
09/2009 – 10/30/2015	Jill Mwenifumbo **Research title**: The evolution of 5-FU drug resistance in colorectal cancer **Current position**: Bioinformatician, CAUSES Research Clinic, BC Children's Hospital Research Institute	Colorectal cancer
09/2009 – 09/30/2012	Maria Mendez-Lago **Research title**: Functional characterization of EZH2 mutations **Current position**: Head of Genomics, Core Facilities and Technology, Institute of Molecular Biology, Mainz, Germany	Follicular lymphoma
01/2009 – 02/2010	Ian Bosdet **Research title:** Genome analysis of pre- and post-treatment lung cancers from patients in a phase II clinical trial of first-line erlotinib **Current position:** Clinical Assistant Professor, Department of Pathology and Laboratory Medicine, UBC; Clinical Scientist, BC Cancer	Lung Cancer
05/2004 – 03/2006	Sean Rogers **Research title**: Gene expression of hESC	Gene Expression
12/2003 – 03/2006	Deryck Persaud **Research title**: Cloning & characterization of novel hESC genes **Current position:** Owner, Infogenetica Bioinformatics, and Biotechnology Consultant	DNA Mapping
02/2000 – 10/2003	Gregory Vatcher **Current position:** Senior Scientist, Gene AC, Beijing, China	Functional Genomics

TRAINEE SCHOLARSHIPS & FELLOWSHIPS:

Date	**Trainee**	**Award**	**Granting Agency**	**CDN$**
01/01/2024 - 12/31/2026	**Signe MacLennan**	CIHR Canada Graduate Scholarship (Doctoral)	CIHR	105,000
09/01/2023 – 09/01/2026	**Michelle Ng, PhD**	Fellowship	CIHR	120,000 +15,000 R&T
09/01/2023 – 08/31/2026	**Michelle Ng, PhD**	Research Trainee Award	MSHRBC	89,250 +2,250 R&T
09/01/2021 – 08/31/2024	**Sander Lambo, PhD**	Research Trainee Award	MSHRBC	135,000 + 13,500 R&T
09/01/2021-08/31/2022	**Signe MacLennan**	CIHR Canada Graduate Scholarship (Master's)	CIHR	17,500
09/01/2022 – 08/31/2023	**Cathy Yan**	CIHR Canada Graduate Scholarship (Master’s)	CIHR	17,500
2020-2022	**Yuka Takemon**	President’s Academic Excellence Initiative PhD Award	UBC	1,080
09/01/2019 - 08/31/2023	**Yuka Takemon**	Four-Year Doctoral Fellowship	UBC	72,800 + full tuition
09/01/2019 - 08/31/2023	**Yuka Takemon**	International Tuition Award	UBC	Full tuition
09/01/2019 - 08/31/2010	**Su min (Lisa) Wei**	BC Graduate Scholarship	UBC	15,000
05/06/2019	**Yuka Takemon**	Faculty of Science Graduate Award (2019S session)	UBC	1,858.92
05/06/2019	**Yuka Takemon**	International Tuition Award (2019S session)	UBC	1,066.66
01/03/2019	**Yuka Takemon**	International Tuition Award (2018W session)	UBC	1,066.67
01/02/2019	**Yuka Takemon**	Faculty of Science Graduate Award (2018W session)	UBC	1,801.56
04/2018 – 08/2018	**Ishika Luthra**	BC Cancer Studentship	BC Cancer	6,000
01/2018 - 03/2020	**Vanessa Porter**	CIHR Canada Graduate Scholarship (Doctoral Award)	CIHR	90,000 + 1,500 R&T
01/2018 – 12/2021	**Vanessa Porter**	UBC Four Year Fellowship	UBC	22,000/yr
11//2016 – 05//2017	**Hye-Jung (Elizabeth) Chun**	Roman M. Babicki Fellowship in Medical Research	UBC	25,000
09/2016 – 08/2018	**Veronique LeBlanc**	Killam Doctoral Scholarship	UBC	50,000 + 2,000 R&T
05/01/2016 – 04/30/2019	**Veronique LeBlanc**	Vanier Canada Graduate Scholarship	CIHR	50,000/yr
05/01/2016 – 04/30/2020	**Veronique LeBlanc**	Four-Year Fellowship	UBC	18,200
09/01/2015 – 04/30/2016	**Emilia Lim**	PhD Student Fellowship	UBC	12,133.34

05/01/2015 – 04/30/2016	**Veronique LeBlanc**	Canada Graduate Scholarship (Master's)	CIHR	17,500
09/2014 – 08/2015	**Veronique LeBlanc**	Faculty of Science Graduate Award	UBC	4,555
09/01/2012 – 08/31/2013	**Ryan Huff**	Frederick Banting and Charles Best Canada Graduate Scholarship (Master's)	CIHR	17,500
09/01/2012 – 08/31/2013	**Farah Zahir, PhD**	Bluma Tischler Postdoctoral Fellowship	UBC	20,400
09/01/2012 – 08/31/2015	**Emilia Lim**	Frederick Banting and Charles Best Canada Graduate Scholarship (Doctoral Award)	CIHR	35,000/yr
07/01/2012 – 06/30/2015	**Farah Zahir**	Postdoctoral Fellowship	CIHR	40,000/yr
05/01/2012 – 04/30/2015	**Julia Pon**	Vanier Canada Graduate Scholarship	CIHR	50,000/yr
05/01/2012 – 08/31/2012	**Daisy Ji**	BC Cancer Studentship	BCCF/CBCF	6,000
09/03/2011 – 04/30/2012	**Olena Morozova**	Roman M Babicki Fellowship in Medical Research	UBC	20,000
09/01/2011 – 08/31/2013	**Maria Mendez-Lago, PhD**	Postdoctoral Fellowship	MSFHR	35,000/yr + 4,000 R&T
09/01/2011 – 08/31/2014	**Rodrigo Goya**	Vanier Canada Graduate Scholarship	CIHR	50,000/yr
09/01/2011 – 08/31/2014	**Jill Mwenifumbo, PhD**	Postdoctoral Fellowship	MSFHR	58,334 + 5,333 R&T
08/01/2011 – 07/31/2013	**Farah Zahir, PhD**	NeuroDevNet Postdoctoral Fellowship	NeuroDevNet	20,000/yr + 2,500 R&T
408/01/2011 – 08/31/2012	**Maria Mendez-Lago, PhD**	Estancias de movilidad posdocto ral en centros extranjeros del Programa Nacional de Movilidad de Recursos Humanos de Investigación	Ministerio de Educacion de España	30,960 Euro/yr
05/01/2011 – 04/30/2013	**Jill Mwenifumbo, PhD**	Postdoctoral Fellowship	CIHR	45,000/yr
05/2011 – 06/2011	**Pierre Cheung**	BC Cancer Studentship	BCCF/CBCF	6,000
09/01-2010 – 08/31/2016	**Julia Pon**	Scriver Family MD/PhD Studentship Award	CIHR	14,667/yr
09/01/2009 – 08/31/2013	**Ryan Morin**	Doctoral Fellowship	UBC	80,000
10/2009 – 09/2011	**Ryan Morin**	Senior Graduate Studentship	MSFHR	14,000
07/2009	**Pierre Cheung**	BC Clinical Genomics Network Studentship	BCCGN	3,750
05/01/2009 – 04/30/2012	**Ryan Morin**	Vanier Canada Graduate Scholarship	CIHR	50,000/yr
04/2009 – 08/2009	**Alison Lee**	BC Cancer Studentship	BCCF	5,400
09/01/2008 – 03/31/2011	**Olena Morozova**	Alexander Graham Bell Canada Postgraduate Scholarship - Doctoral	NSERC	105,000

09/01/2008 – 08/31/2010	**Olena Morozova**	Junior Graduate Studentship	MSFHR	19,000
09/01/2008 – 08/31/2010	**Malachi Griffith**	Research Studentship	NCIC	45,000 + 3,000 R&T
05/01/2008 – 04/30/2010	**Jaswinder Khattra**	Senior Graduate Studentship	MSFHR	38,250
09/01/2007 – 08/31/2008	**Olena Morozova**	Julie Payette Postgraduate Scholarship – Master's	NSERC	25,000
05/01/2007 – 04/30/2010	**Trevor Pugh**	Senior Graduate Studentship	MSFHR	67,500
56 04/01/2007 – 10/31/2007	**Ryan Morin**	Junior Graduate Studentship	MSFHR	22,500
09/01/2006 – 08/31/2009	**Malachi Griffith**	Senior Graduate Studentship	MSFHR	21,000 + 6,000 R&T
09/01/2006 – 08/31/2009	**Sorana Morrissy**	Doctoral Research Award	CIHR	105,000
09/01/2006 – 03/31/2007	**Trevor Pugh**	University Graduate Fellowship	UBC	16,000
01/012006 – 01/01/2009	**Trevor Pugh**	PhD Tuition Award	UBC	11,358
2006	**Trevor Pugh**	IG Grants for Short-Term Competition	CIHR	5,800
10/01/2005 – 10/01/2006	**Trevor Pugh**	Lung Cancer Research Fellowship	Eli Lilly Canada (BCCA)	37,000
09/01/2005 – 08/31/2006	**Sorana Morrissy**	Graduate Scholarship - Master's	CIHR	17,500
04/01/2005 – 05/31/2007	**Sorana Morrissy**	Junior Graduate Studentship	MSHFR	25,458
09/01/2004 – 08/31/2008	**Malachi Griffith**	Postgraduate Scholarship - Doctoral	NSERC	80,300
09/01/2004 – 08/31/2008	**Malachi Griffith**	PhD Tuition Award	UBC	12,800
09/01/2004 – 08/31/2006	**Malachi Griffith**	Junior Graduate Studentship	MSFHR	50,000
09/01/2004 – 08/31/2005	**Malachi Griffith**	Graduate Entrance Scholarship	UBC	3,170
05/01/2004 – 04/30/2005	**Suganthi Chittaranjan**	Senior Graduate Studentship	MSFHR	2,500
09/01/2003 – 08/31/2005	**Malachi Griffith**	Postgraduate Scholarship - Master's	NSERC	17,300/yr
04/01/2002 – 03/31/2004	**Gregory Vatcher, PhD**	Postdoctoral Fellowship	MSFHR	39,000
2000 - 2002	**Gregory Vatcher, PhD**	Postdoctoral Fellowship	NSERC	35,000/yr

TRAINEE TRAVEL AWARDS & STUDENTSHIPS:

Date	**Trainee**	**Award**	**Granting Institution**	**CDN $**
05/06/2024	**Xiao Yu (Cathy) Yan**	GSAT Travel Award to present at Gordon Research Conference	University of Brith Columbia	1,500

03/2023	**Yuka Takemon**	GSAT Travel Award to present at AGBT, Florida	University of Britsh Columbia	1,500
05/2021-06/2021	**Xiao Yu (Cathy) Yan**	FOM Summer Student Research Program ***(Declined)***	University of Britsh Columbia	2,800
05/03/2021-08/20/2021	**Xiao Yu (Cathy) Yan**	BC Cancer Studentship	BC Cancer	6,000
05/01/2021-08/31/2021	**Xiao Yu (Cathy) Yan**	GSAT Summer Studentship ***(Declined)***	University of British Columbia	4,050
05/10/2021-08/27/2021	**Signe MacLennan**	NSERC Undergraduate Student Research Award	Natural Sciences and Engineering Research Council of Canada and University of British Columbia	7,500
2021	**Yuka Takemon**	John Bosdet Memorial Fund Award	BC Cancer Foundation	292
03/23/2020	**Vanessa Porter**	Travel Award (International Papillomavirus Conference)	Canadian Cancer Society Research Institute	2,000
01/03/2020	**Vanessa Porter**	Early Career Investigator Travel Award	International Papillomavirus Society	500 Euros + free registration
03/2018	**Hye-Jung (Elizabeth) Chun**	TCG Trainee Collaboration and Travel Award (International Rhabdoid Tumour Meeting)	University of British Columbia	1,565
09/2017	**Su min (Lisa) Wei**	TCG Travel Award (ASH Annual Meeting)	University of British Columbia	2,250
09/2017	**Hye-Jung (Elizabeth) Chun**	CEEHRC Travel Award (4th Canadian Conference on Epigenetics)	Canadian Epigenetics, Environment and Health Research Consortium Network	500
06/2017	**Su min (Lisa) Wei**	Travel Award (Pathway and Network Analysis of -Omics Data Workshop)	Canadian Bioinformatics Workshop	1,300
03/2017	**Hye-Jung (Elizabeth) Chun**	Travel Award (2nd European Cancer Epigenetics Conference in Heidelberg, Germany)	UBC Faculty of Medicine	1,000
03/15/2017	**Hye-Jung (Elizabeth) Chun**	CEEHRC Travel Award (2nd European Cancer Epigenetics Conference in Heidelberg, Germany)	Canadian Epigenetics, Environment and Health Research Consortium Network	1,000
2/22/2017	**Hye-Jung (Elizabeth) Chun**	Faculty of Science Graduate Award	UBC	500
07/28/2015	**Hye-Jung (Elizabeth) Chun**	Travel Award (CSHL meeting on Epigenetics & Chromatin)	Canadian Cancer Society Research Institute	2,000

05/16/2015	**James Topham**	GSC Graduate Student Travel Award (for the ISMB 2016 Meeting)	John Bosdet Memorial Fund (BCCF)	1,500
11/17/2015	**Emilia Lim**	Travel Award	American Society of Hematology	500
09/01/2015 – 04/30/2016	**Hye-Jung (Elizabeth) Chun**	Faculty of Science Graduate Award	UBC	3,236.22
07/2015	**Hye-Jung (Elizabeth) Chun**	Travel Award (Canadian Cancer Research Conference) Note: Declined by trainee due to personal reason)	CCSRI	2,000
05/2015	**Alessia Gagliardi**	Director's Fund Award (CSHL Symposium "21st Century Genetics: Genes at Work")	CSHL	1,000 USD
08/31/2014 – 04/30/2015	**Hye-Jung (Elizabeth) Chun**	Faculty of Science Graduate Award	UBC	3,407.28
05/2014	**Emilia Lim**	Travel Award (Terry Fox 5th Annual Scientific Meeting)	TFRI	900
04/2014	**Hye-Jung (Elizabeth) Chun**	Graduate Student Travel Award (AACR Annual Meeting)	John Bosdet Memorial Fund (BCCF)	1,500
04/2014	**Hye-Jung (Elizabeth) Chun**	AACR Annual Meeting Travel Award	CCSRI	2,000
11/2013	**Emilia Lim**	CIHR-ICR Travel Award (for the 2013 Canadian Cancer Research Conference)	CIHR Institute of Cancer Research	1,000
11/2013	**Marlo Firme**	Graduate Student Travel Award (for the 2013 Canadian Cancer Research Conference)	John Bosdet Memorial Fund (BCCF)	1,456
11/2013	**Julia Pon**	Graduate Student Travel Award (for the 2013 Canadian Cancer Research Conference)	John Bosdet Memorial Fund (BCCF)	1,290
09/01/2012 – 01/31/2013	**Hye-Jung (Elizabeth) Chun**	College for Interdisciplinary Studies Graduate Award	UBC	2,773
02/2012	**Jill Mwenifumbo, PhD**	Graduate Student Travel Award (for the Advances in Genome Biology and Technology Meeting)	John Bosdet Memorial Fund (BCCF)	2,340 USD
05/01/2011	**Emilia Lim**	Canadian Bioinformatics Workshop Registration Award	OICR	500
05/01/2011	**Jill Mwenifumbo, PhD**	Canadian Bioinformatics Workshop Registration Award	OICR	500
12/2010	**Maria Mendez-Lago, PhD**	Travel Award	American Society of Hematology	500
04/02/2009	**Trevor Pugh**	Travel Award	UBC	400
2006	**Malachi Griffith**	Travel Award for the Canadian Student Health Research Forum	CIHR	250
2004 & 2005	**Suganthi Chittaranjan**	Graduate Student Travel Awards	John Bosdet Memorial Fund (BCCF)	2,200/yr

TRAINEE RESEARCH & TEACHING EXCELLENCE AWARDS:

Date	**Trainee**	**Award**	**Granting Institution**	**CDN $**
2022	**Yuka Takemon**	BC Cancer Research Day Best Poster	BC Cancer	
2022	**Vanessa Porter**	Medical Genetics Teaching Assistant Award	UBC	
2022	**Signe MacLennan**	BC Cancer Summit Poster Prize	TFRI	200
2020	**Vanessa Porter**	Patricia Baird Prize in Medical Genetics	UBC	1,000
11/23/2019	**Veronique LeBlanc**	Poster Award (Cancer biology) 2019 TFRI BC Node Day	TFRI	
11/09/2018	**Vanessa Porter**	First Place, Poster Award, Medical Genetics Research Day	UBC	
06/11/2018	**Veronique LeBlanc**	Second Place, Rapid Fire Talks, 2018 BC Cancer Research Day	BC Cancer	75
05/12/2018	**Veronique LeBlanc**	2018 Young Investigator Award in Basic/Translational Research	18th Biennial Canadian Neuro-Oncology Meeting	1,500
03/09/2018	**Veronique LeBlanc**	Third Place, Poster Prize, B.I.G. Research Day	UBC	50
03/09/2018	**Hye-Jung (Elizabeth) Chun**	First Place, Poster Prize and Lightning Talk Award, B.I.G. Research Day	UBC	300
04/23/2016	**Emilia Lim**	Department of Statistics Award in Data Science (for 2015W session)	UBC	1,000
11/16/2015	**Emilia Lim**	Lloyd Skarsgard Research Excellence Prize	BCCA	1,000
11/12/2014	**Emilia Lim**	Rapid-fire Research Talk, 4th Annual TFRI BC Node Research Day	TFRI	150
10/2013	**Julia Pon**	Best Oral Presentation at the TFRI BC Node Research Day	TFRI	
05/24/2013	**Emilia Lim**	Student Most Groundbreaking Research Oral Presentation Prize	RiboWest 2013 Conference	
10/2011	**Ryan Morin**	Lloyd Skarsgard Research Excellence Prize	BCCA	500
11/26/2010	**Olena Morozova**	One of the recipients of the Best Poster Award at the BC Cancer Agency Annual Cancer Conference	BCCA	
12/2008	**Trevor Pugh**	Genetics and Bioinformatics Retreat Senior Student Poster Award	UBC	150
10/2008	**Malachi Griffith**	Lloyd Skarsgard Research Excellence Prize	BCCA	500
12/2007	**Olena Morozova**	Medical & Bioinformatics Graduate Retreat Best Poster Award (for Bioinformatics category)	UBC	500

12/2007	**Ying-Chen (Claire) Hou**	Medical & Bioinformatics Graduate Retreat Best Poster Award (for Genetics category)	UBC	500
06/2006 – 08/2006	**Malachi Griffith**	CIHR National Research Poster Competition (Honourable Mention)	CIHR	-
2006	**Trevor Pugh**	Research Forum Exchange Poster Award	Genome BC	250
2005	**Trevor Pugh**	Medical Genetics Research Day Student Poster Award (Honourable mention)	UBC	-
2004 & 2003	**Suganthi Chittaranjan**	Medical Genetics Research Day Student Poster Award	UBC	300

TRAINEE PLATFORM / ORAL PRESENTATIONS:

1.	Gordon Research Conference: Single Cell Cancer Biology. Manchester, NH, USA. June 9-14, 2024. **Yan C,** Pleasance E, McConechy M, Shen Y, Nelson J, Laskin J, Marra MA. Single-cell multiomics in precision medicine. **(Oral presentation)**.
2.	Gordon Research Seminar: Viruses and Cells. Barcelona, Spain. May 21-26, 2023. **Porter VL**, O'Neill K, Corbett RD, MacLennan S, Iden M, Mutchler R, Tsaih S-W, Nip, Hamadeh Z, Culibrk L, Fan J, Nip KM, Akbari V, Chan SK, Moore R, Mungall KL, Mungall AJ, Birol I, Jones SJM, Rader JS, Marra MA. Identification of novel genomic structures and regulation patterns at HPV integration events in cervical cancer. **(Oral Presentation)**.
3.	Keystone Symposia: Metastasis (In-person event). Vancouver, BC. May 7-10, 2023. **Yan C**, Marco A. Marra. The origins of metastatic non-small cell lung cancer in primarytumours. **(Oral presentation)**.
4.	35th International Papillomavirus Conference & Basic Science, Clinical Science and Public Health Workshops (IPVC 2023). Washington D.C., USA. Apr 17-21, 2023. **MacLennan SA**, Porter VL, Marra MA. The Genomic Structures and Heterogeneity of Extrachromosomal DNA (ecDNA) in cervical cancer. **(Oral presentation awarded but declined due to illness)**.
5.	Advances in Genome Biology and Technology (In-person event). Fort Lauderdale, FL, USA. Feb 5-9, 2023. **Takemon Y**, Gagliardi A, Chan SY, Diane TL, Topham JT, Huff RD, Hughes CS, Marra MA. Application of an *in silico* framework to map genetic networks and elucidate biological functions of KMT2D, a frequently mutated gene across cancer types. **(Flash talk and poster presentation).**
6.	London Calling (Hybird Event). May 18-20, 2022. **Porter VL**, O'Neill K, Corbett R, Culibrk L, Marissa Iden, Rachel Mutchler, Shirng-Wern Tsain, Ka Ming Nip, Vahid Akbari, Simon K. Chan, Karen L. Mungall, Andrew J. Mungall, Inanc Birol, Steven J. M. Jones, Janet S. Rader, Marco A. Marra. Identification of novel genomic structures and regulation patterns at HPV integration events in cervical cancer. **(Oral presentation).**
7.	London Calling 2022 (Hybrid Event). May 18-20, 2022. **Akbari V**, O'Neill K, Corbett R, **Porter VL**, Pandoh P, Moore R, Marra MA, Hirst M, Jones SJ. DNA Methylation Analysis In Human Tumor Samples Using Nanpore Sequencing. **(Poster presentation).**
8.	London Calling (Hybird Event). May 18-20, 2022. **O'Neill K**, Pleasance E, Dixon K, Akbari V, Fan J, Porter V, Grisdale C, Corbett RD, Taylor G, Shen Y, Mungall KL, Chuah E, Williamson L, Laskin J, Marra MA, Jones S. Nanopore Sequencing for Personalised OncoGenomics. **(Oral presentation).**
9.	BIG 2022 Research Day (Speed Talk). Mar 23, 2022. **Takemon, Y**, **Gagliardi A,** Chan SY, Trinh DL, Topham JT, Huff RD, Hughes CS, Marra, MA. In Silico Genetic Interaction Network Mapping Expands KMT2D's Role in Maintaining Genomic Stability. **(Rapid-fire talk).**
10.	34th International Papillomavirus Conference (Virtual). Nov 15-19, 2021. **Porter VL**, O'Neill K, Nip KM, Culibrk L, Akbari V, Chan SK, Iden M, Tsaih S-W, Corbett R, Mungall KL, Mungall AJ, Birol I, Jones SJM, Rader JS, Marra MA. Analysis of cervical cancers with long-read technology delineates novel genomic structures and regulation patterns at HPV integration events. **(Oral presentation).**

11.	London Calling 2021 (Virtual). May 19-21, 2021. **Porter VL**, O'Neill K, Iden M, Tsaih S-W, Akbari V, Culibrk L, Chan SK, Mungall KL, Mungall AJ, Jones SJM, Rader JS, Marra MA. Nanopore sequencing of cervical cancers uncovers novel host and viral genomic and epigenomic features associated with HPV integration events. **(Oral Presentation)**.
12.	1st International Symposium of CCII -Bioinformatics and its application to cancer and other diseases. (Virtual) Jan 15, 2021. **Chun H-J E**, Johann PD, Milne K, Zapatka M, Buellesbach A, Ishaque N, Iskar M, Erkek S, Wei L, Tessier-Cloutier B, Lever J, Titmuss E, Topham J, Bowlby R, Chuah E, Mungall KL, Ma Y, Mungall AJ, Moore RA, Taylor MD, Gerhard DS, Jones SJM, Korshunov A, Gessler M, Kerl K, Hasselblatt M, Frühwald MC, Perlman EJ, Nelson BH, Pfister SM, Kool M, Marra MA. Comparative analyses of cranial and extra-cranial rhabdoid tumours reveal subgroups with cytotoxic T cell infiltration.
13.	University of British Columbia. Department of Medical Genetics Virtual Research Day 2020. Nov 6, 2020. **Porter VL**, Gagliardi A, Titmuss E,Bowlby R, Zong Z, O'Neill K, Namirembe C, Griner N, Petrello H, Bowen J, Chan S, Culibrk L, Darragh TM, Stoler MH, Wright TC, Gesuwan P, Dyer M, Ma Y, Mungall KL, Jones SJM, Nakisige C, Novik K, Orem J, Origa M, Gastier-Foster JM, Yarchoan R, Casper C, Mills G, Rader JS, Ojesina A, Gerhard DS, Mungall AJ, Marra MA. Analysis of Ugandan cervical carcinomas identifies HPV clade–specific epigenome and transcriptome landscapes. **(Patricia Baird Prize in Medical Genetics Finalist* Presentation. *Winner)**
14.	International Papillomavirus Conference (Virtual Conference due to COVID-19). July 27, 2020. **Porter VL**, Gagliardi A, Titmuss E, Zong Z, Bowlby R, Namirembe C, Griner NB, Petrello H, Bowen J, Chan S, Culibrk L, Darragh TM, Stoler M H, Wright T C, Gesuwan P, Dyer M, Ma Y, Mungall K L, Jones S JM, Nakisige C, Novik K, Orem J, Origa M, Gastier- Foster JM, Yarchoan R, Casper C, Mills GB, Rader JS, Ojesina AI, Gerhard D S, Mungall AJ, Marra MA. Ugandan cervical carcinomas have human papillomavirus clade-specific epigenome and transcriptome landscapes. **(Oral presentation)**
15.	BC Cancer Research Day. Vancouver, BC. June 17, 2019. **LeBlanc VG**, Trinh D, Hughes M, Luthra I, Livingstone D, Blough MD, Cairncross JG, Kelly JJ, Marra MA. Exploring cellular subpopulations in glioblastoma and matched patient-derived organoids using single-cell RNA-seq" **(First place prize for rapid-fire talks)**
16.	Terry Fox PROFYLE Therapeutic Node Meeting. Vancouver, BC. Apr 24, 2019. **Chun H-J E**. Malignant rhabdoid tumours as candidates for immune checkpoint inhibitor therapy. **(Online oral presentation)**
17.	International Human Epigenome Consortium Annual Meeting. Hong Kong, China. Oct 26-28, 2018. **Lee SD**, Song J, Chan SY, Chittaranjan S, Marra MA. Characterization of the Molecular Consequences of CIC-knockout and Neomorphic IDH1-R132H Mutation on Transcriptomic and Epigenomic Landscapes. **(Rapid-fire talk)**
18.	2018 BC Cancer Research Day. Vancouver, BC. June 11, 2018. **LeBlanc VG**, Trinh D, Hughes M, Luthra I, Livingstone D, Blough MD, Cairncross JG, Kelly JJ, Marra MA. Exploring cellular subpopulations in glioblastoma and matched organoids using single-cell RNA-seq. **(Rapid-fire talk)**
19.	18th Biennial Canadian Neuro-Oncology Meeting. Banff, AB. May 10-12, 2018. **LeBlanc VG**, Trinh D, Hughes M, Luthra I, Livingstone D, Blough MD, Cairncross JG, Kelly JJ, Marra MA. Exploring cellular subpopulations in glioblastoma and matched organoids using single-cell RNA-seq. **(Young Investigator Award in Basic/Translational Research).**
20.	International Rhabdoid Tumour Meeting, Lake Louise, AB. Apr 19-22, 2018. **Chun H-J E**. Comparative analyses of cranial ATRTs and extra-cranial MRTs revealed molecular similarities between the MYC-subgroup of ATRTs and MRTs.
21.	B.I.G. Research Day. Vancouver, BC. Mar 9, 2018. **Chun H-J E**. Extra-cranial rhabdoid tumours exhibit molecular similarities to the MYC-subgroup of AT/RTs.
22.	BC Cancer Research Centre's Thursday Oncology Trainee Seminar. Vancouver, BC. Feb 16, 2018. **Chun H-J E**. Comparative analysis of cranial and extra-cranial rhabdoid tumours revealed molecular similarities between subgroups.
23.	The 4th Canadian Conference on Epigenetics, Whistler, BC. Nov 26-29, 2017. **Chun H-J E**. Extra-cranial rhabdoid tumours exhibit molecular similarities to a cranial subtype.

24.	Terry Fox Research Institute 8th Annual Scientific Meeting. Vancouver, BC. Nov 4, 2017. **LeBlanc VG**, Trinh D, Hughes M, Blough MD, Cairncross JG, Kelly JJ, Marra MA. Exploring cellular subpopulations in glioblastoma and matched organoids using single-cell RNA-seq. **(Rapid-fire talk)**
25.	BC Cancer Research Centre's Thursday Oncology Trainee Seminars. Vancouver, BC. May 3, 2017. **LeBlanc VG**, Trinh D, Hughes M, Luthra I, Livingstone D, Blough MD, Cairncross JG, Kelly JJ, Marra MA. Exploring cellular subpopulations in glioblastoma and matched organoids using single-cell RNA-seq.
26.	BC Cancer Research Centre's Thursday Oncology Trainee Seminar. Vancouver, BC. Mar 2, 2017. **LeBlanc VG**. Investigating the role of *CIC* mutations in malignancy.
27.	BC Cancer Research Centre's Thursday Oncology Trainee Seminar. Vancouver, BC. Feb 2, 2017. **Chun H-J E**. Heterogeneous molecular landscapes of malignant rhabdoid tumours uniformly driven by SMARCB1 loss.
28.	58th American Society of Hematology Annual Meeting and Exposition. San Diego, CA. Dec 3-6, 2016. **Lim EL**, Trinh DL, Ries RE, Wang J, Ma Y, Topham J, Hughes M, Pleasance E, Mungall AJ, Moore R, Zhao YJ, Kolb EA, Gamis A, Smith M, Gerhard DS, Alonzo TA, Meshinchi S, Marra MA. A microRNA Expression-based Model Predicts Event Free Survival in Pediatric Acute Myeloid Leukemia. **(Oral presentation)**
29.	2016 American Society of Human Genetics Annual Meeting, Vancouver, B.C. Oct 18-22, 2016. **Lim EL**, Trinh DL, Ries R, Ma Y, Topham J, Hughes M, Pleasance E, Mungall AJ, Moore R, Zhao YJ, Gerhard DS, Kolb EA, Gamis A, Smith M, Alonzo TA, Arceci RJ, Meshinchi S, Marra MA. Pediatric acute myeloid leukemia survival differences revealed by comprehensive miRNA sequence analysis. **(Platform presentation)**
30.	BCCA Monday Noon Seminar Series. Vancouver, BC. Oct 3, 2016. **Lim EL**. miRNA Sequence Analysis Reveals Cancer Subtypes that Correlate With Tumour Characteristics and Patient Outcomes. **(Presentation)**
31.	International Union of Biochemistry and Molecular Biology Annual Meeting. Vancouver, BC. Jul 2016. **Lim EL**, Trinh DL, Ries R, Wang J, Ma Y, Topham J, Hughes M, Pleasance E, Mungall AJ, Moore R, Zhao YJ, Oehler V, Kolb EA, Gamis A, Smith M, Gerhard DS, Arceci RJ, Alonzo TA, Meshinchi S, Marra MA. Comprehensive Sequence Analysis of Relapse & Refractory Pediatric Acute Myeloid Leukemia **(Presentation)**
32.	VanBug Seminar. Vancouver, BC. Mar 2016. **Chun H-J E**, Lim EL, Heravi-Moussavi A, Modaber SS, Moussavi A, Mungall KL, Bilenky M, Carles A, Tse K, Shlafman I, Zhu K, Qian JQ, Harvey D, He An, Long W, Goya R, Ng M, LeBlanc V, Pleasance E, Thiessen N, Wong T, Chuah E, Zhao YJ, Schein JE, Gerhard DS, Taylor MD, Mungall AJ, Moore RA, Ma Y, Jones SJM, Perlman EJ, Hirst M, Marra MA. Heterogeneous epigenetic landscape of extra-cranial malignant rhabdoid tumours. **(Presentation)**
33.	57th American Society of Hematology Annual Meeting. Orlando, FL. Dec 2015. **Lim EL**, Trinh DL, Ries R, Wang J, Ma Y, Topham J, Hughes M, Pleasance E, Mungall AJ, Moore R, Zhao YJ, Oehler V, Kolb EA, Gamis A, Smith M, Gerhard DS, Alonzo TA, Arceci RJ, Meshinchi S, Marra MA. Comprehensive Sequence Analysis of Relapse and Refractory Pediatric Acute Myeloid Leukemia Identifies miRNA and mRNA Transcripts Associated with Treatment Resistance - a Report from the COG/NCI-Target AML Initiative.
34.	BC Cancer Research Centre Thursday Oncology Seminar Series. Vancouver, BC. Nov 2015. **Chun H-J E**, Lim EL, Heravi-Moussavi A, Modaber SS, Moussavi A, Mungall KL, Bilenky M, Carles A, Tse K, Shlafman I, Zhu K, Qian JQ, Harvey D, He An, Long W, Goya R, Ng M, LeBlanc V, Pleasance E, Thiessen N, Wong T, Chuah E, Zhao YJ, Schein JE, Gerhard DS, Taylor MD, Mungall AJ, Moore RA, Ma Y, Jones SJM, Perlman EJ, Hirst M, Marra MA. Extra-cranial malignant rhabdoid tumours have molecularly distinct subgroups.
35.	Children's Oncology Group Annual Meeting. Dallas, TX. Oct 2015. **Lim EL,** Trinh DL, Ries R, Wang J, Ma Y, Topham J, Hughes M, Pleasance E, Mungall AJ, Moore R, Zhao YJ, Oehler V, Kolb EA, Gamis A, Smith M, Gerhard DS, Alonzo TA, Arceci RJ, Meshinchi S, Marra MA. Transcriptome Sequence Analysis of Relapse and Refractory Pediatric Acute Myeloid Leukemia.
36.	Next Generation Sequencing Rounds, Child & Family Research Institute. Vancouver, BC. Sep 25, 2015. **Chun H-J E.** Genomic analyses of extra-cranial malignant rhabdoid tumours.

37.	2nd International GENCODYS Conference Integrative Networks in Intellectual Disabilities. Crete, Greece. Apr 27-28, 2015. **Zahir FR**, Lee L, Makela N, Friedman JM, Marra M. Pathway analyses of whole genome sequence data identifies novel candidate Intellectual Disability genes.
38.	13th International Symposium on Mutation in the Genome: detection, genome sequencing & interpretation. Leiden, The Netherlands. Apr 27-30, 2015. **Zahir FR**, Lee L, Makela N, Friedman JM, Marra M. Pathway analyses of whole genome sequence data identifies novel candidate Intellectual Disability genes.
39.	Genome Informatics 2014. Cambridge, UK. Sep 21-24, 2014. **Lim EL**, Trinh DL, Scott DW, Chu A, Krzywinski M, Robertson G, Mungall AJ, Schein J, Boyle M, Johnson NA, Steidl C, Connors JM, Morin RD, Gascoyne RD, Marra MA. Comprehensive miRNA Sequence Analysis Reveals Survival Differences in Diffuse Large B-cell Lymphoma Patients.
40.	Clinician Investigator Program Research Day. Vancouver, BC. June 2, 2014. **Pon JR**, Wong J, Marra MA. *MEF2B* Mutations Recurrent in Non-Hodgkin Lymphoma Decrease *MEF2B* Transcriptional Activity and Dysregulate Migration and Proliferation. **(Oral presentation)**
41.	University of British Columbia. IOP/BTP/GSAT Research Day. Vancouver, BC. Mar 28, 2014. **Pon JR**, Chittaranjan S, Wong J, Chan S, Trinh D, Tamura-Wells J, Firme M, O'Brien K, Mendez-Lago M, Morin R, Connors JM, Gascoyne RD, Marra M. Regulatory Networks Impacted by *MEF2B* Mutations in Non Hodgkin Lymphoma. **(Oral presentation)**
42.	3rd Annual TFRI-BC Node Research Day. Vancouver, BC. Oct 31, 2013. **Pon JR**, Chittaranjan S, Wong J, Chan S, Trinh D, Tamura-Wells J, Firme M, O'Brien K, Mendez-Lago M, Morin R, Connors JM, Gascoyne RD, Marra M. Regulatory Networks Impacted by *MEF2B* Mutations in Non Hodgkin Lymphoma. **(Awarded Best Oral Presentation)**
43.	RiboWest 2013 Conference. Prince George, BC. May 2013. **Lim EL**, Trinh D, Scott D, Chu A, Morin R, Mungall A, Boyle M, Johnson M, Connors J, Gascoyne R, Marra M. Deep Sequencing of the DLBCL miRnome Reveals Novel Prognostic miRNA. (**Awarded Student Most Groundbreaking Research Oral Presentation Prize)**
44.	Asian Pacific Bioinformatics Conference, Vancouver, BC. Jan 20, 2013. **Chun H-J E**. Interpreting cancer sequencing data in terms of functions, pathways and drug targets. **(Tutorial instruction).**
45.	BC Cancer Agency Research Conference. Vancouver, BC. Nov 2012. **Lim EL**, Morin RD, Chu A, Gascoyne RD, Marra MA. An Integrative Analysis of miRNA:mRNA Interactions Acting in Cancers. **(Awarded Best Bioinformatics Oral Presentation)**
46.	Canadian Association of Genetic Counselors Annual Conference. Saskatoon, SK. Oct 17-20, 2012. **Zahir FR**. Genomics tools at your finger-tips; learning to access and use online available tools for genotype-phenotype correlations. **Invited oral (workshop) presentation**
47.	NeuroDevNet Brain Conference, Toronto, ON. Sep 20-24, 2012. **Zahir FR**, Shen Y, Zhan SH, Adam S, Makela N, Beaulieu C, FORGE Canada Consortium, Gibson W, Patel M, Horvath G, Marra MA, Jones S, Friedman JM. Whole exome sequencing of two families results in identification of novel causative mutations for severe Intellectual Disability. **(Oral presentation)**
48.	Sri Lanka Medical Association 125th Anniversary Conference. Colombo, Sri Lanka. July 2-6, 2012. **Zahir FR**, Adam S, Makela N, FORGE Canada Consortium, Gibson W, Horvath G, Langlois S, Patel W, Marra MA, Jones S, Friedman JM. Cutting edge genomic technologies to diagnose the genetic basis of Intellectual Disability and Major Congenital Anomalies. **(Invited oral presentation)**
49.	Model Organisms to Human Biology- Cancer Genetics Conference. Washington, DC. June 17-20 2012. **Pon JR,** Mendez-Lago M, Mungall AJ, Mungall KL, Bolger-Munro M, Goya R, Hadj Khodabakhshi A, Johnson NA, Chiu R, Jackman S, Krzywinski M, Scott D, Trinh DL, Corbett R, Meissner B, Tse K, Birol I, Holt R, Schein J, Horsman DE, Moore R, Hirst M, Jones SJM, Connors JM, Gascoyne RD, Marra MA, Morin RD. Genomic Profiling of Non-Hodgkin Lymphoma Clinical Samples. **(Oral presentation)**
50.	Pacific North-West Genetics Exchange, Seattle, WA, USA, May 4, 2012. **Zahir FR**, Tucker T, Adam S, Chai D, Tsang E, Delaney A, Eydoux P, Griffith M, Hamdan F, Langlois S, Marra M, Michaud J, Friedman JM. Genomic imbalance of genes encoding epigenetic regulatory proteins is a significant cause of intellectual disability **(Oral presentation)**

51.	BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Dec 2011. **Mwenifumbo JC**, Griffith M, Zhao YJ, Owen D, Gill S, Marra M. Exploring Mutational Evolution in Metastatic Colorectal Cancer. **(Oral presentation)**
52.	11th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. Feb 2010. **Bosdet I**, Pugh T, Sutcliffe M, Ionescu D, Ho C, Sun S, Murray N, Laskin JJ, Marra M. Mutational profiling of pre- and post-treatment lung tumors using whole-transcriptome sequencing and targeted sequence capture. **(Platform presentation)**
53.	Cambridge Healthtech Institute's Next Generation Sequencing Conference. San Diego, CA. Mar 2009. **Pugh T**, Morin RD, Marra MA. Whole transcriptome sequencing of cancer biopsies for concurrent analysis of expression, splicing and mutation **(Platform presentation)**.
54.	10th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. Feb 2009. **Griffith M**, Morin RD, Tang MJ, Pugh TJ, Griffith OL, Ally A, Asano JK, Chan SY, McDonald H, Zhao Y, Zeng T, Delaney A, Hirst M, Tai IT, Marra MA. Transcriptome Sequencing Reveals Alternative Splicing Events in Chemotherapy Resistant Colon Cancer Cells. **(Platform presentation)**
55.	HUGO’s 13th Human Genome Meeting. Hyderabad, India. Sep 2008. **Morozova O**, Morozov V, Hirst M, Marra M. Defining expression signatures of known cancer genes using seriation analysis of SAGE libraries from Cancer Genome Anatomy Project (CGAP). Computational Biology and Structural Proteomics Workshop Presentation. **(Platform presentation)**
56.	The 9th Annual AGBT Conference. Marco Island, FL. Feb 2008. **Morin RD**, O’Connor MD, Griffith M, Kuchenbauer F, Delaney A, Prabhu A-L, Zhao Y, McDonald H, Zeng T, Hirst M, Eaves CJ, Marra MA. Application of Illumina massively parallel sequencing to microRNA profiling and discovery in human embryonic stem cells. **(Platform presentation)**
57.	The 9th Annual AGBT Conference. Marco Island, FL. Feb 2008. **Farnoud N**, Chan S, Flibotte S, Delaney A, Friedman JM, Marra M. DLOH: A Novel Bioinformatics Tool For Detection Of Copy-Number Deletions Using LOH Data. **(Platform presentation)**
58.	Discovery to Diagnostics Conference & Exhibition. Philadelphia, PA. Sep 2007. **Griffith M**. Identification of alternative isoforms associated with chemotherapy resistance. **(Platform presentation**).
59.	HUGO’s 12th Human Genome Meeting. Montreal, QC. May 2007. **Morin RD**, Delaney A, O’Connor M, Prabhu A-L, Zhao Y, McDonald H, Zeng T, Hirst M, Eaves C, Marra MA. Identification of small RNAs important in embryonic stem cells and their differentiation. **(Platform presentation)**

UNDERGRADUATE STUDENTS / OTHER STUDENTS SUPERVISED:

From	To	Student	Status	Degree
09/03/2024 01/10/2024	Present 08/20/2024	Jiajie (Crystal) Shan	Directed Studies Student Co-op Student	BSc (Biochemistry & Molecular Biology) University of British Columbia
05/06/2024	08/30/2024	Rachel Taylor	Summer Student	BSc (Health Sciences in Biomedical Sciences) University of Calgary
04/19/2024	08/30/2024	Rachel Smid	Summer Student	BSc (Health Science) University of Northern British Columbia
09/18/2023	04/12/2024	Emily Flaschner	Directed Studies Student (BMEG 490B)	BSc (Biomedical Engineering) University of British Columbia
05/03/2021 01/2021	08/20/2021 05/02/2021	Xiao Yu (Cathy) Yan	Student Researcher Volunteer Student	BSc Honours (Microbiology & Immunology) University of British Columbia
05/10/2021 01/2021	08/20/2021 05/09/2021	Signe MacLennan	Student Researcher Volunteer Student	BSc (Health Sciences) Simon Fraser University
05/01/2020 &	08/28/2020	Dollina Dodani	Summer Student	BSc (Computing Science) Simon Fraser University

04/29/2019	04/30/2020		Co-op Student	
06/19/2019	08/30/2019	Parsa Seyfourian	Volunteer Student	BSc, 2nd year University of British Columbia
11/21/2018 & 01/02/2018	06/28/2019 08/16/2018	Ishika Luthra	Student Researcher Co-op Student	BSc (Biomedical Engineering) Simon Fraser University
07/23/2018	08/31/2018	Daniel Shirvani	Volunteer Student	High school student, Grade 11 West Vancouver Secondary School
01/15/2018 & 05/01/2017	08/10/2018 08/30/2017	William Brothers	Student Researcher NSERC USRA Student	BSc (Biology) University of British Columbia
06/01/2017	08/31/2017	Heidi Britton	Summer Student	MD Program University of British Columbia
09/08/2015	04/27/2016	Cassia Warren	Directed Studies Student	BSc (Genetics & Physiology) University of British Columbia
09/08/2015	04/29/2016	Amro Anwer	Co-op Student	BSc (Computer Engineering) University of British Columbia
01/05/2015	08/21/2015	Hyun Jung (Adita) Cho	Co-op Student	BSc (Biochemistry, 4th year) University of British Columbia
05/05/2014 & 09/20/2013	08/31/2015 04/30/2014	Min Hye (Angelica) Lee	Co-op Student Volunteer Student	BMLSc (3rd year) University of British Columbia
05/01/2014	04/27/2015	Michelle Ng	Honours Thesis Student	University of British Columbia
09/03/2013	01/18/2015	Jungeun Song	Co-op Student	BSc (Molecular Biology & Biochemistry, final year) Simon Fraser University
05/06/2013	12/20/2013	Jackson Wong	Co-op Student	Faculty of Science (3rd year Biology) University of British Columbia
09/04/2012	08/30/2013	Chi-fu (Kevin) Yang	Co-op Student	BSc Honours (Molecular Biology & Biochemistry, 3rd year) Simon Fraser University
05//2012	08/28/2012	Yisi Daisy Ji	Summer Student	BSc (Pharmacy, 2nd year) University of British Columbia
01/2011 & 05/2007	08/31/2012 09/2008	Cindy Yang	Student Researcher Volunteer Student	BSc (Microbiology & Immunology) University of British Columbia
08/2011	01/2012	Brian Alcock	Student Researcher	BSc Honours (Biology, 4th year) Memorial University, Newfoundland
06/2011	08/2011	Andre Paul Van	Volunteer Student	MSc (Human Genetics) University College London
05/2011 & 05/2009 & 05/2008	06/2012 07/2009 08/2008	Pierre Cheung	Student Researcher Volunteer Student Volunteer Student	BSc Honours (Biochemistry) University of British Columbia
05/2011	08/2011	Sam Whiteley	Volunteer Student	BSc (Mechanical Engineering)

				McGill University
05/2011 & 05/2010	08/2011 08/2010	Madison Bolger-Munro	Student Researcher Volunteer Student	BSc (Microbiology & Immunology, 2nd year) University of British Columbia
03/2011	08/2011	Juan Marlo Firme	Volunteer Student	BSc Honours ((Microbiology & Immunology) University of British Columbia
01/2011	08/2011	Jessica Tamura-Wells	Co-op Student	BSc (Microbiology, 3rd year) University of Victoria
01/2011 & 05/2010	03/2011 09/2010	Eric Zhao	Volunteer Student Summer Student	Faculty of Science University of British Columbia
09/2009 & 05/2009	12/2010 08/2009	Alexandra Maslova	Student Researcher Volunteer Student	Science One Program University of British Columbia
09/2010	12/2010	Ricky Lo	Co-op Student	BSc (Cell Biology & Genetics) University of British Columbia
05/2010	08/2010	Yulia Merkulova	Volunteer Student	Science One Program University of British Columbia
05/2010	08/2010	Brian Cho	Volunteer Student	Science One Program University of British Columbia
10/2009	06/2010	Deborah Chen	Volunteer Student	Science One Program University of British Columbia
02/2009	12/2009	Shaun Drummond	Volunteer Student	Associate Degree in Biology Kwantlen Polytechnique University
05/2009	08/2009	Jasmine Lin	Student Researcher	Bachelor of Arts Cornell University
04/2009 & 09/2008	08/2009 03/2009	Alison Lee	Student Researcher Volunteer Student	BSc Honours (Physiology Program) University of British Columbia
05/2008 & 05/2007	07/2009 08/2007	Jessica Paul	Student Researcher Summer Student	BSc (Honors Biology, minor Biochemistry) Calvin College, Michigan
09/2008	04/2009	Lisa Miao	Student Researcher	BSc (Computer Science) University of British Columbia
04/2008 & 09/2007	06/2008 12/2007	Diane Wu	Summer Student Part-time Research Student	BSc (Mol Biology & Biochem) Simon Fraser University
11/2007	11/2007	Jennifer Puddicombe	Volunteer Student	BSc (Cell Biology & Genetics) University of British Columbia

STUDENT ADVISORY COMMITTEE INVOLVEMENT:

From	**To**	**Student**	**Supervisor**	**Program**
03/2024	Present	Behnaz Salek	Daniel Goldowitz	PhD (Neuroscience), UBC
01/2024	Present	Taghrid Aloraini	Jan Friedman and Inanc Birol	PhD (Bioinformatics), UBC
09/2023	Present	Cassandra Cui	Amina Zoubeidi	PhD (Interdisciplinary Oncology), UBC

09/2023	Present	Umut Berkay Altintas	Nathan Lack	PhD (Bioinformatics), UBC
01/2023	Present	Haley MacDonald	Adi Steif	MSc (Bioinformatics), UBC
11/2022	Present	Johnathan Wong	Inanç Birol	MSc (Bioinformtics)
09/2021	Present	Anne Nathalie Ruth Longakit	Cathy Van Raamsdonk	PhD (Medical Genetics), UBC
04/2021	Present	Elizabeth Stevens	Philip Hieter	PhD (Medical Genetics), UBC
05/2020	Present	Mona Siu	Peter Zandstra	PhD (Medical Genetics), UBC
10/2019	Present	Zeid Hamadeh	Peter Lansdorp	MSc (Genome Science and Technology), UBC
12/2018	Present	Hilary Brewis	Michael Kobor & Peter Stirling	PhD (Medical Genetics), UBC
05/2021	08/2023	Jorge Holguin	Joerg Gsponer	MSc (Bioinformatics), UBC
11/2019	12/2023	Vahid Akbari	Steven Jones	PhD (Medical Genetics), UBC
01/2016	04/2021	Emma Laks	Samuel Aparicio	MSc (Genome Science and Technology), UBC
09/2015	11/2020	Derek Wong	Stephen Yip & David Huntsman	PhD (Pathology and Laboratory Medicine), UBC
11/2010	08/2019	Chandra Lebovitz	Sharon Gorski	PhD (Molecular Biology & Biochemistry), SFU
09/2018	05/2019	Kevin Fan	Steven Jones	MD/PhD Program University of British Columbia
01/2017	04/2018	Kevin Jepson	Carl Hansen	MSc (Genome Science and Technology), UBC
04/2014	12/2016	Sivan Reytan	Philip Hieter	MSc (Medical Genetics), UBC
09/2013	05/2018	Eric Zhao	Steven Jones	MD/PhD Program University of British Columbia
04/2013	04/2018	Hans Zahn	Carl Hansen	PhD (Genome Science and Technology), UBC
04/2013	03/2017	Fong Chun Chan	Sohrab Shah	PhD (Bioinformatics Graduate Program), UBC
01/2013	07/2018	Lauren Tindale	Angela Brooks-Wilson	PhD (Biomedical Physiology and Kinesiology), SFU
12/2010	12/2015	Peter Thompson	Matthew Lorincz	PhD (Medical Genetics), UBC
10/2008	12/2012	Madalene Earp	Angela Brooks-Wilson	PhD (Medical Genetics), UBC
03/2009	02/2012	Mehdi Najafzadeh	Carlo Marra	PhD (Pharmacy Program), UBC
08/2008	07/2009	Ying-Chen (Claire) Hou	Sharon Gorski	PhD (Medical Genetics), UBC
09/2007	07/2010	Lucie Semenec	Jack Chen	MSc (Mol Biol & Biochemistry), SFU
07/2007	03/2012	Anthony Fejes	Steven Jones	PhD (Bioinformatics), UBC

01/2007	06/2012	Dan Fornika	Angela Brooks-Wilson	MSc (Medical Genetics), UBC
01/2007	07/2010	Marco Gallo	Don Riddle	PhD (Medical Genetics), UBC
06/2006	11/2010	Iva Kulic	Aly Karsan	PhD (Experimental Medicine), UBC
05/2006	08/2011	Farah Zahir	Jan Friedman	PhD (Genetics Graduate Program), UBC
05/2005	05/2006	Brianna Melnyk	Robert Holt	MSc (Genetics Graduate Program), UBC
09/2004	11/2011	Yvonne Li	Steven Jones	PhD (CIHR Bioinformatics Program), UBC
09/2004	03/2010	Kelvin Zhang	Francis Ouellette	PhD (CIHR Bioinformatics Program), UBC
12/2003	05/2007	Jessica Lee	Ryan Brinkman	MSc (CIHR Bioinformatics Program), UBC
09/2003	07/2009	David Kent	Connie Eaves	PhD (Medical Genetics), UBC
09/2003	09/2008	Tammy Romanuik	Marianne Sadar	PhD (Pathology and Laboratory Medicine), UBC
09/2003	04/2008	Obi Griffith	Steven Jones	PhD (Medical Genetics), UBC
09/2003	01/2005	Debra Fulton	Fiona Brinkman	MSc (CIHR Bioinformatics Program), SFU
09/2002	08/2004	Perseus Missirlis	Philip Hieter	MSc (Genetics Graduate Program), UBC
03/2002	12/2005	Erin Pleasance	Steven Jones	PhD (Medical Genetics), UBC
09/2001	01/2005	Tom Milne	Hugh Brock, Jay Hess	PhD (Medical Genetics), UBC
09/1999	11/2006	Michael Anglesio	Poul Sorensen	PhD (Pathology), UBC
07/1999	08/2001	Michael Thorne	Steven Jones	MSc (Medical Genetics), UBC
07/1999	05/2001	Sanja Karalic	Carolyn Brown	MSc (Medical Genetics), UBC
09/1998	08/2003	Josette-Renee Landry	Dixie Mager	PhD (Medical Genetics), UBC

COMPREHENSIVE / THESIS EXAMINING COMMITTEE INVOLVEMENT:

Date	Role	Student	Thesis Title	Degree	University
07/31/2024	University Examiner	Chingpan Chu	Preservation and detection of dynamic transcriptional regulatory signals in gene co-expression analysis	PhD (Bioinformatics)	University of British Columbia
11/24/2023	External Examiner	Hiba Omairi	Differential Effects of PDGFA and PDGFC Ligands on Neural Stem and Progenitor Cells	PhD	University of Calgary

10/31/2023	Committee member	Umut Berkay Altintas		PhD	University of British Columbia
08/31/2023	Committee member	Jorge Holguin		PhD	University of British Columbia
08/24/2023	Chair	Chun Wai Cheung	Characterization of DPP4$^+$ fibroadipogenic progenitors in skeletal muscle	Msc (Medical Genetics)	University of British Columbia
04/03/2023	Comprehensive Examiner	Anne Nathalie Ruth Longakit	Life in plastic, it's fantastic: Investigating the role of EMT states on clonal plasticity and metastasis in Uveal Melanoma	Transfer to PhD (MEDG)	University of British Columbia
03/30/2023	Chair	Yana Moscovitz	DICER1 Tumour Predisposition Syndrome Associated Cancers: Somatic TP53 and KRAS Mutations and Cancer Progression	Transfer to PhD (MEDG)	University of British Columbia
03/24/2022	University Examiner	Gillian Vandekerkhove	Circulating Tumour DNA as a Biomarker in Metastatic Bladder Cancer	PhD (Experimental Medicine)	University of British Columbia
12/11/2019	University Examiner	Marjan Farahbod	The interpretation of gene coexpression in systems biology	PhD (Bioinformatics)	University of British Columbia
09/25/2018	Chair (for PhD comprehensive examination)	Katherine Dixon	Molecular pathogenesis of cancer predisposition syndromes and challenges in genetic diagnosis	PhD candidate (Medical Genetics)	University of British Columbia
07/25/2017	University Examiner	Carol Chia-Lu Chen	Interphase histone H3 serine 10 phosphorylation in mouse embryonic stem cells	PhD (Medical Genetics)	University of British Columbia
03/10/2017	University Examiner	Fong Chun Chan	Clinical Implications of Inter-tumour, Intra-tumour, and Tumour Microenvironment Heterogeneity in B-cell Lymphomas	PhD (Bioinformatics Graduate Program)	University of British Columbia

06/10/2015	Chair (for PhD comprehensivee xamination)	Govinda Sharma	The development of a high-throughput methodology for the discovery of cytotoxic T-cell receptor epitopes	PhD candidate (Genome Science & Technology Graduate Program)	University of British Columbia
06/04/2012	External Appraiser	Wigdan Al-Sukhni	Identifying susceptibility genes for Familial Pancreatic Cancer using novel high-resolution genome interrogation platforms	PhD	University of Toronto
04/12/2012	Chair	Jennifer Grants	Gene regulation by CDK8 (for PhD comprehensive examination)	PhD (Medical Genetics)	University of British Columbia
06/28/2011	Chair	Brian Wing Chi Wong	Vascular endothelial growth factor-induced permeability in the pathogenesis of cardiac allograft vasculopathy	PhD (Pathology and Laboratory Medicine)	University of British Columbia
09/04/2009	Chair	Noemie Riendeau	Autism spectrum disorders: Identification of novel microdeletions and microduplications and their associated phenotypes.	MSc (Medical Genetics)	University of British Columbia
07/27/2005	Chair	Jasmeen Merzaban	Formation of functional selection ligands on Activated T Cells and Thymic progenitors: the role of Core 2 ?-6-N-glucosaminyltransferases in the control of lymphocyte trafficking and thymic progenitor homing.	PhD (Experimental Medicine)	University of British Columbia

SIGNIFICANT RESEARCH CONTRIBUTIONS:

Dr. Marra’s significant contributions to genome science are listed below. Publications have been organized into groups of technically or scientifically related topic areas.

I. *Science*, 2009 Apr 24;324(5926):522-528; *Genome Biol*, 2007 Oct 22;8(10):R224; *Science*, 2007 Apr 13;316(5822):222-234; *Science,* 2006 Nov 10;314(5801):941-952; *Science*, 2006 Sep 15;313(5793):1596-1604; *Genome Res*, 2006 Jun;16(6):768-775; *Science*, 2006 Sep 15; 313 (5793):1596-1604. *Proc Natl Acad Sci USA*, 2005 Dec 20;102(51):18526-18531; *Science*, 2005 Jul 15;309(5733):436-442; *Nature*, 2005 Apr 7;434(7034):724-731; *Science,* 2005 Feb 25;307(5713):1321-1324*; Nature*, 2004 Apr 1;428(6982):493-521;

Nature, 2003 Jul 10;424(6945):157-164; *Nature*, 2002 Aug 15;418 (6899):743-750; *Nature Genet*, 2001Oct;29(2):133-134; *Genome Res*, 2001 Feb;11(2):274-280; *Nature*, 2001 Feb 15;409(6822):934-941; *Nature*, 2001 Feb 15; 409(6822):860-921.*Genome Res*, 1997;7:1072-1084.

These selected publications describe large-scale high throughput DNA sequencing conducted via a hierarchical map-based approach. The papers published in the Feb. 15, 2001 issue of Nature, titled "The Human Genome", describe the construction and use of the human genome map to fuel human genome sequencing. Dr. Marra's contribution was to devise and then implement the approaches that led to the construction and use of the map, which served as the centralized coordinating resource for the sequencing effort.

Dr. Marra also led map construction efforts in support of the sequencing of the mouse, rat, bovine, and other genomes, as described in these papers.

II. *Nature*, 2000 Dec 14;408(6814):796-815; *Nature*, 2000;408:823-826; *Cell*, 2000;100:377-386; *Nature*, 1999; 402:769-776; *Science*, 1999;286:2468-2474; *Nature Genet*, 1999;22:265-270; *Nature Genet*, 1999;22:271-275.

This series of papers describes the mapping and sequencing of the *Arabidopsis thaliana* genome. *A. thaliana* is an important model plant used widely to address issues relevant to plant developmental genetics. Dr. Marra was a key member of the Cold Spring Harbor Sequencing Consortium, focused on first leading the effort to map the *A. thaliana* genome and subsequently coordinating aspects of the whole genome sequencing activity.

III. *Emerg Infect Dis*, 2004 Dec;10(12):2192-2195; *Science*, 2003 May;300(5624):1399-1404.

The EID publication describes the sequencing of Avian flu genomes isolated from human patients during an Avian flu outbreak. The Science publication describes the rapid generation of the complete and accurate sequence of the SARS-associated coronavirus. The Genome Sciences Centre generated and end-sequenced cDNAs, and then assembled these sequences into the final ~29 kilobase genome sequence. The entire effort took about six days, demonstrating that genome sequencing of a new viral pathogen could be considered a legitimate part of a "rapid response" to an emerging infectious disease. The Science paper has been cited more than 1,524 times (tracked by Publons); 2,796 times (tracked by Google Scholar) as of Feb 11/22.

IV. Dr. Marra's current efforts are focused on the implementation of genomics approaches to characterize human cancers. He has led and co-led numerous efforts that use genomics sequencing technologies to characterize tumors, leading to the discovery of new cancer-associated mutations, candidate biomarkers, and new therapeutic targets. These efforts resulted in the discovery of mutated genes implicated in **ovarian cancers** e.g. *FOXL2* (*N Engl J Med* 2009 Jun 25;360(26):2719-2729) and *ARID1A* (*N Engl J Med* 2010 Oct 14; 363(16):1532-1543.); **B cell lymphomas** e.g. *EZH2* (*Nat Genet* 2010 Feb ;42(2):181-185), *MLL2*, *MEF2B*, (*Nature* 2011 Jul 27; 476(7360):298-303), *CIITA* (*Nature* 2011 Mar 17;471(7338):377-381.); **brain cancers** (e.g. *CIC* (*J Pathol* 2012 Jan;226(1):7-16), *Proc Natl Acad Sci U S A*. 2019 Sep 17;116(38):19098-19108, *Cancer Cell.* 2022 Apr 11;40(4):379-392.e9); **breast cancers** (e.g. *Nature* 2009 Oct 8;461(7265):809-813 and Nature 2012 Apr 4;486(7403):395-399); **medulloblastomas** (e.g. *Nat Genet* 2017 May;49(5):780-788; *Oncotarget* 2016 May;7(19):28169-28182; *Nature* 2016 Jan;529(7586):351-357; *Cancer Cell* 2014 Jul;26(1):33-47; *Acta Neuropathol* 2013 Mar;125(3):373-384; *Nature* 2012 Aug;488(7409):49-56); **lymphomas** (e.g. *Blood* 2017 Mar 28; *PLoS Med* 2016 Dec 13; *Blood* 2016 Sep;128(9):1206-1213; *Blood* 2015 Oct;126(18):2118-2127; *Blood* 2015 Feb;125(6):959-966; *Genome Biol* 2015 Jan;16(1):18; *Nat Genet* 2014 Apr;46(4):329-335; *Blood* 2013 May;121(18):3666-3674; *Blood* 2013 Apr;121(16):3161-3164; *Blood* 2012 May;119(21):4949-4952; *Blood* 2012 Mar;119(9):1963-1971); **leukemias** (eg *Nat Commun* 2016 Nov;7:1333; *Cancer Cell* 2012 Aug;22(2):153-166); *Cancer Cell* 2023 Dec 11;41(12):2117-2135.e12); **rhabdoid tumours** (e.g. *Cancer Cell* 2016 Mar;29(3):394-406; *Cell Rep*. 2019 Nov 19; 29 (8):2338-2354.e7) and **cervical cancers** (e.g. *Nat Genet*. 2020 Aug;52(8):800-810. doi: 10.1038/s41588-020-0673-7).

Dr. Marra co-leads (with Medical Oncologist Dr. Janessa Laskin) the first proof-of-concept study demonstrating the potential of whole genome and transcriptome analysis in personalized cancer genome medicine. As described in ***Genome Biol*** 2010 Aug 9;11(8):R82, a rare cancer falling outside standard treatment guidelines was analyzed using whole genome and transcriptome sequencing before and after treatment. The sequence data were used to inform the choice of cancer treatment options, which were previously undefined for this rare tumor type. Clinical administration of the selected treatment resulted in shrinkage of the tumor and the establishment of stable disease for several months. Significantly, this study was the first to establish that whole genome and transcriptome sequence characterization of tumors can inform the selection of relevant therapeutic approaches for a cancer patient. This achievement led to the creation of British Columbia's Personalized Oncogenomics (POG) program, which has recruited more than 1,700 patients with advanced cancer, involved >80% of the medical oncologists in BC and published >50 manuscripts, including ***Annals of Oncol.*** 2022 Sept; 33(9):939-949. and ***Nature Cancer*** 2020 Apr 13: 1:452-468.

Dr. Marra continues to develop genomic approaches to stratify patients to personalized treatments, particularly for poor prognosis cancers where current treatment strategies are failing cancer patients and their families.

OTHER MENTORING ACTIVITY:

01/2014	Attended and provided feedback to Interdisciplinary Oncology Program students during their Thursday Oncology Trainee Seminars, as part of ONCO 510 course.
10/2012 – 05/2013	Mentor, Indspire Rivers to Success: Mentoring Indigenous Youth Program
09/2005 – 03/2006	Mentor, Life Sciences Research Tri-Mentoring Program, University of British Columbia
09/2002 – 2012	Mentor/Rotation Supervisor, Bioinformatics Training Program

GRANTS / FUNDING SUPPORT

APPLIED FOR

Granting Agency	Title	Years	Amount	Principal Investigator	Co-Investigator(s)
Terry Fox Research Institute	Marathon of Hope Cancer Centre Network, Pathfinder Phase II	05/01/2023 to 10/31/2024	Total amount: $218,868	Steven Jones (NPI)	Marco Marra
BC Cancer	Targeting Drivers of Lethal Glioma Brain Tumours	07/01/2024 to 06/30/2027	Total amount: $1,200,000	Carol Chen (NPI)	Marco Marra, Rebecca Harrison, Poul Sorensen, Peter Stirling, Stephen Yip, Mostafa Fatehi Hassanabad
Terry Fox Research Institute	Shaping precision medicine initiatives in BC and beyond through patient empowerment: a multimedia project	11/01/2024 to 11/30/2025	Total amount: $250,000	Natalie LeVasseur	Janessa Laskin, Marco Marra, and Steven Jones
Canada Foundation for Innovation	Multi-omic Analysis of Treatment Resistance and Cancer Heterogeneity (MATCH) *(Equipment grant)*	01/01/2025 to 12/31/2029	Total amount: $1,000,000	Marco Marra	
Canada Foundation for Innovation	A Pathogen-ready Arsenal of Next-generation lipid nanoparticle (LNP) messenger RNA (mRNA) therapeutics (PAN-RNA)	01/01/2025 to 12/31/2029	Total amount: $12,301,710	Eric Jan (NPI), Sabrina Leslie (NPI), and	

	(Equipment grant)			Marco Marra	
Cancer Research Society	Liver transplantation in metastatic colorectal cancer (mCRC) **-** A pilot study and correlative analysis characterizing tumor heterogeneity to inform ctDNA assays in CRC	09/01/2024 to 08/31/2025	Total amount: $130,000	Jonathan Loree	Marco Marra

CURRENTLY HELD

Granting Agency	Title	Years	Amount	Principal Investigator	Co-Applicant(s)
BC Cancer Foundation	Personalized OncoGenomics	07/01/2012 to 03/31/2025	Total amount: $40,700,000 $3,130769/yr GSC amount: $34,700,000 $2,669,230/yr	Marco Marra and Janessa Laskin	Karen Gelmon, Howard Lim, and Steven Jones
Canadian Institutes of Health Research	Exploring the relationship between the genome and the epigenome in cancers	07/01/2015 to 03/31/2025	Total amount: $4,149,777 $592,825/yr	Marco Marra	Program Experts: Joseph Connors, Randy Gascoyne, Gregory Cairncross, Michael McManus, Cheryl Arrowsmith, Gregg Morin, and Pamela Hoodless
Terry Fox Research Institute	The Enhanced Pancreatic Cancer Profiling for Individualized Care project	07/01/2017 to 06/30/2025	Total amount: $4,085,288 $510,661/yr GSC amount: $0	Daniel Renouf, David Schaeffer, Stephen Gallinger, George Zogopoulos, and Oliver Bathe	Gregg Morin, Steven Jones, Jennifer Knox, Sandra Fischer, Marco Marra, Chris O'Callaghan, and Malcolm Moore

Terry Fox Research Institute	Marathon of Hope BC Cancer Consortium-BC2C (MOHCCN)	06/11/2020 to 03/31/2025	Total amount: $13,056,160 $2,611,232/yr	Marco Marra and Daniel Renouf (Consortium Co-leads)	Christian Steidl, David Scott, Steven Jones, Janessa Laskin, David Schaeffer, Aly Karsan, David Sanford, Martin Hirst, Torsten Neilsen, Samuel Aparicio, Stephen Chia, Rebecca Deyell, and Rod Rassekh
Canada Foundation for Innovation	Cancer Single Cell Dynamics Observatory *(Equipment grant)*	01/01/2021 to 12/31/2025	Total amount: $5,992,026 $1,198,405/yr	Samuel Aparicio (NPI)	Alexander Bouchard-Cote, Connie Eaves, Marco Marra, Karen Cheung, David Huntsman, Peter Lansdorp, Megan Levings, Josef Penninger, and Christian Steidl
Genome BC	Genome BC Marathon of Hope Cancer Centre program (MOH002)	04/01/2022 to 03/31/2025	Total amount: $2,000,000 $1,000,000/yr	Marco Marra and Daniel Renouf	Steven Jones
Canada Foundation for Innovation	CGEn – A National Platform for Genome Sequencing and Analysis *(Equipment grant)*	04/01/2022 to 03/31/2026	Total amount: $28,655,584 $7,163,896/yr GSC amount $6,490,601 $1,622,650/yr	Stephen Scherer (NPI), Steven Jones, and Mark Lathrop	Marco Marra, Guillaume Bourque, Linlea Armstrong, Nada Jabado, Ioannis Ragoussis, and Lisa Strug
Canadian Institutes of Health Research	Discovery of HPV-associated genomic alterations in cervical cancer	07/01/2022 to 03/31/2027	Total amount: $420,750 $140,250/yr	Marco Marra	Steven Jones
National Institutes of Health	Enlisting HPV integration events to illuminate drivers and target treatment in invasive cervical cancer	07/01/2022 to 06/30/2027	Total amount: $183,226 USD $36,645 USD/yr	Janet Rader	Marco Marra

Terry Fox Research Institute	The Terry Fox New Frontiers Program Project Grant in Modeling lymphoma evolution and clinical trajectory using multiomics	09/01/2022 to 08/31/2028	Total amount: $6,000,000 $1,000,000/yr GSC amount: $1,486,196 $247,699//yr	Christian Steidl (NPI), Andrew Roth, Andrew Weng, David Scott, Ryan Morin, Graham Slack, and Marco Marra	Laura Hilton, Connie Eaves, Jeffrey Craig, Andrew Mungall, Adi Steif, and Kerry Savage
Canadian Institutes of Health Research	Dissecting the determinants and dynamics of cellular states promoting glioma evolution	04/01/2023 to 03/31/2028	Total amount: $1,040,400 $208,080/yr GSC amount: $0	Federico Gaiti	Marco Marra
Canadian Institutes of Health Research	The impact of chromosomal instability on ovarian cancer progression	04/01/2023 to 03/31/2029	Total amount: $902,700 $150,450/yr	Adi Steif	Marco Marra
Terry Fox Research Institute	Terry Fox Leader in Cancer Genome Science Award	10/01/2023 to 09/30/2028	Total amount: $5,000,000 $1,000,000/yr	Marco Marra	
Canada Foundation for Innovation	CGEn – Canada's national platform for genome sequencing and analysis *(Equipment grant)*	01/01/2024 to 12/31/2028	Total amount: $18,496,520 $4,624,130/yr GSC amount: $5,942,140	Stephen Scherer (NPI), Steven Jones, Mark Lathrop	Nada Jabado, Guillaume Bourque, Marco Marra, Kasmintan Schrader, Lisa Strug, Padmaja Subbarao, Ioannis Ragoussis
Alberta Cancer Foundation	A patient-derived organoid platform for next level breast cancer research	04/01/2024 to 03/31/2028	Total amount: $1,250,000	Ing Swie Goping	Marco Marra

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Granting Agency	**Title**	**Years**	**Amount**	**Principal Investigator**	**Co-Applicant(s)**
National Institutes of Health (USA) / NHGRI	The Human Genome Sequence: A pilot project	07/1996 to 06/1999	Total amount: $18,806,979 USD $626,899/yr	Robert H. Waterston	Marco Marra

			($28,210,468 CAD $940,348/yr)		
National Institutes of Health (USA) / NHGRI	Enhancing the Value of the *C. elegans* Genome	01/1998 to 01/2001	Total amount: $1,091,412 USD $363,804/yr ($1,637,118 CAD $545,706/yr)	Robert H. Waterston	Marco Marra
National Institutes of Health (USA) / NHGRI	Human BAC clone mapping	07/1998 to 06/2000	Total amount: $1,580,220 USD $790,110/yr ($2,370,330 CAD $1,185,165/yr)	Robert H. Waterston	Marco Marra
National Institutes of Health (USA) / NHGRI	Isolation of Mouse BAC Clones Anchored to the RH Map	07/1998 to 06/1999	Total amount: $351,376 USD ($527,064 CAD) (one year)	Robert H. Waterston	Marco Marra
National Institutes of Health (USA)	Zebrafish Genomic Resource Development	09/1998 to 09/2001	Total amount: $743,163 USD $247,721/yr ($1,114,744 CAD $371,581/yr)	S. Johnson	Marco Marra
National Institutes of Health (USA) / NHGRI	Sequencing the Human Genome	03/1999 to 02/2004 (ending 2000 for Marco)	Total amount: $27,184,915 USD $543,698/yr ($40,777,732 CAD $815,547/yr)	Robert H. Waterston	Marco Marra
National Institutes of Health (USA) / NHGRI	Sequencing the Mouse Genome	09/1999 to 10/2001	Total amount: $2,881,731 USD $960,577/yr ($4,411,211 CAD $1,470,403/yr)	John McPherson	Marco Marra

National Institutes of Health (USA) / NHGRI	ESTs Obtained for the Tumor Gene Index	04/1999 to 12/2002	Total amount: $2,042,784 USD $680,928/yr ($3,064,176 CAD $1,021,392/yr)	Robert H. Waterston	Marco Marra
Natural Sciences and Engineering Research Council of Canada	Genome and Transcriptome Analysis of the Human Pathogen *Cryptococcus neoformans* Grant #:228249-99	02/2000 to 01/2003	Total amount: $616,337 $205,445/yr GSC amount: $465,572 $155,190/yr	James Kronstad	Marco Marra, Steven Jones
Canada Foundation for Innovation	Team Leaders for Genome Sequence Centre *(Equipment grant)*	04/2000 to 03/2002	Total amount: $700,000 (one time amt.)	Marco Marra	Steven Jones
National Cancer Institute of Canada	Identifying Molecular Targets for Prevention and Treatment of Lung Cancer	06/2000 to 06/2003	Total amount: $874,321 $291,440/yr GSC amount: $165,927 $55,309/yr	Stephen Lam	Marco Marra, Wan Lam, Calum MacAulay, and Jean LeRiche
National Institutes of Health (USA) / NCI	A Molecular Classification of Brain Tumors	08/2000 to 01/2003	Total amount: $241,191 USD $80,397/yr ($370,452 CAD $123,484/yr)	Greg Riggins	Marco Marra
National Institutes of Health (USA)/ NCI / SAIC	Full Length cDNA Sequencing Contract #:20XS180	08/16/2000 to 02/29/2004	Total amount: $4,067,426 USD $1,208,659/yr ($6,124,809 CAD) $1,749,945/yr	Marco Marra	Steven Jones

National Institutes of Health (USA) / NIA	Genes with Major Effects on Life Span in *C. elegans* Sub-contract #99154561-1 *(Contract)*	08/01/2000 to 07/31/2007	Total amount: $375,000 USD $75,000/yr ($532,500 CAD $76,071/yr)	Don Riddle	Marco Marra
US Department of Agriculture (USDA)	High Throughput Fingerprinting of BAC Clones to Develop a Bovine Physical Map Agreement #58-5438-0-F143	09/2000 to 08/2003	Total amount: $1,100,000 USD $366,666/yr ($1,665,000 CAD $555,000/yr)	Marco Marra	
Agriculture and Agri-Food Canada	Bovine Genome Project	03/2001 to 03/2004	Total amount: $500,000 $166,666/yr	Stephen Moore	Marco Marra, Steven Jones, and Bernie Benkel
Agriculture and Agri-Food Canada	Sequencing and Evaluation of Random Expressed Sequence Tag (EST) Clones from Wheat Leaf Rust, *Puccinia triticina*, cDNA Libraries	04/2001 to 03/2002	Total amount: $69,850 (one year)	Guus Bakkaren	Steven Jones, Marco Marra, and Guanggan Hu
National Institutes of Health (USA) / NHGRI	Sequencing the Rat Genome	04/2001 to 03/2003	Total amount: $1,192,316 USD $397,438/yr ($1,877,124 CAD $625,708/yr)	John McPherson	Marco Marra
Genome Canada / Genome British Columbia	Genome BC Sequencing and Mapping platform – Competition I, II, Other	10/01/2001 to 12/31/2005	Total amount of Operating & Equipment: $24,260,478 $4,852,095/yr	Marco Marra	
Genome Canada / Genome British Columbia	Cancer Genomics – A multidisciplinary approach to the large-scale high throughput identification of genes involved in early stage cancer	10/01/2001 to 03/31/2006	Total amount: $16,740,911 $3,348,182/yr GSC Amount: $500,850 $111,300/yr	Victor Ling, Marco Marra, and Connie Eaves	Allen Eaves, Richard Gallagher, Keith Humphries, Jaclyn Hung, David Huntsman, Marco Marra, Steven Jones, Stephen Lam, Wan Lam, Calum MacAulay, Miriam Rosi,

					Juergen Vielkind, Jaclyn Hung, Wilf Jeffries, Peter Lansdorp, Nhu Le, James Piret, Neal Poulin, Marianne Sadar, and Isabella Tai
Michael Smith Foundation for Health Research	Supplemental Training Program Award (CIHR: Bioinformatics training for health research) Award #TP-SUP-006011	03/01/2002 to 02/28/2007	Total amount: $300,000 $75,000/yr	Steven Jones	David Baillie, Philip Hieter, Marco Marra, Fiona Brinkman, Jenny Bryan, Anne Condon, Arvind Gupta, Francis Ouellette, and Frederic Pio
Canadian Institutes of Health Research	Bioinformatics Training for Health Research Training Program STP-53919	03/01/2002 to 08/31/2009	Total amount: $2,020,821 $224,535/yr GSC amount: $1,800,000 $225,000/yr	Steven Jones	David Baillie, Phil Hieter, Marco Marra, Fiona Brinkman, Jenny Bryan, Anne Condon, Arvind Gupta, Francis Ouellette, and Frederic Pio
Natural Sciences and Engineering Research Council of Canada	Cloning and Characterization of Inxs and Echinus, Two Genes Involved in Programmed Cell Death in *Drosophila*	04/01/2002 to 03/31/2007	Total amount: $211,400 $42,280/yr	Marco Marra	
Genome Canada / Genome British Columbia	Comparative and Functional Genomics of the Human Pathogen *Cryptococcus neoformans*	07/01/2002 to 03/30/2005	Total amount: $1,079,279 $359,757/yr	James Kronstad	Robert Brunham, Marco Marra, Steven Jones, and Colleen Nelson
Genome Canada / Genome British Columbia	Expression Profiles of Cells and Tissues in *C. elegans*	07/01/2002 to 03/31/2005	Total amount: $3,000,000 $1,000,000/yr GSC Amount: $706,426	David Baillie	Don Moerman, Marco Marra, Steven Jones, Francis Ouellette, Claes Wahlestedt, Erik Sonnhammer, Robert Olafson, Ana Vas Gomes, and Thomas Burglin

Genome Canada / Genome British Columbia	Bioinformatics of Mammalian Gene Expression	07/01/2002 to 03/31/2006	Total amount: $6,134,386 $1,533,596/yr	Steven Jones and Marco Marra	
Canadian Institutes of Health Research	Genomics, Genetics, & Gerontology (G3): A multidisciplinary team for the study of healthy aging	10/2002 to 03/2003	Total amount: $5,000	Marco Marra	Angela Brooks-Wilson
Prostate Cancer Research Foundation of Canada	SAGE Analysis of Androgen-Independent Prostate Cancer	01/2003 to 12/2003	Total amount: $50,000 GSC amount: $0	Marianne Sadar	Marco Marra
Genome Canada	SARS – High throughput sequencing and analysis of an emerging pathogen	03/2003 to 04/2003	Total amount: $58,400	Marco Marra	
National Institutes of Health (USA) / NCI (SAIC)	SAGE Sequencing of Mouse Genome to Develop an Atlas of Gene Expression Sub-contract # 23XS007	04/01/2003 to 03/31/2006	Total amount: $1,000,000 USD $333,333/yr ($1,300,000 CAD $433,333/yr)	Marco Marra	
Canadian Institutes of Health Research	Genomics, Genetics & Gerontology (G3): A multidisciplinary team for the study of healthy aging Grant #: 116074	04/01/2003 to 03/31/2009	Total amount: $1,159,844 $231,969/yr	Marco Marra and Angela Brooks-Wilson	Steven Jones, Nhu Le, Joseph Connors, and Graydon Meneilly
National Institutes of Health (USA) / NHGRI	Improvements in BAC Fingerprinting and End Sequencing	04/09/2003 to 11/30/2006	Total amount: $4,316,678 USD $1,438,893/yr ($5,902,812 CAD $1,987,020/yr)	Marco Marra	Steven Jones and Jacqueline Schein
British Columbia Government / Michael Smith Foundation for Health Research	SAVI (SARS Accelerated Vaccine Initiative)	05/2003 to 10/2003	Total amount: $2,600,000 GSC amount: $0	Brett Finlay and Robert Brunham	Marco Marra and Caroline Astell

Michael Smith Foundation for Health Research	Institutional Infrastructure Proposal for Health Research for the BCCA *(Infrastructure grant)*	06/2003 to 03/2006	Total amount: $2,198,038 $1,099,019/yr GS amount: $0	Victor Ling	M Bally, D Banerjee, A Brooks-Wilson, K Chi, L Chiu, A Coldman, J Connors, S Dedhar, R Doll, R Durand, A Eaves, C Eaves, R Gallagher, D Garner, R Gascoyne, K Gelmon, D Hogge, R Holt, P Hoodless, K Humphries, D Huntsman, S Jones, A Karsan, R Kay, T Keane, G Krystal, S Lam, W Lam, P Lansdorp, W Linden, V Ling, C MacAulay, D Mager, M Marra, L Mayer, M McBride, N Murray, MB Nelson, S O’Reilly, P Olive, I Olivotto, M Rosin, T Ruth, M Sadar, C Smith, and J Spinelli
Genome Canada / Genome British Columbia	A Quantitative and Comprehensive Atlas of Gene Expression in Mouse Development	07/01/2003 to 03/31/2006	Total amount: $13,195,524 $4,398,508/yr GSC Amount: $4,578,549 $1,526183/yr	Marco Marra and Pamela Hoodless	Elizabeth Simpson, Gregory Riggins, Steven Jones, and Cheryl Helgason
Canadian Institutes of Health Research	SARS: A scientific collaborative to support public health response through vaccination	08/2003 to 08/2004	Total amount: $500,000 GSC amount: $0	Danuta Skowronski	Bob Brunham, David Patrick, Marco Marra, Timothy Booth, David Scheifele, Martin Petric, Babak Pourboholoul, Caroline Astell,

					Lorne Babiuk, Yosssef Av-Gay, William Bowie, Mel Krajden, Steven Jones, Monka Naus, Valencia Remple, James Russell, Christopher Richardson, Raymond Tellier, Lauren Meyesers, Allison McGeer, Theresa Tam, and Michael Drebot
National Institutes of Health (USA) / NHGRI	Sequencing the Mouse Genome (Xenopus full-length cDNA sequencing)	11/01/2003 to 10/31/2004	Total amount: $800,000 USD ($1,040,000 CAD)	Richard Wilson	Marco Marra
National Institutes of Health (USA) / NCI (SAIC)	Creation of a Publicly Available SAGE Dataset from NIH Approved Human ES Cell Lines	12/10/2003 to 05/09/2005	GSC amount: $330,000 USD $165,000/yr ($409,200 CAD) ($204,600/yr)	Marco Marra and Connie Eaves	
National Institutes of Health (USA)	Genomic and Proteomic Analysis of Androgen Independent Prostate Cancer Grant #: 1R01CA105304-01	04/01/2004 to 02/28/2010	Total amount: $1,078,854 USD $215,770/yr ($1,383,750 CAD $276,750/yr)	Marianne Sadar	Marco Marra, Steven Jones, Yuzhou Wang, and Robert Holt
NCI-FCRDC / SAIC	Mammalian Gene Collection (MGC) Solicitation S03-105 *(Contract)*	06/14/2004 to 09/25/2008	Total amount: $7,566,411 USD $1,891,602/yr	Marco Marra	
Michael Smith Foundation for Health Research	Cancer, the Environment and Occupation (CEO); the program of the Cancer Control Research Unit at the BCCA *(Infrastructure grant)*	07/01/2004 to 03/31/2009	Total amount: $724,311 $160,958/yr GSC Amount: $0	Richard Gallagher	Angela Brooks-Wilson, Marco Marra, Steven Jones, John Spinelli, Nhu Le, and Chris Bajdik

Genome Canada	Bovine Genome Project: Full Insert cDNA Sequencing Plan	08/01/2004 to 07/31/2007	Total amount: $6,046,272 $2,015,424/yr GSC amount: $4,725,523 $1,575,174/yr	Marco Marra, Robert Holt, Steven Jones, and Stephen Moore	
National Institutes of Health (USA)	Optical Systems for In Vivo Molecular Imaging of Cancer	09/01/2004 to 08/31/2009	Total amount: $8,583,213 USD $1,716,642/yr ($10,471,519 CAD) GSC amount: $133,000 USD ($162,260 CAD)	Michael Descour, Rebecca Richards-Kortum, Calum MacAulay, and Konstantin Sokolov	Karen Adler-Storthz, Steven Jones, Stephen Lam, Wan Lam, Peter Lansdorp, Marco Marra, Wadih Arap, Neely Atkinson, Lezlee Coghlan, Michele Follen, Ann Gillenwated, Martial Guillaud, Walter Hittelman, Miaden Korbelik, Brian Korgel, Mia Markey, Renata Pasqualini, Miriam Rosin, Krishnendu Roy, and William Satterfield
Genome Canada	Genomic Tools for Diagnosis and Evaluation of Mental Retardation	10/01/2004 to 09/30/2007	Total amount: $5,558,741 $2,779,731/yr GSC amount: $2,117,504 $705,834/yr	Jan Friedman and Marco Marra	Steven Jones, Sylvie Langlois, Patrice Eydoux, Bartha Knoppers, Carlo Marra, and Robert Holt Key personnel: Agnes Baross and Allen Delaney
Genome Canada	A Genomic Approach to the Identification of the Genetic and Environmental Components Underlying Berry Quality in Grapevine	11/01/2004 to 10/31/2007	Total amount: $3,134,481 $1,044,827/yr GSC amount: $890,195 $222,548/yr	Jose Martinez-Zapater, and Stephen Lund	Marco Marra, Steven Jones, Patricia Bowen, Robert Olafson, and Joerg Bohlmann
Genome Canada	Genome BC Sequencing and Mapping Platform (Applied Genomics & Proteomics)	01/05/2005 to 12/31/2007	Total amount: $1,486,231 $495,410/yr	Marco Marra	

National Cancer Institute of Canada	Biology of Cancer: Follicular lymphoma as a model of cancer progression	07/01/2005 to 06/30/2008	Total amount: $3,540,067 $1,180,022/yr GSC amount: $1,892,414 $630,804/yr	Joseph Connors	Randy Gascoyne, Douglas Horsman, and Marco Marra
Canada Foundation of Innovation	CMCP (Canadian Molecular Cytogenetics Platform) *(Equipment grant)*	07/01/2005 to 12/31/2009	Total amount: $11,215,190 $2,803,797/yr GSC amount: $2,500,000 $625,000/yr	Jan Friedman	Marco Marra, Oliver Cohen, Regen Drouin, Bartha Knoppers, Peter Lansdorp, Sabine Mai, Guy Rouleau, Jeremy Squire, and Rosanna Weksberg
Western Economic Diversification	Next generation sequencing *(Equipment grant)*	12/01/2005 to 12/01/2006	Total amount: $1,075,000	Marco Marra	
Stem Cell NCE & StemCell Technologies	Development of Technologies for the Derivation, Propagation and Differentiation of hESC	10/01/2005 to 09/30/2008	Total amount: $1,722,000 $574,000/yr GSC amount: $74,618 $24,872/yr	James Piret, Mick Bhatia, Connie Eaves, and Andras Nagy	Keith Humphries, Aly Karsan, Derek van deer Kooy, Peter Lansdorp, Stephen Lye, Marco Marra, Derrick Rancourt, Janet Rossant, and Peter Zandstra
Genome British Columbia / Genome Canada	Genome BC: Large-scale High-throughput Genomics Platforms at BCCA – GSC	01/01/2006 to 12/31/2008	Total amount: $8,907,686 $2,969,288/yr	Marco Marra, Steven Jones, and Robert Holt	Asim Siddiqui, Martin Hirst, Inanc Birol, Martin Krzywinski, Allen Delaney, Francis Ouellette, and Jacqueline Schein
Genome Canada	High Resolution Analysis of Follicular Lymphoma Genomes	01/01/2006 to 12/31/2009	Total amount: $9,341,856 $2,335,464/yr	Marco Marra, Joseph Connors, and Randy Gascoyne	Douglas Horsman, Martin Krzywinski, Jacqueline Schein, Robert Holt, Steven Jones, and Carlo Marra

Genome Canada	Dissecting Gene Expression Networks in Mammalian Organogenesis	01/01/2006 to 06/30/2010	Total amount: $7,770,032 $1,726,673/yr	Pamela Hoodless and Marco Marra	Aly Karsan, Cheryl Helgason, Steven Jones, Sidney Katz, and Ed Levy
Vancouver Foundation	Enriching Genomics in High School Science Curricula	07/01/2006 to 11/30/2007	Total amount: $23,500 GSC amount: $0	Sidney Katz	Marco Marra
Michael Smith Foundation for Health Research	BC Clinical Genomics Network (formerly Expression of Interest for a Family Studies Platform) *(Infrastructure grant)*	04/01/2007 to 09/30/2014	Total amount: $3,550,000 $710,000/yr GSC amount: $0	Jan Friedman and Michael Hayden	Laura Arbour, Jehannine Austin, Leigh Field, Sylvie Langlois, Carlo Marra, Marco Marra, and Sian Spacey
Heart and Stroke Foundation of Canada	Dissecting Gene Regulatory Networks in Cardiac Cushion Development	07/01/2007 to 06/30/2010	Total amount: $376,416 $124,472/yr GSC amount: $0	Aly Karsan	Pamela Hoodless, Marco Marra, and Steven Jones
Michael Smith Foundation for Health Research	Model Systems and Cancer Therapeutics *(Infrastructure grant)*	07/01/2007 to 06/30/2011	Total amount: $800,000 $200,000/yr GSC amount: $250,000 $62,500/yr	Philip Hieter	Samuel Aparicio, David Huntsman, Marco Marra, Don Riddle, Michel Roberge, and Ann Rose
National Institutes of Health (USA)	A comprehensive catalog of human DnaseI hypersensitive sites	09/30/2007 to 01/31/2010	Total amount: $15,031,440 USD $110,766/yr Direct cost: $410,704 USD $102,676/yr GSC amount: $0	John Stamatoyannopolous	Marco Marra and Steven Jones
Genome British Columbia	The mountain pine beetle epidemic	01/01/2008 to 12/31/2009	Total amount: $4,063,524 $2,031,762/yr GSC amount: $800,000	Joerg Bohlmann and Janice Cooke	Brian Aukema, Colette Breuil, Gary Bull, David Coltman, Richard Hamelin, Robert Holt, Dezene

			$400,000/yr		Huber, Steven Jones, Chris Keeling, Martin Luckert, Marco Marra, and Felix Sperling
Genome Canada	Production-scale deployment of next-generation sequencing instruments	04/01/2008 to 03/31/2010	Total amount: $1,912,521 $956,260/yr	Marco Marra, Robert Holt, and Steven Jones	Martin Hirst
Genome Canada	Towards single cell genomics	04/01/2008 to 03/31/2010	Total amount: $1,824,278 $912,139/yr GSC amount: $990,304 $495,152/yr	Carl Hansen and Marco Marra	Samuel Aparicio, Steven Jones, Robert Holt, and Martin Hirst
Canadian Institutes of Health Research	SynTarg Discovery Program: Use of a Genome Wide siRNA Screen To Identify Targets that will Enhance Platinum-Containing Chemotherapy when used in First Line Therapy of Non-Small Cell Lung Cancer	07/01/2008 to 06/30/2011	Total amount: $477,534 $159,178/yr	Marcel Bally	Samuel Aparicio, Steven Jones, Janessa Laskin, and Marco Marra
Canadian Cancer Society Research Institute (formerly National Cancer Institute of Canada)	Biology of Cancer: Insights from Genomic Analyses of Lymphoid Neoplasms	07/01/2008 to 06/30/2013	Total amount: $6,284,994 $1,256,998/yr GSC amount: $2,370,516 $474,103/yr	Joseph Connors, Randy Gascoyne, Douglas Horsman, and Marco Marra	Steven Jones Key personnel: Jacqueline Schein, Martin Hirst, Allen Delaney, and Ryan Morin
National Institutes of Health (USA) - SAIC - Frederick	Sequencing for Discovery of Candidate Mutations in Lymphoma Transcriptomes *(Contract)*	07/01/2008 to 06/30/2014	Total amount: $ 14,213,780 USD $2,368,963/yr GSC amount: $10,842,220 USD $1,807,036/yr	Marco Marra	Steven Jones, Martin Hirst
Canadian Breast Cancer Foundation	Alternative spliced genes in CrkRS/Her2 co-amplified breast cancer	09/01/2008 to 08/31/2010	Total amount: $140,000 $70,000/yr	Gregg Morin	Marco Marra

National Institutes of Health (USA)	Integrated epigenetic maps of human embryonic and adult cells	09/30/2008 to 06/30/2014	Total amount: $14,075,540 USD $2,815,108/yr GSC amount: $3,890,144 USD $778,028/yr	Marco Marra and Joseph Costello	Steven Jones, Martin Hirst, Robyn Roscoe, Arturo Alvarez-Buylla, Peggy Farnham, Susan Fisher, David Haussler, James Kent, Michael McManus, Thea Tlsty, Ting Wang, Arthur Weiss, Allan Balmain, Pieter De Jong, Joe W. Gray, Gary Karpen, Pui-Yan Kwok, Barbara Panning, Dan Pinkel, Mark Segal, Scott VandenBerg, and Keith Yamamoto
US Army Department of Defense	Dissecting genomic and epigenomic heterogeneity in metastatic breast tumors	01/01/2009 to 06/30/2010	Total amount: $301,460 USD $150,730/yr ($317,437 CAD $158,718/yr)	Samuel Aparicio	Marco Marra and Carl Hansen
Genome British Columbia	Genome BC Genomics Platforms at BC Cancer Agency Genome Sciences Centre	01/01/2009 to 06/30/2011	Total amount: $6,471,892 $2,588,756/yr	Marco Marra, Steven Jones, and Robert Holt	Inanc Birol, Allen Delaney, Martin Hirst, Richard Moore, and Jacqueline Schein
Natural Sciences and Engineering Research Council of Canada	Graduate Program in High-Throughput Biology	09/01/2009 to 04/01/2015	Total amount: $1,650,000 $275,000/yr	Stephen Withers	Joerg Bohlmann, Lindsay Eltis, Leonard Foster, Robert Hancock, Carl Hansen, Philip Hieter, Marco Marra, Andre Marziali, and Michel Roberge

Canadian Institutes of Health Research	Bioinformatics Training for Health Research	09/01/2009 to 08/31/2015	Total amount: $1,950,000 $325,000/yr	Steven Jones and Fiona Brinkman	Paul Pavlidis, David Baillie, Anne Condon, Jack (Nansheng) Chen, Wyeth Wasserman, Cenk Sahinalp, Jenny Bryan, and Marco Marra
National Institutes of Health (USA)	Cancer transcriptome characterization using massively parallel DNA sequencing (TCGA) *(Contract)*	09/29/2009 to 06/30/2016	Total amount: $10,876,230 USD $1,776,158/yr	Marco Marra	Key personnel: Steven Jones, Martin Hirst, Richard Moore, Yongjun Zhao, Allen Delaney, Ryan Morin, Robert Holt, and Robyn Roscoe
Canada Foundation for Innovation	Ultra-high-throughput DNA Sequencing Platform for Large Scale Genome Analysis **(Grant #: 20070)** *(Equipment grant)*	01/01/2010 to 03/31/2016	Total amount: $ 25,810,880 $5,162,176/yr	Marco Marra	Steven Jones, Robert Holt, Samuel Aparicio, David Huntsman, David Baillie, Joerg Bohlmann, Robert Brunham, Philip Hieter, and Jan Friedman
British Columbia Knowledge Development Fund	Ultra-high-throughput DNA sequencing platform for large-scale genome analysis *(Equipment grant)*	02/19/2010 to 03/31/2015	Total amount: (Please refer to CFI grant)	Marco Marra	Steven Jones, Robert Holt, Samuel Aparicio, David Huntsman, David Baillie, Joerg Bohlmann, Robert Brunham, Philip Hieter, and Jan Friedman
Canadian Institutes of Health Research	Massively parallel genomic sequencing for clinical identification of mutations that cause intellectual disability	04/01/2010 to 03/31/2013	Total amount: $450,873 $150,291/yr GSC amount: $316,491 $105,497/yr	Jan Friedman	Cornelius Boerkoel and Marco Marra
California Institute for Regenerative Medicine	Development of Highly Active Anti-Leukemia Stem Cell Therapy (HALT)	04/01/2010 to 03/31/2015	Total amount: $18,859,590 CAD $4,714,897/yr GSC amount:	Dennis Carson and John Dick	Catriona Jamieson, Jean Wang, Jayne Danska, and Thomas Kipps, **Collaborators:** Thomas Hudson

			$4,204,507 CAD $1,051,126/yr		Kelly Fraser and Marco Marra
Canadian Institutes of Health Research	The Terry Fox New Frontiers Program Project Grant in the genomics of forme fruste tumours: new vistas on cancer biology and management	07/01/2010 to 06/30/2013	Total amount: $3,126,365 $1,042,121/yr GSC amount: $486,000 $162,000/yr	David Huntsman, Samuel Aparicio, Peter Lansdorp, Marco Marra, Torsten Nielsen, Carl Hansen, Poul Sorensen, and Tully Underhill	Sohrab Shah, Martin Hirst, and Stephen Yip
Genome British Columbia	Linking Cholesterol Metabolism, Callousness and Conduct Disorder	09/01/2010 to 08/31/2011	Total amount: $120,770	Cornelius Boerkoel and Marco Marra	Beatrice Golomb, Richard Kelley, and Christele du Souich
Cancer Research Society	Characterizing cell-based models for non-Hodgkin's lymphoma	09/01/2010 to 08/31/2012	Total amount: $119,964 $59,982/yr	Marco Marra	Andrew Mungall and Ryan Morin
BC Cancer Foundation	BC Cancer Foundation Innovation Support Fund-2010 *(Equipment grant)*	01/01/2011 to 03/31/2011	Total amount: $11,977	Marco Marra	
Western Economic Diversification Canada	High throughput DNA sequencers at the BC Cancer Agency Genome Sciences Centre *(Equipment grant)*	02/01/2011 to 03/31/2013	Total amount: $3,935,000 $1,967,500/yr	Marco Marra	
Genome Canada	Genomics Innovation Centre at the BC Cancer Agency	04/01/2011 to 03/31/2013	Total amount: $6,626,905 $3,313,452/yr	Marco Marra, Steven Jones, and Robert Holt	
Ontario Institute for Cancer Research	Strategic Plan Initiative Project - Medulloblastoma Advanced Genomics International Consortium	04/01/2011 to 03/31/2014	Total amount: $299,726 $74,931/yr	Michael Taylor, Marco Marra, and	

			GSC amount: $215,508 $71,836/yr	David Malkin	
Canadian Breast Cancer Research Alliance	Genome heterogeneity in predictive models of drug action in triple negative breast cancer	04/01/2011 to 03/31/2015	Total amount: $1,153,953 $288,488/yr	Samuel Aparicio	Stephen Chia, Connie Eaves, Karen Gelmon, Tak Mak, Marco Marra, Montgomery Martin, and Sohrab Shah
National Institutes of Health – SAIC – Frederick	HIV tumour molecular characterization project *(Contract)*	07/08/2011 to 05/31/2017	Total amount: $15,690,530 USD $2,615,088/yr	Marco Marra	Steven Jones and Martin Hirst
National Institutes of Health (USA)	RNAseq and miRNA seq for ovarian cancer samples as part of TCGA *(Contract)*	07/11/2011 to 07/10/2012	Total amount: $621,103 USD	Marco Marra	
Genome Canada/ Canadian Institutes of Health Research	The Canadian Pediatric Cancer Genomic Consortium: Translating next-generation sequencing technologies into improved therapies for high-risk childhood cancer	07/01/2011 to 09/30/2013	Total amount: $2,827,359 $1,413,679/yr GSC amount: $1,384,135 $692,067/yr	Poul Sorensen, Conrad Fernandez, Cynthia Hawkins, Annie Huang, Nada Jabado, David Malkin, Daniel Sinnett, and Michael Taylor	Guillaume Bourque, Steven Jones, Marco Marra, Alexandre Montpetit, Kirk Schultz, and Stephen Yip
Genome British Columbia	Genomics applied to the management of high-risk AML/myelodysplastic syndromes	07/01/2011 to 03/30/2014	Total amount: $3,113,494 $1,556,747/yr	Aly Karsan and Marco Marra	Donna Hogge, Steven Jones, Keith Humphries, Stuart Peacock, Peter Chow-White, and Andrew Feenberg
Genome Canada	Stratifying and Targeting Pediatric Medulloblastoma Through Genomics (MAGIC)	07/01/2011 to 03/31/2015	Total amount: $9,856,814 $3,285,604/yr GSC amount: $5,244,176	Marco Marra, Michael Taylor, and David Malkin	Carlo Marra, Donald Mabbott, Steven Jones, Stephen Scherer, Cynthia Hawkins, Eric

			$1,748,059/yr		Bouffet, James Rutka, Jennifer Chan, Jennifer Chan, Stephan Pfister, Gary Bader, Yoon-Jae Cho, Scott Pomeroy, and Stephen Clifford
Canadian Institutes of Health Research	Centre for Epigenome Mapping Technologies	01/01/2012 to 12/31/2016	Total amount: $6,000,000 $1,200,000/yr GSC amount: $5,161,843 $1,032,368/yr	Marco Marra, Martin Hirst, and Steven Jones	Samuel Aparicio, Max Cynader, Connie Eaves, Randy Gascoyne, David Huntsman, Aly Karsan, and Michael Kobor, Joseph Connor, Christian Steidl, Andrew Weng, and Sam Wiseman
Lions Club International Foundation	Lions Club International Foundation Equipment Award *(Equipment grant)*	06/01/2012 to 05/31/2012	Total amount: $147,041	Marco Marra	
Terry Fox Research Institute	Modeling and Therapeutic Targeting of the Clinical and Genetic Diversity of Glioblastoma	07/01/2012 to 06/30/2018	Total amount: $8,178,787 $3,716,846/yr GSC amount: $ 1,858,423 $464,605/yr	Gregory Cairncross	Marco Marra, Steven Jones, Samuel Weiss, Stephen Robbins, David Kaplan, and David Mason
BC Cancer Foundation	Graduate student support for lymphoma research in the ANGELYC project	09/26/2012 to 09/25/2017	Total amount: $125,000 $25,000/yr	Marco Marra and Joseph Connors	
BC Cancer Foundation	BC Cancer Foundation Innovation Support Fund - The Milan and Maureen Ilich Foundation *(Equipment grant)*	12/01/2012 to 03/31/2013	Total amount: $31, 636	Marco Marra and Angela Brooks-Wilson	
NIH-SAIC-Frederick	Molecular characterization and validation of pediatric cancers *(Contract)*	04/01/2013 to 03/31/2015	Total amount: $3,801,971 USD $1,900,985/yr GSC amount: $3,009,173	Marco Marra	

			USD $1,504,586/yr		
Genome Canada	Genome Canada Science and Technology Innovation Centre 2013	04/01/2013 to 09/30/2015	Total amount: $ 8,983,109 $4,491,554/yr	Marco Marra, Steven Jones, and Robert Holt	
Canada Foundation for Innovation	Compute Canada GSC Node	04/01/2013 to 03/31/2017	Total amount: $942,116 $235,529/yr GSC amount: $711,499 $177,874/yr	Marco Marra	
Genome Canada	Personalized Treatment of Lymphoid Cancer: British Columbia as Model Province	04/01/2013 to 03/31/2018	Total amount: $10,232,800 $2,558,200/yr GSC amount: $ 3,777,648 $944,412/yr	Joseph Connors, Marco Marra, and Randy Gascoyne	Stuart Peacock, Steven Jones, and Christian Steidl
BC Cancer Foundation	Pediatric Personalized Genomics	04/10/2013 to 03/31/2022	Total amount: $703,889 $100,555/yr	Marco Marra	
University of British Columbia	Moving the needle for glioblastoma multiforme	07/01/2013 to 06/30/2018	$563,142 $112,628/yr	Marco Marra	Key personnel: Suganthi Chittaranjan
NIH-SAIC-Frederick	Response to Solicitation X13-1093 for additional sequencing in TCGA *(Contract)*	07/03/2013 to 08/15/2014	Total amount: $357,725 USD	Marco Marra	
The Leukemia and Lymphoma Society of Canada	MLL2 interactions in Non-Hodgkin Lymphomas	07/01/2013 to 06/30/2015	Total amount: $120,000 $60,000/yr	Marco Marra	Samuel Aparicio

Terry Fox Research Institute	The Terry Fox New Frontiers Program Project in Molecular Correlates of Treatment Failure in Lymphoid Cancers	07/01/2013 to 06/30/2016	Total amount: $3,885,626 $971,406//yr GSC amount: $1,453,617 $363,404/yr	Randy Gascoyne, Joseph Connors, Marco Marra, Sohrab Shah, and Christian Steidl	Steven Jones
American Association of Cancer Research	Immunogenomics to create new therapies for high-risk childhood cancers	07/01/2013 to 06/30/2017	Total amount: $1,816,044 USD $454,011/yr GSC amount: $348,704 USD $87,176/yr	John Maris, Malcolm Brenner, Donald Parsons, Nabil Ahmed, William Weiss, Stephan Grupp, Javed Khan, Crystall Mackall, Marco Marra, Poul Sorensen, Michael Taylor, and Michael Jensen	
Terry Fox Research Institute	The Terry Fox New Frontiers Program Project in The Genomics of Forme Fruste Tumours: New Vistas on Cancer Biology and Treatment	07/01/2013 to 06/30/2018	Total amount: $7,500,000 $1,500,000/yr GSC amount: $486,000 $97,200/yr	David Huntsman, Samuel Aparicio, Carl Hansen, Martin Hirst, Marco Marra, Gregg Morin, Ryan Morin, Torsten Nielsen, Sohrab Shah, Poul Sorensen, T. Michael Underhill, and Anna Tinker	Stephen Yip, Jessica McAlpine, and Cheng-Han Lee

Canada Foundation for Innovation	Genomics approaches to personalizing cancer diagnosis and treatment *(Equipment grant)*	04/01/2014 to 12/31/2017	Total amount: $14,204,540 $4,734,846/yr GSC amount: $14,140,000 $1,713,333/yr	Marco Marra, Steven Jones, Robert Holt, Aly Karsan, Samuel Aparicio, David Huntsman, Karen Gelmon, Janessa Laskin, Paul Rogers, and Brian Toyota	
National Institutes of Health	Princess Margaret Phase 1 Consortium	04/07/2014 to 02/28/2019	Total amount: $1,756,985 USD $351,397/ yr	Lillian L. Siu, Daniel Sullivan, Sebastian Hotte, and Kim Chi	Key Personnel: Samuel Aparicio, David Huntsman, Steven Jones, Marco Marra, Daniel Renouf, Christian Kollmannsberger, Anna Tinker, and 38 others
Genome Canada	Sequencing Platform at the BC Cancer Agency Genome Sciences Centre-Genomics Innovation Network Node	04/01/2015 to 03/31/2017	Total amount: $2,000,000 $1,000,000/yr	Robert Holt	Marco Marra
Canada Foundation for Innovation	Canada's Genomics Enterprise (CGEn): A national genomic tools network for transforming life science research *(Equipment grant)*	04/01/2015 to 03/31/2020	Total amount: $58,435,140 $11,687,028/yr GSC amount: $ 20,910,670 $4,182,134/yr	Steven Jones, Stephen Scherer, Mark Lathrop, Guillaume Bourque, Michael Brudno, Robert Holt, Aly Karsan, Marco Marra, Jiannis Ragoussis, and Michael Taylor	
Stand-up to Cancer (Canada) /	Translational development of novel drugs targeting tumor vulnerabilities	09/01/2015 to 08/31/2019	Total amount: $9,000,000 CAD $2,250,000/yr	Tak Mak, Samuel Aparicio, Morag Park,	Francois Benard, Marco Marra, Sohrah Shah, Montgomery

American Association for Cancer Research			GSC amount: $0	Kathleen Pritchard, and Karen Gelmon	Martin, Stephen Chia, and Wendie den Brok
Genome Canada	Methods and Technology Development at the Sequencing Platform at the BC Cancer Agency Genome Sciences Centre	10/01/2015 to 09/30/2017	Total amount: $2,000,000 $1,000,000/yr	Robert Holt and Marco Marra	Steven Jones, Inanc Birol, Carl Hansen, Robin Coope, Andrew Mungall, Ryan Morin, and Robyn Roscoe
Stand-up to Cancer (Canada) / American Association for Cancer Research	Targeting Brain Tumour Stem Cell Epigenetic and Molecular Networks	10/01/2015 to 09/30/2020	Total amount: $11,791,833 CAD $2,947,958/yr GSC amount: $1,372,095 $343,023/yr	Peter Dirks, Samuel Weiss, Marco Marra, Mathieu Lupien, Amy Caudy, Michael Tyers, Michael Salter, Michael Taylor, Warren Mason, Trevor Pugh, Nada Jabado, Cheryl Arrowsmith, Gary Bader, and Eric Bouffet	
Genome British Columbia	Northern Biobank Initiative: Phase 2	10/01/2015 to 03/31/2022	Total amount: $1,250,000 $312,500/yr	Nadine Caron	Marco Marra
Canadian Institutes of Health Research	Development of an automated end-to-end next generation sequencing assay to detect all classes of genetic variant in a single diagnostic test	04/01/2016 to 03/31/2022	Total amount: $906,304 $302,101/yr	Aly Karsan and Marco Marra	Inanc Birol, Richard Moore, Yongjun Zhao, Robin Coope, Peter Watson, Hagen Kennecke, Cheryl Ho, Ian Bosdet, and Lucas Swanson
Terry Fox Research Institute	The Terry Fox Precision Oncology For Young peopLE	04/01/2016 to 03/31/2023	Total amount: $5,000,000 $1,000,000/yr	David Malkin	Gregg Morin, Steven Jones and Marco Marra

			GSC amount: $565,767 $113,153/yr		
Genome Canada	Automated Tumour Pathology	07/01/2016 to 09/30/2018	Total amount: $409,858 $204,929/yr GSC amount: $363,569 $181,784/yr	Marco Marra and Robin Coope	Calum MacAulay
Terry Fox Research Institute	Overcoming treatment failure in lymphoid cancers	07/01/2016 to 12/31/2022	Total amount: $7,500,000 $1,500,000/yr GSC amount: $ 2,361,102 $472,220/yr	Christian Steidl, Joseph Connors, Marco Marra, Ryan Morin, David Scott, Andrew Weng, Sohrab Shah, and Pedro Farinha	Andrew Mungall, Gregg Morin, Carl Hansen, and Graham Slack
National Institutes of Health	Contract 14X292 (Molecular characterization of HIV malignancies)	08/19/2016 to 04/12/2024	Total amount: $3,443,583 USD $573,930/yr	Marco Marra	
Genome British Columbia	Personalized OncoGenomics 3.0	10/31/2016 to 03/31/2020	Total amount: $2,000,000 $500,000/yr	Janessa Laskin and Marco Marra	Steven Jones and Dean Regier
Canadian Institutes of Health Research	Centre for Epigenome Mapping Technologies	02/01/2017 to 01/31/2023	Total amount: $4,534,483 $906,896/yr GSC amount: $1,727,800 $345,560/yr	Martin Hirst, Marco Marra, and Steven Jones	Samuel Aparicio, Connie Eaves, Pascal Lavoie, Daniel Renouf, and Kirk Schultz
Terry Fox Research Institute	Terry Fox Canadian Comprehensive Cancer Centre Network Pilot (T4CN Pilot)	04/01/2017 to 03/31/2020	Total amount: $2,000,000 $1,000,000/yr	Francois Benard and Bradley Wouters	Marco Marra, Trevor Pugh, Brad Nelson, Pamela Ohashi, David Jaffray, Alejandro Berlin and Steven Jones
Genome Canada	BC Cancer Agency Genome Sciences Centre Genomics Technology Platform	04/01/2017 to 03/31/2023	Total amount: $9,641,002 $1,606,833yr GSC amount: $8,753,776	Marco Marra, Steven Jones, Martin Hirst and Corey Nislow	

			$1,458,962/yr		
Genome Canada	Tackling Childhood Brain Cancer at the root to improve survival and quality of life	04/01/2018 to 03/31/2023	Total amount: $12,997,400 $2,599,480/yr GSC amount: $343,634 $68,726/yr	Nada Jabado, Jacek Majewski, and Michael Taylor	Claudia Kleinman, Aled Edwards, Cheryl Arrowsmith, Steven Jones, Livia Garzia, Jean Lachanie, Trevor Pugh, Peter Dirks, Marco Marra, Ioannis Ragoussis, Guillaume Bourque, Mathieu Lupien, Mathieu Blanchette, Alexandre Montpetit, Maryam Fouladi, Michael Sundsrom, Lillian Siu, and Vijay Ramaswamy
Genome Canada	Silent Genomes: Reducing health care disparities and improving diagnostic success for children with genetic diseases from Indigenous populations	04/01/2018 to 03/31/2024	Total amount: $10,400,000 $1,733,333/yr	Laura Arbour, Nadine Caron and Wyeth Wasserman	Maja Tarailo-Graovac, Marco Marra, Sonia Anand, Anna Lehman, Jeff Reading, Dean Regier, Stuart Peacock, and Josee Lavoie
Genome Canada	Deciphering the genome biology of relapsed lymphoid cancers to improve patient management	04/01/2018 to 03/31/2024	Total amount: $11,926,360 $1,987,726/yr GSC amount: $4,724,884 $787,480/yr	Christian Steidl, Marco Marra, David Scott	Joseph Connors, Ryan Morin, Dean Regier, Aly Karsan, and Robert Kridel
Canadian Cancer Society Research Institute / Canadian Institutes of Health Research	Dissecting tumour heterogeneity using single cell genomics, epigenomics and transcriptomics	08/01/2018 to 07/31/2021	Total amount: $199,150 $99,575/yr	Marco Marra	Samuel Aparicio and Richard Moore Key personnel: Robin Coope, Yongjun Zhao and Simon Haile Merhu

University of British Columbia	Dermatology Point-of-Care Intelligent Imaging Network-Digital Pathology	08/01/2019 to 06/30/2022	Total amount: $423,074 $211,537/yr	Marco Marra, Steven Jones, and Stephen Yip	Robin Coope (Key personnel)
BC Cancer Foundation	Hereditary male breast cancer: characterization of known and novel familial predispositions using short and long reads sequencing technologies	03/03/2020 to 09/30/2022	Total amount: $74,891 $37,445yr	Steven Jones and Kashmintan Schrader	MyLinh Thibodeau, Sophie Sun, Aly Karsan, Stephen Yip, Janessa Laskin and Marco Marra
Genome British Columbia	Securing Reagent Supplies and Scaling COVID-19 testing in BC	04/01/2020 to 12/31/2020	Total amount: $250,000	Martin Hirst, Mel Krajden, and Natalie Prystajecky	Marco Marra, Robin Coope, Mayor Thibault, Sheila Teves, Ivan Sadowski, Gregg Morin, and Robert Holt
Canada Foundation for Innovation	Preparing for the Next Wave: Technology to Detect and Analyze SARS-CoV-2	11/20/2020 to 09/30/2021	Total amount: $401,238	Marco Marra (NPI), Steven Jones, Martin Hirst, and Natalie Prystajecky	
Canadian Cancer Society Research Institute	Long read DNA methylation sequencing for early detection of pancreatic adenocarcinoma	01/15/2021 to 01/14/2022	Total amount: $150,000	Marco Marra (NPI) and Steven Jones	David Schaeffer, Daniel Renouf, and Parveen Bhatti
Michael Smith Foundation for Health Research	Creative Knowledge Translation to Support BC Cancer's Personalized OncoGenomics Program	02/01/2021 to 01/31/2022	Total amount: $15,000 GSC amount: $0	Janessa Laskin	Marco Marra
National Institutes of Health	Contract 21X014F	02/02/2021 to 08/30/2022	Total amount: $735,352 USD	Marco Marra	
Genome BC	Genome BC Marathon of Hope Cancer Centre program (MOH001)	10/01/2021 to 09/30/2022	Total amount: $1,000,000	Marco Marra and Daniel Renouf	Steven Jones

PATENTS:

1. Provisional Patent application “Novel methods for the prediction of treatment response in cancer”. Inventors: **Marco Marra** and Yuka Takemon. USPTO Application # 63/679/964, Aug 06, 2024.

2. Patents entitled “Novel biomarkers and targets for ovarian carcinoma”**.** Inventors: Huntsman DG, **Marra M**, Wiegand K, Hirst M, Shah SP. Filed Apr 22, 2011. Granted in Europe, as patent No. EP2561351

(validated in Germany, France and United Kingdom), Canada (patent No. 2797291), China (patent No. 103026227), Brazil (patent No. 112012027104) and Hong Kong (patent No. HK1181846).

3. Patents entitled "Biomarkers for non-hodgkin lymphomas and uses thereof". Inventors: Morin RD, **Marra MA**, Mungall AJ, Hirst M, Mendez-Lago M, Gascoyne RD, Connors JM. Filed June 23, 2011. Granted in Canada (patent No. 2841142) and the United States (patents No. 9,045,801 and 10,113,199). Pending US patent application No. 16/148,576.

BOOK CHAPTERS

(The names of Dr. Marra's trainees are underlined.)

1. Firme M and **Marra M**. CIC (capicua transcriptional repressor). ***Atlas Genet & Cytogenet Oncol Haematol.*** Jean-Loup Huret (Editor-in-Chief). 2016, 20(5): 250-255. DOI : 10.4267/2042/62773.
2. Zahir FR and Marra MA. Use of Affymetrix Arrays in the Diagnosis of Gene Copy-Number Variation. ***Curr Protoc Hum Genet.*** 2015 Apr 1;85:8.13.11-8.13.13.
3. Pon JR and **Marra MA**. Driver and Passenger Mutations in Cancer. ***Annu. Rev. Pathol. Mech. Dis***. Jocelyn Rice (Ed.) Annual Reviews. 2015 Jan 24;10:25–50.
4. Chun HJ, Khattra J, Krzywinski M, Aparicio SA, **Marra MA**. Second-generation sequencing for cancer genome analysis. ***Cancer Genomics: From Bench to Personalized Medicine***. Dellaire GD, Berman JN, Arceci RJ. (Eds). 1st Ed. Elsevier. 2013 Dec. Part 2, pp 13-30.
5. Morin RD and **Marra M**. Transcriptomics in the Age of High-Throughput Sequencing. ***Genomic and Personalized Medicine***. Ginsburg G and Huntington FW (Eds). Elsevier. 2nd Edition. 2012 Oct 30. Vol 1. Chapter 12: 145-155.
6. Morrissy S, Zhao YJ, Delaney A, Asano J, Dhalla N, Li I, McDonald H, Pandoh P, Prabhu A-L, Tam A, Hirst M, **Marra M**. Tag-Seq: Next-generation Tag Sequencing for Gene Expression Profiling. ***Tag-based Next Generation Sequencing***. Harbers M and Kahl G (Eds). Wiley-VCH Verlag & Co. Weinheim, Germany. 2012. Part One, Chapter 13, pp 211-241.
7. Goya R, Meyer IM, and **Marra MA**. Applications of High-Throughput Sequencing. ***Bioinformatics for High Throughput Sequencing***. Rodriguez-Espeleta N, Hackenberg M, Aransay AM (Eds.) Springer, NY. 2012, 27-53.
8. Tucker T, **Marra M**, Friedman JM. Massively Parallel Sequencing. ***Molecular Analysis & Genome Discovery***, Ralph Rapley and Stuart Harbron (Eds.). 2nd Edition. John Wiley & Sons, Ltd. 2011 Oct, pp 114-132.
9. Morin RD, Zhao YJ, Prabhu AL, Dhalla N, McDonald H, Pandoh P, Tam A, Zeng T, Hirst M**, Marra MA**. Preparation and Analysis of MicroRNA Libraries Using the Illumina Massively Parallel Sequencing Technology. ***RNAi and microRNA-Mediated Gene Regulation in Stem Cells. Methods, Protocols, and Applications.*** Zhang, Baohong, Stellwag, Edmund J. (Eds.). 1st Edition. Humana Press Inc. Clifton, New Jersey, USA. 2010 Sep. Vol 650 Part 3, Chapter 14, pp 173-199.
10. Morin RD, Kuchenbauer F, Humphries RK, **Marra MA.** Massively Parallel MicroRNA Profiling in the Haematologic Malignancies. ***MicroRNA Profiling in Cancer: A Bioinformatics Perspective.*** Gusev Y (Ed). Pan Stanford Publishing Pte Ltd. 2010 Oct 01. pp 71-94.
11. Morrissy SA, Zhao YJ, Delaney A, Asano J, Dhalla N, Li I, McDonald H, Pandoh P, Prabhu A-L, Tam A, Hirst M, **Marra MA**. Digital Gene Expression by Tag Sequencing on the Illumina Genome Analyzer. ***Curr Protoc Hum Genet.*** Haines JL, Korf BR, Morton CC, Seidman CE, Seidman JG, and

Smith DR (Eds.) John Wiley & Sons, Inc. Hoboken, New Jersey, USA. 2010 Apr 1; Chapter 11:Unit 11.11.1-11.11.36.

12. Pugh TJ and **Marra MA.** Trisomy 9. ***Encyclopedia of Molecular Mechanisms of Disease***. Florian Lang (Ed). Springer, Berlin, Heidelberg. 2009; 1, pp 2112-2113.

13. Petrescu AS and **Marra MA.** Genomic approaches for identifying mammalian cis-encoded antisense transcripts. ***Res Adv in Nucleic Acids Res.*** 2, 2008.

14. Delaney AD, Qian H, Friedman JM, **Marra MA**. Use of Affymetrix Mapping Arrays in the Diagnosis of Gene Copy Number Variation. ***Curr Protoc Hum Genet.*** John Wiley & Sons, Inc. 2008 Oct 1; Chapter 8:Unit 8:13.

15. Griffith M and **Marra MA**. Alternative expression analysis: Experimental and bioinformatics approaches for the analysis of transcript diversity. ***Genes, Genomes and Genomics.*** Thangadurai D, Tang W, Papavassiliou AG, Anupama M (Eds), Regency Publications, New Delhi, India, 2007; 2, pp. 201-242**.**

16. Mathewson CA, Schein JE, **Marra MA**. Large-Scale BAC Clone Restriction Digest Fingerprinting. ***Curr Prot Hum Genet***. D. Smith (ed), John Wiley & Sons, Inc., Hoboken, NJ, 2007 Apr; Chapter 5:Unit 5.19.1-5.19.21.

17. Halaschek-Weiner JV, **Marra MA**, Brooks-Wilson AR. Gene Expression Analysis in Pharmacogenetics and Pharmacogenomics. ***Pharmacogenomics*** 2nd Edition. Kalow W, Meyer UA, Tyndale RF (Eds) Marcel Dekker Inc. New York, USA, 2005; Vol. 156, pp. 389-406.

18. Astell CR, Holt RA, Jones SJM, **Marra MA.** Genome Organization and Structural Aspects of the SARS-related Virus. **A*dv Infect Dis.*** Schmidt A, Wolff MH, Weber O (Eds), Birkhauser Verlag, Basel, Switzerland, 2005; Vol. 1, pp. 101-128.

19. Schein J, Kucaba T, Sekhon M, Smailus D, Waterston R, **Marra M**. High throughput BAC fingerprinting. ***Bacterial Artificial Chromosomes: Vol 1 Library Construction, Physical Mapping, & Sequencing.*** Zhao S, Stodolsky M (Eds), Humana Press, Clifton, NJ, 2004; Vol. 255, pp. 143-156.

RESEARCH PUBLICATIONS AND REVIEWS:

IN PREPARATION

1. Sharma K, Ehman M, Weymann D, Maroilley T, Mohajeri A, Lehman A, Tarailo-Graovac M, Jones S, **Marra MA**, Wasserman W, Caron N, Arbour L, Regier DA. The cost trajectory of genomic sequencing and analysis for Indigenous children with suspected rare diseases.

2. Grewal J, Pleasance E, Csizmok V, Williamson L, Wee K, Bleile D, Shen Y, Tessier-Cloutier B, Yip S, Renouf D, Laskin J, **Marra M**, Jones S. Single-sample pathway analysis using Pathway Impact Evaluation (PIE) of machine-learning based cancer classifiers.

3. Dixon K, Shen Y, Hoeschen C, Wong H, Cremin C, Senz J, Lum A, O'Neill K, Ch'ng C, Hong Q, Karasinska J, Topham J, Pleasance ED, Jones M, Zhao E, Young S, Mungall K, Mungall AJ, Moore R, Ma YP, Fok A, Nelson J, Lee MKC, Yip S, Lim H, Karsan A, Jones SJM, Laskin J, **Marra MA**, Schaeffer DF, Renouf DJ, Huntsman DG, Schrader KA. Genomic and transcriptomic landscape of familial pancreatic cancer and implications for altered glucose metabolism in moderate-penetrance cancer susceptibility.

4. Luka Culibrk, Jasleen Kaur Grewal, Erin Pleasance, Laura Williamson, Karen Mungall, Janessa Laskin, **Marco Marra,** Steven Jones. Robust somatic copy number estimation using coarse-to-fine segmentation. ***bioRxiv preprint doi: https://doi.org/10.1101/2021.08.06.455329***

5. Yuka Takemon, Alessia Gagliardi, Erin D. Pleasance, Veronika Csizmok, Andrew J. Mungall, Richard A. Moore, Eric Chuah, Karen L. Mungall, Eleanor Lewis, Howard J. Lim, Daniel J. Renouf, Steven JM. Jones, Janessa Laskin, **Marco A. Marra**. Using KMT2D deficiency as a COMPASS to identify cancer cell vulnerabilities. In revision.

6. Veronika Csizmok, Cameron J. Grisdale, Laura M. Williamson, Howard J. Lim, Lawrence Lee, Alannah Smrke, Steven J.M. Jones, **Marco A. Marra**, Janessa Laskin. Clinical activity of alectinib in a metastatic osteosarcoma case with a FUS-TFCP2 fusion and a novel ALK deletion.

7. Cathy Yan, **Marco A. Marra**. When Less is More: Less Invasive Sample Acquisition Methods for Genomic Profiling of Metastatic Non-Small Cell Lung Cancer.

8. Melika Hanos, Alannah Smrke, Erin Pleasance, Sara Sadeghi, Karen L. Mungall, Eric Chuah, Richard A. Moore, Andy J. Mungall, Howard J. Lim, Daniel J. Renouf, Michael Wright, Torsten Neilsen, Ren Yuan, Chris Jensen**,** Steven J.M. Jones, **Marco A. Marra**, and Janessa Laskin. Pemigatinib is an effective treatment for a novel *FGFR2* fusion associated metastatic gastrointestinal stromal tumour.

9. Glenn Chang, Vanessa L. Porter, Kieran O'Neill, Luka Culibrk, Vahid Akbari, **Marco A. Marra**, Steven J. M. Jones. IMPALA: A Comprehensive Pipeline for Detecting and Elucidating Mechanisms of Allele Specific Expression in Cancer.

IN REVIEW

1. Topham JT, Karasinska JM, Metcalfe A, Ali H, Kalloger SE, Kevorkova M, Titmuss E, Jang GH, O'Kane GM, Moore RA, Mungall AJ, Loree JM, Notta F, Wilson JM, Bathe OF, Tang PA, Goodwin R, Knox JJ, Gallinger S, Laskin J, **Marra MA**, Jones SJM, Renouf DJ, Schaeffer DF. Focal amplification and overexpression of E3 ubiquitin ligase genes CBLC and SMURF1 in patients with pancreatic ductal adenocarcinoma**.** ***Cancer Cell***.

2. *Wee K, *Yang KC, Schaeffer DF, Zhou C, Leung E, Feng X, Laskin J, Marra MA, Loree JM, Gorski SM. Genomic and transcriptomic landscapes of metastatic neuroendocrine neoplasms from distinct primary sites and their clnical implications. Submitted, Dec 2023 (in review, npj Precision Oncology). *co-first authors

3. LeVasseur N, Csizmok V, Bonakdar M, Shen Y, Zibrik L, Williamson L, Zhao EY, Mungall KL, Chuah E, Moore RA, Mungall AJ, Jones SJM, Sun S, Gelmon KA, Laskin J, **Marra MA,** Chia SK. Whole genome sequencing and beyond - The clinical experience with applied multi-omics sequencing in metastatic breast cancer patients. ***JCO Precis Oncol.***

4. Chiu K, Dixon K, Chan S, Ng T, Shen Y, Pleasance E, Young S, Portigal-Todd C, Schaeffer DF, Yip S, Jones SJM, Laskin J, **Marra MA**, Lim HJ, Schrader KA. Succinate dehydrogenase-deficient gastric adenocarcinoma associated with carrier status for SDHB. ***NPJ Genom Med.***

PUBLISHED

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564. Sarkozy C, Wu S, Takata K, Aoki T, Neriah SB, Milne K, Goodyear T, Strong C, Rastogi T, Hilton LK, Lai D, Sehn LH, Farinha P, Nelson BH, Weng A, **Marra MA**, Scott DW, Craig JW, Steidl C, Roth A. Integrated single cell analysis reveals co-evolution of malignant B cells and tumor micro-environment in transformed follicular lymphoma. ***Cancer Cell.*** 2024 Aug 13:S1535-6108(24)00292-7. doi: 10.1016/j.ccell.2024.07.012. PMID: 39151424

563. Deyell RJ, Shen Y, Titmuss E, Dixon K, Williamson LM, Pleasance E, Nelson J, Abbasi S, Mungall KL, Chuah E, Moore RA, Mungall AJ, Zhao Y, Lee A, Dunham C, Armstrong L, Virani A, Rogers P, Young S, Schrader KA, Fok A, Ma Y, Ch'ng C, Bonakdar M, Wee K, Jones M, Jones SJM, Laskin J, **Marra MA,** Rassekh SR. Whole genome and transcriptome integrated analyses guide clinical care of pediatric poor prognosis cancers. ***Nat Commun.*** 2024 May 16;15(1):4165. doi: 10.1038/s41467-024-48363-5. PMID: 38755180 **(This article is featured in Nature Communications Editors' Highlights webpage** https://www.nature.com/ncomms/editorshighlights).

562. Titmuss E, Yu IS, Pleasance ED, Williamson LM, Mungall K, Mungall AJ, Renouf DJ, Moore R, Jones SJM, **Marra MA**, Laskin JJ, Savage KJ. Exploration of germline correlates and risk of immune related adverse events in advanced cancer patients treated with immune checkpoint inhibitors. ***Curr Oncol***. 2024 Mar 30; 31(4), 1865-1875; https://doi.org/10.3390/curroncol31040140.
PMID: 38668043

561. Coope RJ, Pleasance S, Pandoh P, Schlosser C, Corbett RD, **Marra MA**. Rapid microdissection of tissue sections via laser ablation. ***J Clin Pathol***. 2024 May 17;77(6):430-434. doi: 10.1136/jcp-2023.
PMID: 38429092

560. Sabatini PJB, Bridgers J, Huang S, Downs G, Zhang T, Sheen C, Park N, Kridel R**, Marra MA**, Steidl C, Scott DW, Karsan A. Multisite clinical cross-validation and variant interpretation of a next generation sequencing panel for lymphoid cancer prognostication. ***J Clin Pathol***. 2024 Jan 5:jcp-2023-209262. doi: 10.1136/jcp-2023-209262. Online ahead of print. PMID: 38182402

559. Grants JM, May C, Bridgers J, Huang S, Gillis S, Meissner B, Boyle M, Ben-Neriah S, Hung S, Duns G, Hilton L, Gerrie AS, **Marra M**, Kridel R, Sabatini PJB, Steidl C, Scott DW, Karsan A. Chronic Lymphocytic Leukemia IGHV Somatic Hypermutation Detection by Targeted Capture Next-Generation Sequencing. ***Clin Chem***. 2024 Jan 4;70(1):273-284. doi: 10.1093/clinchem/hvad147. PMID: 38175592

558. Lambo S, Trinh DL, Ries RE, Jin D, Setiadi A, Ng M, LeBlanc VG, Loken MR, Brodersen LE, Dai F, Pardo LM, Ma X, Vercauteren SM, Meshinchi S, **Marra MA**. A longitudinal single-cell atlas of treatment response in pediatric AML. ***Cancer Cell***. 2023 Dec 11;41(12):2117-2135.e12. doi: 10.1016/j.ccell.2023.10.008. PMID: 37977148.

557. Hilton LK, Ngu HS, Collinge B, Dreval K, Ben-Neriah S, Rushton CK, Wong JCH, Cruz M, Roth A, Boyle M, Meissner B, Slack GW, Farinha P, Craig JW, Gerrie AS, Freeman CL, Villa D, Rodrigo JA, Song K, Crump M, Shepherd L, Hay AE, Kuruvilla J, Savage KJ, Kridel R, Karsan A, **Marra MA**, Sehn LH, Steidl C, Morin RD, Scott DW. Relapse timing is associated with distinct evolutionary dynamics in diffuse large B cell lymphoma. ***J Clin Oncol.*** 2023 Sep 1;41(25):4164-4177. doi: 10.1200/JCO.23.00570. PMID: 37319384.

556. Dreval K, Hilton LK, Cruz M, Shaalan H, Ben-Neriah S, Boyle M, Collinge B, Coyle KM, Duns G, Farinha P, Grande BM, Meissner B, Pararajalingam P, Rushton CK, Slack GW, Wong J, Mungall AJ, **Marra MA**, Connors JM, Steidl C, Scott DW, Morin RD. Genetic subdivisions of follicular lymphoma defined by distinct coding and noncoding mutation patterns. ***Blood***. 2023 Aug 10;142(6):561-573. doi: 10.1182/blood.2022018719. PMID: 37084389.

555. Romero JM, Titmuss E, Wang Y, Vafiadis J, Pacis A, Jang GH, Zhang A, Golesworthy B, Lenko T, Williamson LM, Grünwald B, O'Kane GM, Jones SJM, **Marra MA**, Wilson JM, Gallinger S, Laskin J, Zogopoulos G. Chemokine expression predicts T cell-inflammation and improved survival with checkpoint inhibition across solid cancers. ***NPJ Precis Oncol***. 2023 Aug 9;7(1):73. doi: 10.1038/s41698-023-00428-2. PMID: 37558751.

554. Xu J, Pandoh PK, Corbett RD, Smailus D, Bowlby R, Brooks D, McDonald H, Haile S, Chahal S, Bilobram S, Mungall KL, Mungall AJ, Coope R, Moore RA, Zhao Y, Jones SJ, **Marra MA**. A high-throughput pipeline for DNA/RNA/small RNA purification from tissue samples for sequencing. ***Biotechniques***. 2023 Aug;75(2):47-55. doi: 10.2144/btn-2023-0011. PMID:37551834

553. Takemon Y, **Marra MA.** GRETTA: an R package for mapping in silico genetic interaction and essentiality networks. ***Bioinformatics***. 2023 Jun 1;39(6):btad381. doi: 10.1093/bioinformatics/btad381. PMID: 37326978.

552. MacLennan SA, **Marra MA**. Oncogenic Viruses and the Epigenome: How Viruses Hijack Epigenetic Mechanisms to Drive Cancer. ***Int J Mol Sci***. 2023 May 31;24(11):9543. doi: 10.3390/ijms24119543. PMID: 37298494.

551. Takemon Y, LeBlanc VG, Song J, Chan SY, Lee SD, Trinh DL, Ahmad ST, Brothers WR, Corbett RD, Gagliardi A, Moradian A, Cairncross JG, Yip S, Aparicio SAJR, Chan JA, Hughes CS, Morin GB, Gorski SM, Chittaranjan S, **Marra MA**. Multi-Omic Analysis of CIC's Functional Networks Reveals Novel Interaction Partners and a Potential Role in Mitotic Fidelity. ***Cancers*** (Basel). 2023 May 17;15(10):2805. doi: 10.3390/cancers15102805. PMID: 37345142.

550. Tsang ES, Csizmok V, Williamson LM, Pleasance E, Topham J, Karasinska J, Titmuss E, Schrader I, Yip S, Tessier-Cloutier B, Mungall K, Ng T, Sun S, Lim HJ, Loree JM, Laskin J, **Marra MA**, Jones SJM, Schaeffer DF, Renouf DJ. Homologous Recombination Deficiency Signatures in Gastrointestinal and Thoracic Cancers Correlate with Platinum Therapy Duration. ***NPJ Precis Oncol***. 2023 Mar 24;7(1):31. doi: 10.1038/s41698-023-00368-x. PMID: 36964191.

549. Titmuss E, Milne K, Jones MR, Ng T, Topham JT, Brown SD, Schaeffer DF, Kalloger S, Wilson D, Corbett RD, Williamson LM, Mungall K, Mungall AJ, Holt RA, Nelson BH, Jones SJM, Laskin J, Lim HJ and **Marra MA**. Immune Activation following Irbesartan Treatment in a Colorectal Cancer Patient: A Case Study. ***Int. J. Mol. Sci.*** 2023 24, 5869. https://doi.org/10.3390/ijms24065869. PMID: 36982943

548. Thomas N, Dreval K, Gerhard DS, Hilton LK, Abramson JS, Ambinder RF, Barta S, Bartlett NL, Bethony J, Bhatia K, Bowen J, Bryan AC, Cesarman E, Casper C, Chadburn A, Cruz M, Dittmer DP, Dyer MA, Farinha P, Gastier-Foster JM, Gerrie AS, Grande BM, Greiner T, Griner NB, Gross TG, Harris NL, Irvin JD, Jaffe ES, Henry D, Huppi R, Leal FE, Lee MS, Martin JP, Martin MR, Mbulaiteye SM, Mitsuyasu R, Morris V, Mullighan CG, Mungall AJ, Mungall K, Mutyaba I, Nokta M, Namirembe C, Noy A, Ogwang MD, Omoding A, Orem J, Ott G, Petrello H, Pittaluga S, Phelan JD, Ramos JC, Ratner L, Reynolds SJ, Rubinstein PG, Sissolak G, Slack G, Soudi S, Swerdlow SH, Traverse-Glehen A, Wilson WH, Wong J, Yarchoan R, ZenKlusen JC, **Marra MA**, Staudt LM, Scott DW, Morin RD. Genetic subgroups inform on pathobiology in adult and pediatric Burkitt lymphoma. ***Blood***. 2023 Feb 23;141(8):904-916. doi: 10.1182/blood.2022016534. PMID: 36201743

547. Topham J, Tsang E, Karasinska J, Metcalfe A, Ali H, Kalloger S, Csizmok V, Williamson L, Titmuss E, Jang G-H, Denroche R, Wong H-L, O'Kane G, Moore R, Mungall A, Loree J, Notta F, Wilson J, Bathe O, Tang P, Goodwin R, Knox J, Gallinger S, Laskin J, **Marra M**, Jones S, Schaeffer D, Renouf D. Integrative analysis of KRAS wildtype pancreatic ductal adenocarcinoma reveals mutation and expression-based similarities to cholangiocarcinoma. ***Nat Commun***. 2022 Oct 8;13(1):5941. doi: 10.1038/s41467-022-33718-7. PMID: 36209277

546. Weymann D, Laskin J, Jones SJM, Roscoe R, Lim HJ, Renouf DJ, Schrader KA, Sun S, Yip S, **Marra MA**, Regier DA. Early-stage economic analysis of research-based comprehensive genomic sequencing for advanced cancer care. ***J Community Genet***. 2022 Oct;13(5):523-538. doi: 10.1007/s12687-021-00557-w. PMID: 34843087

545. Porter VL and **Marra MA**. The Drivers, Mechanisms, and Consequences of Genome Instability in HPV-Driven Cancers. ***Cancers*** 2022 Sep 23;14(19):4623. doi: 10.3390/cancers14194623. PMID: 36230545

544. Hendrikse LD, Haldipur P, Saulnier O, Millman J, Sjoboen AH, Erickson AW, Ong W, Gordon V, Coudière-Morrison L, Mercier AL, Shokouhian M, Suárez RA, Ly M, Borlase S, Scott DS, Vladoiu MC, Farooq H, Sirbu O, Nakashima T, Nambu S, Funakoshi Y, Bahcheli A, Diaz-Mejia JJ, Golser J, Bach K, Phuong-Bao T, Skowron P, Wang EY, Kumar SA, Balin P, Visvanathan A, Lee JJY, Ayoub R, Chen X,

Chen X, Mungall KL, Luu B, Bérubé P, Wang YC, Pfister SM, Kim SK, Delattre O, Bourdeaut F, Doz F, Masliah-Planchon J, Grajkowska WA, Loukides J, Dirks P, Fèvre-Montange M, Jouvet A, French PJ, Kros JM, Zitterbart K, Bailey SD, Eberhart CG, Rao AAN, Giannini C, Olson JM, Garami M, Hauser P, Phillips JJ, Ra YS, de Torres C, Mora J, Li KKW, Ng HK, Poon WS, Pollack IF, López-Aguilar E, Gillespie GY, Van Meter TE, Shofuda T, Vibhakar R, Thompson RC, Cooper MK, Rubin JB, Kumabe T, Jung S, Lach B, Iolascon A, Ferrucci V, de Antonellis P, Zollo M, Cinalli G, Robinson S, Stearns DS, Van Meir EG, Porrati P, Finocchiaro G, Massimino M, Carlotti CG, Faria CC, Roussel MF, Boop F, Chan JA, Aldinger KA, Razavi F, Silvestri E, McLendon RE, Thompson EM, Ansari M, Garre ML, Chico F, Eguía P, Pérezpeña M, Morrissy AS, Cavalli FMG, Wu X, Daniels C, Rich JN, Jones SJM, Moore RA, **Marra MA**, Huang X, Reimand J, Sorensen PH, Wechsler-Reya RJ, Weiss WA, Pugh TJ, Garzia L, Kleinman CL, Stein LD, Jabado N, Malkin D, Ayrault O, Golden JA, Ellison DW, Doble B, Ramaswamy V, Werbowetski-Ogilvie TE, Suzuki H, Millen KJ, Taylor MD. Failure of human rhombic lip differentiation underlies medulloblastoma formation. ***Nature***. 2022 Sep;609(7929):1021-1028. doi: 10.1038/s41586-022-05215-w. PMID: 36131014

543. Titmuss E, Corbett RD, Davidson S, Abbasi S, Williamson LM, Pleasance E, Shlien A, Renouf DJ, Jones SJM, Laskin J, **Marra MA**. TMBur: A Distributable Tumor Mutation Burden Approach. ***Genome Biol.*** 2022 Sept 7; 15 (190). doi: https://doi.org/10.1186/s12920-022-01348-z. PMID: 36071521

542. Pleasance E, Bohm A, Williamson LM, Nelson JMT, Shen Y, Bonakdar M, Titmuss E, Csizmok V, Wee K, Hosseinzadeh S, Grisdale CJ, Reisle C, Taylor GA, Lewis E, Jones MR, Bleile D, Sadeghi S, Zhang W, Davies A, Pellegrini B, Wong T, Bowlby R, Chan SK, Mungall KL, Chuah E, Mungall AJ, Moore RA, Zhao YJ, Deol B, Fisic A, Fok A, Regier DA, Weymann D, Schaeffer DF, Young S, Yip S, Schrader K, Levasseur N, Taylor SK, Feng X, Tinker A, Savage KJ, Chia S, Gelmon K, Sun S, Lim H, Renouf DJ, Jones SJM, **Marra MA***, Laskin J.* Whole genome and transcriptome analysis enhances precision cancer treatment options. ***Annals of Oncol.*** 2022 Sept; 33(9):939-949. Doi: 10.1016/j.annonc.2022.05.522. *Co-senior authors. PMID: 35691590

541. Coope RJN, Matic N, Pandoh PK, Corbett RD, Smailus DE, Pleasance S, Lowe CF, Ritchie G, Chorlton SD, Young M, Ally AA, Asano JK, Carlsen RE, Chahal SS, Zhao YJ, Holmes DT, Romney MG, Jones SJM, **Marra MA**. Automated Library Construction and Analysis Pipelines for High-throughput ARTIC Amplicon SARS-CoV-2 Sequencing on MinION. ***JALM.*** 2022 Sep 1;7(5):1025-1036. doi: 10.1093/jalm/jfac054. doi: 10.1093/jalm/jfac054. PMID: 35723286

540. Yu ISW, Wee K, Williamson L, Titmuss E, An J, Naderi-Azad S, Metcalf C, Yip S, Horst B, Jones S, Paton K, Nelson BH, **Marra M**, Laskin JJ, Savage KJ. Exceptional response to combination ipilimumab and nivolumab in metastatic uveal melanoma: Insights from genomic analysis. ***Melanoma Res.*** 2022 Aug 1;32(4):278-285. doi: 10.1097/CMR.0000000000000810. PMID: 35726793

539. Akbari V, Garant J-M, O'Neill K, Pandoh P, Moore R, **Marra MA**, Hirst M, Jones SJM. Genome-wide detection of imprinted differentially methylated regions using nanopore sequencing. ***eLife*** 2022;11:e77898. https://elifesciences.org/articles/77898.
PMID: 35787786

538. Tessier-Cloutier B, Grewal JK, Jones MR, Pleasance E, Shen Y, Cai E, Dunham C, Hoang L, Horst B, Huntsman DG, Ionescu D, Karnezis AN, Lee AF, Lee CH, Lee TH, Twa DD, Mungall AJ, Mungall K, Naso JR, Ng T, Schaeffer DF, Sheffield BS, Skinnider B, Smith T, Williamson L, Zhong E, Regier DA, Laskin J, **Marra MA**, Gilks CB, Jones SJ, Yip S. The impact of whole genome and transcriptome analysis (WGTA) on predictive biomarker discovery and diagnostic accuracy of advanced malignancies. ***J Pathol Clin Res***. 2022 Jul;8(4):395-407. doi: 10.1002/cjp2.265. PMID: 35257510

537. Lau T, Sefid Dashti ZJ, Titmuss E, Pender A, Topham JT, Bridgers J, Loree JM, Feng X, Pleasance ED, Renouf D J, Schrader KA, Sun S, Ho C, **Marra MA**, Laskin J, Karsan A. The Neoantigen Landscape of the Coding and Noncoding Cancer Genome Space. ***J Mol Diagn***. 2022 June;24(6):609-618. doi: https://doi.org/10.1016/j.jmoldx.2022.02.004. PMID: 35367630

536. Lavoie MJ *, Csizmok V*, Williamson LM, Culibrk L, Wang G, **Marra MA**, Laskin J, Jones SJM, Renouf DJ, Kollmannsberger CK. Whole-genome and transcriptome analysis of advanced adrenocortical cancer highlights multiple alterations affecting epigenome and DNA repair pathways. ***Cold Spring Harb Mol Case Stud.*** 2022 Apr 28;8(3):a006148. doi:10.1101/mcs.a006148. PMID: 35483882

535. Dodani DD, Nguyen MH, Morin RD, **Marra MA***, Corbett RD*. Combinatorial and Machine Learning Approaches for Improved Somatic Variant Calling from Formalin-Fixed Paraffin-Embedded Genome Sequence Data. ***Front Genet.*** 2022 Apr 27;13:834762. doi: 10.3389/fgene.2022.834764. *Co-senior authors. PMID: 35571031

534. LeBlanc VG, Trinh DL, Aslanpour S, Hughes M, Livingstone D, Jin D, Ahn BY, Blough MD, Cairncross JG, Chan JA, Kelly JJP, **Marra MA**. Single-cell landscapes of primary glioblastomas and matched explants and cell lines reveal variable retention of inter- and intra-tumor heterogeneity. ***Cancer Cell.*** 2022 Apr 11;40(4):379-392.e9. **(This article is featured on the cover of the journal. Featured in Preview: Patient derived explants as tumor models. CG Hubert and JN Rich, *Cancer Cell* 40, April 11, 2022).** PMID: 35303420

533. Lee SD, Song J, LeBlanc VG, **Marra MA**. Integrative multi-omic analysis reveals neurodevelopmental gene dysregulation in CIC-knockout and IDH1 mutant cells. ***J Pathol.*** 2022 Mar;256(3):297-309. doi: 10.1002/path.5835. PMID: 34767259

532. Regier DA, Chan B, Costa S, Scott DW, Steidl C, Connors JM, Karsan A, **Marra MA**, Kridel R, Cromwell I, Pollard S. Cost-Effectiveness of Molecularly Guided Treatment in Diffuse Large B-Cell Lymphoma (DLBCL) in Patients under 60. ***Cancers*** (Basel). 2022 Feb 12;14(4):908. doi: 10.3390/cancers14040908. PMID: 35205656

531. Reisle C, Williamson LM, Pleasance E, Davies A, Pellegrini B, Bleile DW, Mungall KL, Chuah E, Jones MR, Ma Y, Lewis E, Beckie I, Pham D, Matiello Pletz R, Muhammadzadeh A, Pierce BM, Li J, Stevenson R, Wong H, Bailey L, Reisle A, Douglas M, Bonakdar M, Nelson JMT, Grisdale CJ, Krzywinski M, Fisic A, Mitchell T, Renouf DJ, Yip S, Laskin J, **Marra MA**, Jones SJM. A Platform for Oncogenomic Reporting and Interpretation. ***Nat Commun***. 2022 Feb 9;13(1):756. doi: 10.1038/s41467-022-28348-y. PMID: 35140225

530. Milella M, Luchini C, Lawlor RT, Johns AL, Casolino R, Yoshino T, Biankin AV; ICGC-ARGO (incl **Marra MA**). ICGC-ARGO precision medicine: familial matters in pancreatic cancer. ***Lancet Oncol***. 2022 Jan;23(1):25-26. doi: 10.1016/S1470-2045(21)00703-8. PMID: 34973218

529. Haile S, Nikiforuk AM, Pandoh PK, Twa DDW, Smailus DE, Nguyen J, Pleasance S, Wong A, Zhao YJ, Eisler D, Moksa M, Cao Q, Wong M, Su E, Krzywinski M, Nelson J, Mungall AJ, Tsang F, Prentice LM, Jassem A, Manges AR, Jones SJM, Coope RJ, Prystajecky N, **Marra MA**, Krajden M, Hirst M. Optimization of magnetic bead-based nucleic acid extraction for SARS-CoV-2 testing using readily available reagents . ***J Virol Methods.*** 2022 Jan; 299:114339. doi: 10.1016/j.jviromet.2021.114339. PMID: 34687784

528. Williamson LM, Rive CM, Di Francesco D, Titmuss E, Chun HE, Brown SD, Milne K, Pleasance E, Lee AF, Yip S, Rosenbaum DG, Hasselblatt M, Johann PD, Kool M, Harvey M, Dix D, Renouf DJ, Holt RA, Nelson BH, Hirst M, Jones SJM, Laskin J, Rassekh SR, Deyell RJ, **Marra MA**. Clinical response to nivolumab in an INI1-deficient pediatric chordoma correlates with immunogenic recognition of brachyury. ***NPJ Precis Oncol***. 2021 Dec 20;5(1):103. doi: 10.1038/s41698-021-00238-4. PMID: 34931022

527. Zhang Y, Chen F, Pleasance E, Williamson L, Grisdale CJ, Titmuss E, Laskin J, Jones SJM, Cortes-Ciriano I, **Marra MA**, Creighton CJ. Rearrangement-mediated cis-regulatory alterations in advanced patient tumours reveal interactions with therapy. ***Cell Rep***. 2021 Nov 16;37(7):110023. doi: 10.1016/j.celrep.2021.110023. PMID: 34788622

526. Yang KC, Kalloger SE, Aird JJ, Lee MCK, Rushton C, Mungall KL, Mungall AJ, Gao D, Chow C, Xu J, Karasinska JM, Colborne S, Jones SJM, Schrader J, Morin RD, Loree JM, **Marra MA**, Renouf DJ, Morin GB, Schaeffer DF, Gorski SM. Proteotranscriptomic classification and characterization of pancreatic neuroendocrine neoplasms. ***Cell Rep.*** 2021 Oct 12;37(2):109817. doi: 10.1016/j.celrep.2021.109817. PMID: 34644566

525. Guenter J, Abadi S, Lim H, Chia S, Woods R, Jones M, Rebic N, Renouf DJ, Laskin J, **Marra M**. Evaluating genomic biomarkers associated with resistance or sensitivity to chemotherapy in patients with advanced breast and colorectal cancer. ***J Oncol Pharm Pract***. 2021 Sep;27(6):1371-1381. doi: 10.1177/1078155220951845. PMID: 32847480

524. Weymann D, Pollard S, Chan B, Titmuss E, Bohm A, Laskin J, Jones SJMS, Pleasance E, Nelson J, Fok A, Lim H, Karsan A, Renouf DJ, Schrader KA, Sun S, Yip S, Schaeffer DF, **Marra MA**, Regier DA. Clinical and cost outcomes following genomics-informed treatment for advanced cancers. ***Cancer Med.*** 2021 Aug;10(15):5131-5140. doi: 10.1002/cam4.4076. PMID: 34152087

523. Salehi S, Kabeer F, Ceglia N, Andronescu M, Williams MJ, Campbell KR, Masud T, Wang B, Biele J, Brimhall J, Gee D, Lee H, Ting J, Zhang AW, Tran H, O'Flanagan C, Dorri F, Rusk N, de Algara TR, Lee SR, Cheng BYC, Eirew P, Kono T, Pham J, Grewal D, Lai D, Moore R, Mungall AJ, **Marra MA**; IMAXT Consortium, McPherson A, Bouchard-Côté A, Aparicio S, Shah SP. Clonal fitness inferred from time-series modelling of single-cell cancer genomes. ***Nature***. 2021 Jul;595(7868):585-590. doi: 10.1038/s41586-021-03648-3. PMID: 34163070

522. Haile S, Corbett RD, Leblanc V, Wei L, Pleasance S, Bilobram S, Nip KM, Brown K, Trinh E, Smith J, Trinh D, Bala M, Chuah E, Coope RJ, Moore RA, Mungall AJ, Mungall K, Zhao YJ, Hirst M, Aparicio S, Birol I, Jones SJ, **Marra MA**. A scalable strand-specific protocol enabling full-length total RNA sequencing from single cells. ***Front Genet***. 2021 Jun 3;12:665888. doi: 10.3389/fgene.2021.665888. eCollection 2021. PMID: 34149808

521. Zhang B, Kim MY, Elliot G, Zhou Y, Zhao G, Li D, Lowdon RF, Gormley M, Kapidzic M, Robinson JF, McMaster M, Hong C, Mazor T, Hamilton E, Sears RL, Pehrsson EC, **Marra MA**, Jones SJM, Bilenky M, Hirst M, Wang T, Costello JF, Fisher SJ. Human placental cytotrophoblast epigenome dynamics over gestation and alterations in placental disease. ***Dev Cell***. 2021 May 3;56(9):1238-1252.e5. doi: 10.1016/j.devcel.2021.04.001. PMID: 33891899

520. Isaev K, Ennishi D, Hilton L, Skinnider B, Mungall KL, Mungall AJ, Bakhtiari M, Tremblay-LeMay R, Silva A, Ben-Neriah S, Boyle M, Villa D, **Marra MA**, Steidl C, Gascoyne RD, Morin R, Savage KJ, Scott DW, Kridel R. Molecular Attributes Underlying Central Nervous System and Systemic Relapse in Diffuse Large B-cell Lymphoma. ***Haematologica.*** 2021 May 1;106(5):1466-1471. doi: 10.3324/haematol.2020.255950. PMID: 32817292

519. Docking TR, Parker JDK, Jädersten M, Duns G, Chang L, Jiang J, Pilsworth JA, Swanson LA, Chan SK, Chiu R, Nip KM, Mar S, Mo A, Wang X, Martinez-Høyer S, Stubbins RJ, Mungall KL, Mungall AJ, Moore RA, Jones SJM, Birol I, **Marra MA**, Hogge D, Karsan A. A Clinical Transcriptome Approach to Patient Stratification and Therapy Selection in Acute Myeloid Leukemia. ***Nat Commun***. 2021 Apr 30;12(1):2474. doi: 10.1038/s41467-021-22625-y. PMID: 33931648

518. Collinge BJ, Ben-Neriah S, Chong LC, Boyle M, Jiang A, Miyata-Takata T, Farinha P, Craig JW, Slack GW, Ennishi D, Mottok A, Meissner B, Chavez EA, Gerrie AS, Villa D, Freeman CL, Savage KJ, Sehn LH, Morin RD, Mungall AJ, Gascoyne RD, **Marra MA**, Connors JM, Steidl C, Scott DW. Impact of *MYC* and *BCL2* structural variants in tumors of DLBCL morphology and mechanisms of false-negative *MYC IHC*. ***Blood***. 2021 Apr 22;137(16):2196-2208. doi: 10.1182/blood.2020007193. PMID: 33120427

517. Skowron P, Farooq H, Cavalli FMG, Morrissy AS, Ly M, Hendrikse LD, Wang EY, Djambazian H, Zhu H, Mungall KL, Trinh QM, Zheng T, Dai S, Stucklin ASG, Vladoiu MC, Fong V, Holgado BL, Nor C, Wu X, Abd-Rabbo D, Bérubé P, Wang YC, Luu B, Suarez RA, Rastan A, Gillmor AH, Lee JJY, Zhang

XY, Daniels C, Dirks P, Malkin D, Bouffet E, Tabori U, Loukides J, Doz FP, Bourdeaut F, Delattre OO, Masliah-Planchon J, Ayrault O, Kim SK, Meyronet D, Grajkowska WA, Carlotti CG, de Torres C, Mora J, Eberhart CG, Van Meir EG, Kumabe T, French PJ, Kros JM, Jabado N, Lach B, Pollack IF, Hamilton RL, Rao AAN, Giannini C, Olson JM, Bognár L, Klekner A, Zitterbart K, Phillips JJ, Thompson RC, Cooper MK, Rubin JB, Liau LM, Garami M, Hauser P, Li KKW, Ng HK, Poon WS, Yancey Gillespie G, Chan JA, Jung S, McLendon RE, Thompson EM, Zagzag D, Vibhakar R, Ra YS, Garre ML, Schüller U, Shofuda T, Faria CC, López-Aguilar E, Zadeh G, Hui CC, Ramaswamy V, Bailey SD, Jones SJ, Mungall AJ, Moore RA, Calarco JA, Stein LD, Bader GD, Reimand J, Ragoussis J, Weiss WA, **Marra MA**, Suzuki H, Taylor MD. The transcriptional landscape of Shh medulloblastoma. ***Nat Commun***. 2021 Mar 19;12(1):1749. doi: 10.1038/s41467-021-21883-0. PMID: 33741928

516. Britton H, Levine A, Shen Y, Mungall K, Serrano J, Snuderl M, Pleasance E, Jones S, Laskin J, **Marra M**, Rassekh S, Deyell R, Yip S, Cheng S, Dunham C. NTRK2 Fusion Driven Pediatric Glioblastoma: Identification of Oncogenic Drivers via Integrative Genome and Transcriptome Profiling. ***Clin Case Rep.*** 2021 Feb 10;9(3):1472-1477. doi: 10.1002/ccr3.3804. PMID: 33768871

515. Richards LM, Whitley OKN, MacLeod H, Cavalli FMG, Coutinho FJ, Jaramillo JE, Svergun N, Riverin M, Croucher DC, Kushida M, Yu K, Guilhamon P, Rastegar N, Ahmadi M, Bhatti JK, Bozek DA, Li N, Lee L, Che C, Luis E, Park NI, Xu Z, Ketela T, Moore RA, **Marra M**, Spears J, Cusimano MD, Das S, Bernstein M, Haibe-Kains B, Lupien M, Luchman HA, Weiss S, Angers S, Dirks PB, Bader GD, Pugh TJ. Gradient of developmental and injury-response transcriptional states defines functional vulnerabilities underpinning glioblastoma heterogeneity. ***Nat Cancer***. 2021 Feb;2(2):157-173. doi: 10.1038/s43018-020-00154-9. PMID: 35122077

514. Akbari V, Garant JM, O'Neill K, Pandoh P, Moore R, **Marra MA**, Hirst M, Jones SJM. Megabase-scale methylation phasing using nanopore long reads and NanoMethPhase. ***Genome Biol***. 2021 Feb 22;22(1):68. doi: 10.1186/s13059-021-02283-5. PMID: 33618748

513. Coope RJN, Schlosser C, Corbett RD, Pleasance S, Tessier-Cloutier B, Pandoh P, Kirk H, Haile S, Zhao YJ, Mungall AJ, **Marra MA**. Whole-Slide Laser Microdissection for Tumour Enrichment. ***J Pathol.*** 2021 Feb;253(2):225-233. doi: 10.1002/path.5575. PMID: 33135777

512. Naso J, Topham J, Karasinska J, Lee M, Kalloger S, Wong H-L, Nelson J, Moore R, Mungall A, Jones S, Laskin J, **Marra M**, Renouf D, Schaeffer D. Tumor Infiltrating Neutrophils and Gland-Formation Predict Overall Survival and Molecular Subgroups in Pancreatic Ductal Adenocarcinoma. ***Cancer Med.*** 2021 Feb;10(3):1155-1165. doi: 10.1002/cam4.3695. PMID: 33372414

511. Tsang ES, Grisdale CJ, Pleasance ED, Topham JT, Mungall KL, Reisle CR, Choo C, Carreira M, Bowlby R, Karasinska JM, MacMillan D, Williamson LM, Chuah E, Moore RA, Mungall AJ, Zhao Y, Tessier-Cloutier B, Ng T, Sun S, Lim H, Schaeffer DF, Renouf DJ, Yip S, Laskin J, **Marra MA**, Jones SJ, Loree JM. Uncovering Clinically Relevant Gene Fusions with Integrated Genomic and Transcriptomic Profiling of Metastatic Cancers. ***Clin Cancer Res.*** 2021 Jan 15;27(2):522-531. doi: 10.1158/1078-0432.CCR-20-1900. PMID: 33148671

510. Tsang ES, Topham JT, Karasinska JM, Lee MKC, Williamson LM, Mendis S, Denroche RE, Jang GH, Kalloger SE, Moore RA, Mungall AJ, Laskin J, O'Kane GM, Knox JJ, Goodwin R, Loree JM, Gallinger S, Jones SM, **Marra MA**, Schaeffer DF, Renouf DJ. Delving into Early Onset Pancreatic Ductal Adenocarcinoma: How Does Age Fit In? ***Clin Cancer Res.*** 2021 Jan 1;27(1):246-254. doi: 10.1158/1078-0432.CCR-20-1042. PMID: 32958704

509. Topham JT, Karasinska JM, Lee MKC, Csizmok V, Williamson LM, Jang GH, Denroche RE, Tsang E, Kalloger SE, Wong H-l, O'Kane GM, Moore RA, Mungall AJ, Loree JM, Bathe O, Tang P, Goodwin R, Knox JJ, Gallinger S, Laskin J, **Marra MA**, Jones SJM, Renouf DJ, Schaeffer DF. Subtype-discordant pancreatic ductal adenocarcinoma tumors show intermediate clinical and molecular characteristics. ***Clin Cancer Res***. 2021 Jan 1;27(1):150-157. doi: 10.1158/1078-0432.CCR-20-2831. PMID: 33051307

508. Pender A, Titmuss E, Pleasance E, Fan K, Pearson H, Brown S, Grisdale C, Topham J, Shen Y, Bonakdar M, Taylor G, Williamson L, Mungall K, Chuah E, Mungall A, Moore R, Lavoie J-M, Yip S, Lim H, Renouf D, Sun S, Holt R, Jones S, **Marra M**, Laskin J. Genome and transcriptome biomarkers of response to immune checkpoint inhibitors in advanced solid tumours. ***Clin Cancer Res.*** 2021 Jan 1;27(1):202-212. doi: 10.1158/1078-0432.CCR-20-1163. PMID: 33020056

507. Weymann D, Laskin J, Jones SJM, Lim H, Renouf DJ, Roscoe R, Schrader KA, Sun S, Yip S, **Marra MA**, Regier DA. Matching methods in precision oncology: An introduction and illustrative example. ***Mol Genet Genomic Med***. 2021 Jan;9(1):e1554. doi: 10.1002/mgg3.1554. PMID: 33237632

506. Thibodeau ML, O'Neill K, Dixon K, Reisle C, Mungall KL, Krzywinski M, Shen Y, Lim HJ, Cheng D, Tse K, Wong T, Chuah E, Fok A, Sun S, Renouf D, Schaeffer DF, Cremin C, Chia S, Young S, Pandoh P, Pleasance S, Pleasance E, Mungall AJ, Moore R, Yip S, Karsan A, Laskin J, **Marra MA**, Schrader KA, Jones SJM. Improved structural variant interpretation for hereditary cancer susceptibility using long-read sequencing. ***Genet Med***. 2020 Nov;22(11):1892-1897. doi: 10.1038/s41436-020-0880-8. PMID: 32624572

505. Wong D, Sogerer L, Lee SS, Wong V, Lum A, **Marra MA**, Yip S. TRIM25 promotes Capicua degradation independently of ERK in the absence of ATXN1L. ***BMC Biol***. 2020 Oct 28;18(1):154. doi: 10.1186/s12915-020-00895-0. PMID: 33115448

504. De Boeck A, Ahn BY, D'Mello C, Lun X, Alsherhi M, Szulzewsky F, Shen Y, Khan L, Dang NH, Reichardt E, Goring KA, King J, Grinshtein N, Hamardzumyan D, Reilly KM, Blough MD, Cairncross JG, Yong VW, **Marra MA**, Jones SJM, Kaplan DR, McCoy K, Holland EC, Bose P, Chan JA, Robbins SM, Senger DL. Glioma-derived IL-33 orchestrates an inflammatory brain tumor microenvironment that accelerates glioma progression. ***Nat Commun***. 2020 Oct 5;11(1):4997. doi: 10.1038/s41467-020-18569-4. PMID: 33020472

503. Lavoie J-M, Mitchell T, Lee S-E, Deol B, Chia SK, Gelmon KA, Kollmannsberger CK, Tinker AV, Jones SJM, **Marra M,** Laskin J, Renouf DJ. Patient Selection for a Developmental Therapeutics Program Using Whole Genome and Transcriptome Analysis. ***Invest New Drugs***. 2020 Oct;38(5):1601-1604. doi: 10.1007/s10637-020-00892-8. PMID: 3190773

502. Dixon K, Young S, Shen Y, Thibodeau ML, Fok A, Pleasance E, Zhao E, Jones M, Aubert G, Armstrong L, Virani A, Regier D, Gelmon K, Renouf D, Chia S, Bosdet I, Rassekh SR, Deyell RJ, Yip S, Fisic A, Titmuss E, Abadi S, Jones SJM, Sun S, Karsan A, **Marra M**, Laskin J, Lim H, Schrader KA. Establishing a framework for the clinical translation of germline findings in precision oncology. ***JNCI Cancer Spectr***. 2020 Oct;4(5):pkaa045. doi: 10.1093/jncics/pkaa045. PMID: 33134827

501. Bailey MH, Meyerson WU, Dursi LJ, Wang L-B, Dong G, Liang W-W, Weerasinghe A, Li S, Kelso S, Saksena G, Ellrott K, Wendl MC, Wheeler DA, Getz G, Simpson JT, Gerstein MB, Ding L, PCAWG Consortium. Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. ***Nat Commun***. 2020 Sep 21;11(1):4748. doi: 10.1038/s41467-020-18151-y. PMID: 32958763

500. Calvente L, Tremblay-LeMay R, Xu W, Chan FC, Hong M, Zhang T, Yhim HY, Kuruvilla J, Crump M, Kukreti V, Prica A, Regier D, **Marra MA**, Karsan A, Steidl C, Scott DW, Sabatini P, Kridel R. Validation of the RHL30 digital gene expression assay as a prognostic biomarker for relapsed Hodgkin lymphoma. ***Br J Haematol***. 2020 Sep;190(6):864-868. doi: 10.1111/bjh.16777. PMID: 32510594

499. Topham JT, Titmuss E, Pleasance ED, Williamson LM, Karasinska JM, Culibrk L, Lee MK, Mendis S, Denroche RE, Jang GH, Kalloger SE, Wong HL, Moore RA, Mungall AJ, O'Kane GM, Knox JJ, Gallinger S, Loree JM, Mager DL, Laskin J, **Marra MA**, Jones SJ, Schaeffer DF, Renouf DJ. Endogenous Retrovirus Transcript Levels are Associated with Immunogenic Signatures in Multiple Metastatic Cancer Types. ***Mol Cancer Ther***. 2020 Sep;19(9):1889-1897. doi: 10.1158/1535-7163.MCT-20-0094. PMID: 32518206

498. Li CH, Prokopec SD, Sun RX, Yousif F, Schmitz N; PCAWG Tumour Subtypes and Clinical Translation, Boutros PC; PCAWG Consortium. Sex differences in oncogenic mutational processes. ***Nat Commun.*** 2020 Aug 28;11(1):4330. doi: 10.1038/s41467-020-17359-2. PMID: 32859912

497. Gagliardi A, Porter VL, Zong Z, Bowlby R, Titmuss E, Namirembe C, Griner NB, Petrello H, Bowen J, Chan S, Culibrk L, Darragh TM, Stoler MH, Wright TC, Gesuwan P, Dyer M, Ma Y, Mungall KL, Jones S, Nakisige C, Novik K, Orem J, Origa M, Gastier-Foster JM, Yarchoan R, Casper C, Mills GB, Rader JS, Ojesina AI, Gerhard DS, Mungall AJ, **Marra MA**. Analysis of Ugandan cervical carcinomas reveals human papillomavirus clade-specific epigenome and transcriptome landscapes. ***Nat Genet***. 2020 Aug;52(8):800-810. doi: 10.1038/s41588-020-0673-7. **(This article was featured on the cover of the journal.)** PMID: 32747824

496. Pararajalingam P, Coyle KM, Arthur S, Thomas N, Alcaide M, Meissner B, Boyle M, Qureshi Q, Grande BM, Rushton C, Slack GW, Mungall A, Tam C, Agarwal R, Dawson SJ, Lenz G, Balasubramanian S, Gascoyne RD, Steidl C, Connors J, Villa D, Audas TE, **Marra MA**, Johnson NA, Scott DW, Morin RD. Coding and non-coding drivers of mantle cell lymphoma identified through exome and genome sequencing. ***Blood***. 2020 Jul 30;136(5):572-584. doi: 10.1182/blood.2019002385. PMID: 32160292

495. Rushton CK, Arthur SE, Alcaide M, Cheung M, Jiang A, Coyle KM, Thomas N, Hilton L, Michaud N, Daigle S, Davidson J, Bushell K, Yu S, Rhys R, Jain M, Shepherd L, **Marra MA**, Kuruvilla J, Crump M, Mann K, Assouline S, Cleary KLS, Connors JM, Steidl C, Cragg MS, Scott DW, Johnson NA, Morin RD. Genetic and evolutionary patterns of treatment resistance in relapsed B-cell lymphoma. ***Blood Adv.*** 2020 Jul 14; 4 (13): 2886–2898. doi: 10.1182/bloodadvances.2020001696. PMID: 32589730

494. Mendis S, Alcaide M, Topham JT, Johnson B, Morin RD, Chu J, Bosdet I, Kopetz S, Karsan A, Gill S, Laskin J, Jones SJM, **Marra MA**, Schaeffer DF, Renouf DJ, Loree JM. Integration of Whole-Genome Sequencing With Circulating Tumor DNA Analysis Captures Clonal Evolution and Tumor Heterogeneity in Non-V600 BRAF Mutant Colorectal Cancer. ***Clin Colorectal Cancer***. 2020 Jun;19(2):132-136.e3. doi: 10.1016/j.clcc.2020.02.001. PMID: 32151517

493. Li L, Maire CL, Bilenky M, Carles A, Heravi-Moussavi A, Hong C, Tam A, Kamoh B, Cho S, Cheung D, Li I, Wong T, Nagarajan RP, Mungall AJ, Moore R, Wang T, Kleinman CL, Jabado N, Jones SJ, **Marra MA**, Ligon KL, Costello JF, Hirst M. Epigenomic programming in early fetal brain development. ***Epigenomics***. 2020 Jun;12(12):1053-1070. doi: 10.2217/epi-2019-0319. PMID: 32677466

492. Pleasance E, Titmuss E, Williamson L, Kwan H, Zhao EY, Dixon K, Fan K, Culibrk L, Bowlby R, Jones MR, Shen Y, Grewal JK, Ashkani J, Wee K, Grisdale CJ, Thibodeau ML, Bozoky Z, Pearson H, Majounie E, Vira T, Shenwai R, Mungall KL, Chuah E, Davies J, Warren M, Reisle C, Bonakdar M, Taylor GA, Csizmok V, Chan SK, Zong S, Bilobram S, Muhammadzadeh A, D'Souza D, Corbett RD, MacMillan D, Carreira M, Choo C, Bleile D, Sadeghi S, Zhang W, Wong T, Cheng D, Brown SD, Holt RA, Moore RA, Mungall AJ, Zhao YJ, Nelson J, Fok A, Ma Y, Lee MKC, Lavoie J-M, Mendis S, Karasinska JM, Deol B, Fisic A, Schaeffer DF, Yip S, Schrader K, Regier DA, Weymann D, Chia S, Gelmon K, Tinker A, Sun S, Lim H, Renouf DJ, Jones SJM, Laskin J, **Marra MA**. Pan-cancer analysis of advanced patient tumors reveals interactions between therapy and genomic landscapes. ***Nat Cancer***. 2020 Apr 13: 1:452-468. (https://doi.org/10.1038/s43018-020-0050-6) **(This article was featured on the cover of the journal.)**

491. Ennishi D, Healy S, Bashashati A, Saberi S, Hother C, Mottok A, Chan FC, Chong L, Kridel R, Boyle M, Meissner B, Aoki T, Takata K, Woolcock B, Vigano E, Libin, Gold M, Telenius A, Madero A, Farinha P, Slack G, Ben-Neriah S, Lai D, Zhang A, Salehi S, Hennady, Chiu D, Mostafavi S, Gerrie A, Villa D, Sehn L, Savage K, Mungall A, Weng A, Bally M, Morin RD Cohen G, Connors J, **Marra M**, Shah S, Gascoyne R, Scott D. *TMEM30A* loss-of-function mutations drive lymphomagenesis and confer therapeutically exploitable vulnerability in B-cell lymphoma. ***Nat Med.*** 2020 Apr;26(4):577-588. doi: 10.1038/s41591-020-0757-z. PMID: 32094924

490. Chan-Seng-Yue M, Kim JC, Wilson GW, Ng K, Figueroa EF, O'Kane GM, Connor AA, Denroche RE, Grant RC, McLeod J, Wilson JM, Jang GH, Zhang A, Liang SB, Borgida A, Chadwick D, Kalimuthu S, Lungu I, Bartlett JMS, Krzyzanowski PM, Sandhu V, Tiriac H, Froeling FEM, Karasinska JM, Topham JT, Renouf DJ, Schaeffer DF, Jones SJM, **Marra MA**, Laskin J, Chetty R, Stein LD, Zogopoulos G, Haibe-Kains B, Campbell PJ, Tuveson DA, Knox JJ, Fischer SE, Gallinger S, Notta F. Transcription phenotypes of pancreatic cancer are driven by genomic events during tumor evolution. ***Nat Genet***. 2020 Apr;52(4):463. doi: 10.1038/s41588-020-0588-3. PMID: 31932696

489. Ghaedi M, Shen ZY, Orangi M, Martinez-Gonzalez I, Wei L, Lu X, Das A, Heravi-Moussavi A, **Marra MA**, Bhandoola A, Takei F. Single-cell analysis of RORα tracer mouse lung reveals ILC progenitors and effector ILC2 subsets. ***J Exp Med***. 2020 Mar 2;217(3): jem.20182293. doi: 10.1084/jem.20182293. PMID: 31816636

488. Majounie E, Wee K, Williamson LM, Jones MR, Pleasance E, Lim HJ, Ho C, Renouf DJ, Yip S, Jones SJM, **Marra MA**, Laskin J. Fluorouracil sensitivity in a head and neck squamous cell carcinoma with a somatic DPYD structural variant. ***Cold Spring Harb Mol Case Stud***. 2020 Feb 3;6(1)::a004713. doi: 10.1101/mcs.a004713. PMID: 31871216

487. ICGC/TCGA Pan-Cancer Analysis of Whole Genomes Consortium. Pan-cancer analysis of whole genomes. ***Nature***. 2020 Feb;578(7793):82-93. doi: 10.1038/s41586-020-1969-6. PMID: 32025007

486. Karasinska JM, Topham JT, Kalloger S, Jang GH, Denroche RE, Culibrk L, Williamson LM, Wong HL, Lee MK, O'Kane GM, Moore RA, Mungall AJ, Moore MJ, Warren C, Metcalfe A, Notta F, Knox JJ, Gallinger S, Laskin JJ, **Marra MA**, Jones SJ, Renouf DJ, Schaeffer DF. Altered gene expression along the glycolysis-cholesterol synthesis axis is associated with outcome in pancreatic cancer. ***Clin Cancer Res***. 2020 Jan 1;26(1):135-146. doi: 10.1158/1078-0432.CCR-19-1543. PMID: 31481506

485. Laks E, McPherson A, Zahn H, Lai D, Steif A, Brimhall J, Biele J, Wang B, Masud T, Ting J, Grewal D, Nielsen C, Leung S, Bojilova V, Smith M, Golovko O, Poon S, Eirew P, Kabeer F, Ruiz de Algara T, Lee SR, Taghiyar MJ, Huebner C, Ngo J, Chan T, Vatrz-Watts S, Walters P, Abrar N, Chan S, Wiens M, Martin L, Scott RW, Underhill TM, Chavez E, Steidl C, Da Costa D, Ma Y, Coope RJN, Corbett R, Pleasance S, Moore R, Mungall AJ, Mar C, Cafferty F, Gelmon K, Chia S, CRUK IMAXT Grand Challenge Team, **Marra MA,** Hansen C, Shah SP, Aparicio S. Clonal Decomposition and DNA Replication States Defined by Scaled Single-Cell Genome Sequencing. ***Cell***. 2019 Nov 14;179 (5), 1207-1221.e22. PMID: 31730858

484. Chun HE, Johann PD, Milne K, Zapatka M, Buellesbach A, Ishaque N, Iskar M, Erkek S, Wei L, Tessier-Cloutier B, Lever J, Titmuss E, Topham JT, Bowlby R, Chuah E, Mungall KL, Ma Y, Mungall AJ, Moore RA, Taylor MD, Gerhard DS, Jones SJM, Korshunov A, Gessler M, Kerl K, Hasselblatt M, Frühwald MC, Perlman EJ, Nelson BH, Pfister SM, **Marra MA**, Kool M. Identification and Analyses of Extra-Cranial and Cranial Rhabdoid Tumor Molecular Subgroups Reveal Tumors with Cytotoxic T Cell Infiltration. ***Cell Rep***. 2019 Nov 19; 29 (8):2338-2354.e7. doi: 10.1016/j.celrep.2019.10.013. PMID: 31708418

483. Negri GL, Grande BM, Delaidelli A, El-Naggar A, Cochrane D, Lau CC, Triche TJ, Moore RA, Jones SJM, Montpetit A, **Marra MA**, Malkin D, Morin RD, Sorensen PH. Integrative genomic analysis of matched primary and metastatic pediatric osteosarcoma. ***J Pathol.*** 2019 Nov;249(3):319-331. PMID: 31236944

482. Haile S, Corbett RD, Bilobram S, Mungall K, Grande BM, Kirk H, Pandoh P, MacLeod T, McDonald H, Bala M, Coope RJ, Moore RA, Mungall AJ, Zhao YJ, Morin RD, Jones SJ, **Marra MA**. Evaluation of protocols for rRNA depletion-based RNA sequencing of nanogram inputs of mammalian total RNA. ***PLoS One***. 2019 Oct 31;14(10):e0224578. doi: 10.1371/journal.pone.0224578. PMID: 31671154

481. Vaske OM, Bjork I, Salama SR, Beale H, Tayi Shah A, Sanders L, Pfeil J, Lam DL, Learned K, Durbin A, Kephart ET, Currie R, Newton Y, Swatloski T, McColl D, Vivian J, Zhu J, Lee AG, Leung SG,

Spillinger A, Liu HY, Liang WS, Byron SA, Berens ME, Resnick AC, Lacayo N, Spunt SL, Rangaswami A, Huynh V, Torno L, Plant A, Kirov I, Zabokrtsky KB, Rassekh SR, Deyell RJ, Laskin J, **Marra MA**, Sender LS, Mueller S, Sweet-Cordero EA, Goldstein TC, Haussler D. Comparative Tumor RNA Sequencing Analysis for Difficult-to-Treat Pediatric and Young Adult Patients With Cancer. ***JAMA Netw Open***. 2019 Oct 2;2(10):e1913968. doi: 10.1001/jamanetworkopen.2019.13968. PMID: 31651965

480. Suzuki H, Kumar SA, Shuai S, Diaz-Navarro A, Gutierrez-Fernandez A, De Antonellis P, Cavalli FMG, Juraschka K, Farooq H, Shibahara I, Vladoiu MC, Zhang J, Abeysundara N, Przelicki D, Skowron P, Gauer N, Luu B, Daniels C, Wu X, Forget A, Momin A, Wang J, Dong W, Kim SK, Grajkowska WA, Jouvet A, Fèvre-Montange M, Garrè ML, Rao AAN, Giannini C, Kros JM, French PJ, Jabado N, Ng HK, Poon WS, Eberhart CG, Pollack IF, Olson JM, Weiss WA, Kumabe T, López-Aguilar E, Lach B, Massimino M, Van Meir EG, Rubin JB, Vibhakar R, Chambless LB, Kijima N, Klekner A, Bognár L, Chan JA, Faria CC, Ragoussis J, Pfister SM, Goldenberg A, Wechsler-Reya RJ, Bailey SD, Garzia L, Morrissy AS, **Marra MA**, Huang X, Malkin D, Ayrault O, Ramaswamy V, Puente XS, Calarco JA, Stein L, Taylor MD. Recurrent non-coding U1-snRNA mutations drive cryptic splicing in Shh medulloblastoma. ***Nature.*** 2019 Oct;574(7780):707-711. doi: 10.1038/s41586-019-1650-0. PMID: 31664194

479. Shen Y, Grisdale CJ, Islam SA, Bose P, Lever J, Zhao EY, Grinshtein N, Ma Y, Mungall AJ, Moore RA, Lun X, Senger DL, Robbins SM, Wang AY, MacIsaac JL, Kobor MS, Luchman HA, Weiss S, Chan JA, Blough MD, Kaplan DR, Cairncross JG, **Marra MA**, Jones SJM. Comprehensive genomic profiling of glioblastoma tumors, BTICs, and xenografts reveals stability and adaptation to growth environments. ***Proc Natl Acad Sci U S A***. 2019 Sep 17;116(38):19098-19108. **(This paper had a write up in the Highlights from the Literature in the Feb 2020 issue of Neuro-Oncology**. https://academic.oup.com/neuro-oncology/article/22/2/177/5741687 **)** PMID: 31471491

478. Mottok A, Hung SS, Chavez EA, Woolcock B, Telenius A, Chong LC, Meissner B, Nakamura H, Rushton C, Viganò E, Sarkozy C, Gascoyne RD, Connors JM, Ben Neriah S, Mungall A, **Marra MA**, Siebert R, Scott DW, Savage KJ, Steidl C. Integrative genomic analysis identifies key pathogenic mechanisms in primary mediastinal large B-cell lymphoma. ***Blood***. 2019 Sep 5;134(10):802-813. PMID: 31292115

477. Thorsson V, Gibbs DL, Brown SD, Wolf D, Bortone DS, Ou Yang TH, Porta-Pardo E, Gao GF, Plaisier CL, Eddy JA, Ziv E, Culhane AC, Paull EO, Sivakumar IKA, Gentles AJ, Malhotra R, Farshidfar F, Colaprico A, Parker JS, Mose LE, Vo NS, Liu J, Liu Y, Rader J, Dhankani V, Reynolds SM, Bowlby R, Califano A, Cherniack AD, Anastassiou D, Bedognetti D, Rao A, Chen K, Krasnitz A, Hu H, Malta TM, Noushmehr H, Pedamallu CS, Bullman S, Ojesina AI, Lamb A, Zhou W, Shen H, Choueiri TK, Weinstein JN, Guinney J, Saltz J, Holt RA, Rabkin CE; Cancer Genome Atlas Research Network, Lazar AJ, Serody JS, Demicco EG, Disis ML, Vincent BG, Shmulevich L. The Immune Landscape of Cancer. ***Immunity.*** . 2019 Aug 20;51(2):411-412. doi: 10.1016/j.immuni.2019.08.004. PMID: 31433971

476. Wong D, Shen Y, Levine AB, Pleasance E, Jones M, Mungall K, Thiessen B, Toyota B, Laskin J, Jones SJM, **Marra MA**, Yip S. The pivotal role of sampling recurrent tumors in the precision care of patients with tumors of the central nervous system. ***Cold Spring Harb Mol Case Stud***. 2019 Aug 1;5(4). pii: a004143. doi: 10.1101/mcs.a004143. PMID: 31371350

475. Johnston M, Nikolic A, Ninkovic N, Guilhamon P, Cavalli F, Seaman S, Zemp F, Lee J, Abdelkareem A, Ellestad K, Murison A, Kushida M, Coutinho F, Ma Y, Mungall A, Moore R, **Marra M**, Taylor M, Dirks P, Pugh T, Morrissy S, St Croix B, Mahoney D, Lupien M, Gallo M. High-resolution structural genomics reveals new therapeutic vulnerabilities in glioblastoma. ***Genome Res***. 2019 Aug;29(8):1211-1222. PMID: 31249064

474. Jones MR, Williamson LM, Topham JT, Lee MKC, Goytain A, Ho J, Denroche RE, Jang G-H, Pleasance ED, Shen Y, Karasinska JM, McGhie JP, Gill S, Lim H, Moore MJ, Wong H-L, Ng T, Yip S, Zhang W, Sadeghi S, Reisle CR, Mungall AJ, Mungall KL, Moore RA, Ma Y, Knox JJ, Gallinger S,

Laskin J, **Marra MA**, Schaeffer DF, Jones SJM, Renouf DJ. *NRG1* gene fusions are recurrent, clinically actionable gene rearrangements in KRAS wild-type pancreatic ductal adenocarcinoma. ***Clin Cancer Res.*** 2019 Aug 1;25(15):4674-4681. doi: 10.1158/1078-0432.CCR-19-0191. PMID: 31068372

473. Vladoiu M, El-Hamamy I, Donovan L, Farooq H, Holgado B, Ramaswamy V, Mack S, Lee J, Kumar S, Przelicki D, Michealraj KA, Juraschka K, Skowron P, Luu B, Suzuki H, Morrissy S, Cavalli F, Garzia L, Daniels C, Wu X, Qazi M, Singh S, Chan J, **Marra M**, Malkin D, Dirks P, Pugh T, Notta F, Kleinman C, Jabado N, Stein L, Taylor MD. Childhood Cerebellar Tumors Mirror Conserved Fetal Transcriptional Programs. ***Nature.*** 2019 Aug;572(7767):67-73. PMID: 31043743

472. Kwan HH, Culibrk L, Taylor GA, Leelakumari S, Tan R, Jackman SD, Tse K, MacLeod T, Cheng D, Chuah E, Kirk H, Pandoh P, Carlsen R, Zhao Y, Mungall AJ, Moore R, Birol I, **Marra MA**, Rosen DAS, Haulena M, Jones SJM. The Genome of the Steller Sea Lion (*Eumetopias jubatus*). ***Genes*** (Basel). 2019 Jun 26;10(7). pii: E486. doi: 10.3390/genes10070486. PMID: 31248052

471. Feng X, Pleasance E, Zhao EY, Ng T, Grewal J, Mohammad N, Taylor SK, Simmons C, Srikanthan A, Rassekh, SR, Deyell R, Rauw R, Knowling M, Khoo K, Lee U, Noonan K, Hart J, Tonseth RP, Shen Y, Titmuss E, Jones M, Bonakdar M, Reisle C, Taylor GA, Chan S, Mungall R, Chuah E, Zhao YJ, Mungall A, Moore R, Lim H, Renouf DJ, Gelmon K, Yip S, Jones SJM, **Marra M**, Laskin J. Therapeutic implication of genomic landscape of adult metastatic sarcoma. ***JCO PO.*** 2019 Jun;3:1-25. doi: 10.1200/PO.18.00325. PMID: 35100702

470. Williamson LM, Steel M, Grewal JK, Thibodeau ML, Zhao EY, Loree JM, Yang KC, Gorski SM, Mungall AJ, Mungall KL, Moore RA, **Marra MA**, Laskin J, Renouf DJ, Schaeffer DF, Jones SJM. Genomic characterization of a well-differentiated grade 3 pancreatic neuroendocrine tumor. ***Cold Spring Harb Mol Case Stud***. 2019 Jun 3;5(3). pii: a003814. doi: 10.1101/mcs.a003814. PMID: 31160355

469. Ahmad ST, Rogers AD, Chen MJ, Dixit R, Adnani L, Frankiw LS, Lawn SO, Blough MD, Alshehri M, Wu W, **Marra MA**, Robbins SM, Cairncross JG, Schuurmans C, Chan JA. Capicua regulates neural stem cell proliferation and lineage specification through control of Ets factors. ***Nat Commun***. 2019 May 1;10(1):2000. PMID: 31043608

468. Hoffman M, Gillmor AH, Kunz DJ, Johnston MJ, Nikolic A, Narta K, Zarrei H, King JC, Ellestad K, Dang NH, Cavalli FM, Kushida M, Coutinho FJ, Luu B, Ma Y, Mungall AJ, Moore RA, **Marra MA**, Taylor MD, Pugh TJ, Dirks PB, Scherer SW, Senger DL, Simons BD, Chan JA, Morrissy AS, Gallo M. Intratumoral genetic and functional heterogeneity in pediatric glioblastoma. ***Cancer Res***. 2019 May 1;79(9):2111-2123. PMID: 30877103

467. Yasin H, Gibson WT, Langlois S, Stowe RM, Tsang ES, Lee L, Poon J, Tran G, Tyson C, Wong CK, **Marra MA**, Friedman JM, Zahir FR. A Distinct Neurodevelopmental Syndrome with Intellectual Disability, Autism Spectrum Disorder, Characteristic Facies and Macrocephaly is caused by defects in CHD8. ***J Hum Genet.*** 2019 Apr;64(4):271-280. PMID: 30670789

466. Grewal JK, Tessier-Cloutier B, Jones M, Gakkhar S, Ma Y, Moore R, Mungall AJ, Taylor MD, Gelmon K, Lim H, Renouf D, Laskin J, **Marra M**, Yip S, Jones SJM. Application of a Neural Network Whole Transcriptome-Based Pan-Cancer Method for Diagnosis of Primary and Metastatic Cancers. ***JAMA Netw Open.*** 2019 Apr 5;2(4):e192597. doi: 10.1001/jamanetworkopen.2019.2597. PMID: 31026023

465. Thibodeau ML, Zhao EY, Reisle C, Ch'ng C, Wong HL, Shen Y, Jones MR, Lim HJ, Young S, Cremin C, Zhang W, Holt R, Eirew P, Karasinska J, Kalloger S, Taylor G, Majounie E, Bonakdar M, Zong Z, Bleile D, Chiu R, Birol I, Gelmon K, Lohrisch C, Mungall KL, Mungall AJ, Moore R, Ma YP, Fok A, Yip S, Karsan A, Huntsman D, Schaeffer DF, Laskin J, **Marra MA,** Renouf DJ, Jones SJM, Schrader KA. Base excision repair deficiency signatures implicate germline and somatic *MUTYH* aberrations in pancreatic ductal adenocarcinoma and breast cancer oncogenesis. ***Cold Spring Harb Mol Case Stud.*** 2019 Apr 1;5(2). pii: a003681. doi: 10.1101/mcs.a003681. PMID: 30833417

464. Ennishi D, Takata K, Beguelin W, Duns G, Mottok A, Farinha P, Bashashati A, Saberi S, Boyle M, Meissner B, Ben-Neriah S, Woolcock BW, Telenius A, Lai D, Teater M, Kridel R, Savage KJ, Sehn LH, Morin RD, **Marra MA**, Shah SP, Connors JM, Gascoyne RD, Scott DW, Melnick AM, Steidl C. Molecular and Genetic Characterization of MHC Deficiency Identifies EZH2 as Therapeutic Target for Enhancing Immune Recognition. ***Cancer Discov.*** 2019 Apr; 9(4):546-563. PMID: 30705065

463. Grande BM, Gerhard DS, Jiang A, Griner NB, Abramson JS, Alexander TB, Allen H, Ayers LW, Bethony JM, Bhatia K, Bowen J, Casper C, Choi JK, Culibrk L, Davidsen TM, Dyer MA, Gastier-Foster JM, Gesuwan P, Greiner TC, Gross TG, Hanf B, Harris NL, He Y, Irvin JD, Jaffe ES, Jones SJM, Kerchan P, Knoetze N, Lea FE, Lichtenberg TM, Ma Y, Martin JP, Martin M-R, Mbulaiteye SM, Mullighan CG, Mungall AJ, Namirembe C, Novik K, Noy A, Ogwang MD, Omoding A, Orem J, Reynolds SJ, Rushton CK, Sandlund JT, Schmitz R, Taylor C, Wilson WH, Zhao EY, **Marra MA**, Morin RD, Staudt LM. Genome-wide discovery of somatic coding and non-coding mutations in pediatric endemic and sporadic Burkitt lymphoma. ***Blood.*** 2019 Mar 21;133(12):1313-1324. PMID: 30617194

462. Bolouri H, Farrar JE, Triche T Jr, Ries RE, Lim EL, Alonzo TA, Ma Y, Moore R, Mungall AJ, **Marra MA**, Zhang J, Ma X, Liu Y, Liu Y, Auvil JMG, Davidsen TM, Gesuwan P, Hermida LC, Salhia B, Capone S, Ramsingh G, Zwaan CM, Noort S, Piccolo SR, Kolb EA, Gamis AS, Smith MA, Gerhard DS, Meshinchi S. The molecular landscape of pediatric acute myeloid leukemia reveals recurrent structural alterations and age-specific mutational interactions. ***Nat Med***. 2019 Mar;25(3):530. doi: 10.1038/s41591-019-0369-7. PMID: 30705421

461. Pandoh PK, Corbett RD, McDonald H, Smailus D, Alcaide M, Kirk H, Trinh E, Haile S, MacLeod T, Bilobram S, Mungall AJ, Ma Y, Moore RA, Coope R, Zhao YJ, Jones SJ, Holt R, Karsan A, Morin R, **Marra MA**. A High Throughput Protocol for Isolating Cell-Free Circulating Tumor DNA from Peripheral Blood. ***Biotechniques***. 2019 Feb;66(2):85-92. PMID: 30744412

460. Tsang ES, Shen Y, Chooback N, Ho C, Jones M, Renouf DJ, Lim H, Sun S, Yip S, Pleasance E, Ionescu DN, Mungall K, Kasaian K, Ma Y, Zhao Y, Mungall A, Moore R, Jones SJM, **Marra M**, Laskin J. Clinical Outcomes after Whole Genome Sequencing in Patients with Metastatic Non-Small Cell Lung Cancer. ***Cold Spring Harb Mol Case Stud***. 2019 Feb 1;5(1). pii: a002659. doi: 10.1101/mcs.a002659. PMID: 30514790

459. Haile S, Corbett RD, Bilobram S, Bye MH, Kirk H, Pandoh P, Trinh E, MacLeod T, McDonald H, Bala M, Miller D, Novik K, Coope RJ, Moore RA, Zhao Y, Mungall AJ, Ma Y, Holt RA, Jones SJ, **Marra MA.** Sources of erroneous sequences and artifact chimeric reads in next generation sequencing of genomic DNA from formalin-fixed paraffin-embedded samples. ***Nucleic Acids Res***. 2019 Jan 25;47(2):e12. PMID: 30418619

458. Ennishi D, Jiang A, Boyle M, Collinge B, Grande BM, Ben-Neriah S, Rushton C, Tang J, Thomas N, Slack GW, Farinha P, Takata K, Miyata-Takata T, Craig J, Mottok A, Meissner B, Saberi S, Bashashati A, Villa D, Savage KJ, Sehn LH, Kridel R, Mungall AJ, **Marra MA**, Shah SP, Steidl C, Connors JM, Gascoyne RD, Morin RD, Scott DW. Double-Hit Gene Expression Signature Defines a Distinct Subgroup of Germinal Center B-Cell-Like Diffuse Large B-Cell Lymphoma. ***J Clin Oncol.*** 2019 Jan 20;37(3):190-201. PMID: 30523716

457. Wong D, Lounsbury K, Lum A, Song J, Chan S, LeBlanc V, Chittaranjan S, **Marra MA**, Yip S. Transcriptomic analysis of CIC and ATXN1L reveal a functional relationship exploited by cancer. ***Oncogene.*** 2019 Jan;38(2):273-290. doi: 10.1038/s41388-018-0427-5. PMID: 30093628

456. Ko JJ, Grewal J, Ng T, Lavoie JM, Thibodeau ML, Shen Y, Mungall AJ, Taylor G, Schrader KA, Jones SJM, Kollmannsberger C, Laskin J, **Marra MA.** Whole genome and transcriptome profiling of a metastatic thyroid-like follicular renal cell carcinoma. ***Cold Spring Harb Mol Case Stud.*** 2018 Dec 17;4(6). pii: a003137. doi: 10.1101/mcs.a003137. PMID: 30446580

455. Hmeljaki J, Sanchez-Vega F, Hoadley KA, Shih J, Stewart C, Heiman D, Tarpey P, Danilova L, Drill E, Gibb EA, Bowlby R, Kanchi R, Osmanbeyoglu HU, Sekido Y, Takeshita J, Newton Y, Graim K, Gupta M, Gay CM, Diao L, Gibbs DL, Thorsson V, Iype L, Kantheti H, Severson DT, Ravegnini G, Desmeules P, Jungbluth AA, Travis WD, Dacic S, Chirieac LR, Galateau-Sallé F, Fujimoto J, Husain AN, Silveira HC, Rusch VW, Rintoul RC, Pass H, Kindler H, Zauderer MG, Kwiatkowski DJ, Bueno R, Tsao AS, Creaney J, Lichtenberg T, Leraas K, Bowen J; TCGA Research Network, Felau I, Zenklusen JC, Akbani R, Cherniack AD, Byers LA, Noble MS, Fletcher JA, Robertson AG, Shen R, Aburatani H, Robinson BW, Campbell P, Ladanyi M. Integrative Molecular Characterization of Malignant Pleural Mesothelioma. ***Cancer Discov***. 2018 Dec;8(12):1548-1565. PMID: 30322867

454. Taylor GA, Kirk H, Coombe L, Jackman SD, Chu J, Tse K, Cheng D, Chuah E, Pandoh P, Carlsen R, Zhao Y, Mungall AJ, Moore R, Birol I, Franke M, **Marra MA**, Dutton C, Jones SJM. The Genome of the North American Brown Bear or Grizzly: Ursus arctos ssp. horribilis. ***Genes*** (Basel). 2018 Nov 30;9(12). PMID: 30513700

453. Wang Y, Xu X, Maglic D, Dill MT, Mojumdar K, Ng PK, Jeong KJ, Tsang YH, Moreno D, Bhavana VH, Peng X, Ge Z, Chen H, Li J, Chen Z, Zhang H, Han L, Du D, Creighton CJ, Mills GB; Cancer Genome Atlas Research Network, Camargo F, Liang H. Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. ***Cell Rep***. 2018 Oct 30;25(5):1304-1317.e5. PMID: 30380420

452. Korkut A, Zaidi S, Kanchi RS, Rao S, Gough NR, Schultz A, Li X, Lorenzi PL, Berger AC, Robertson G, Kwong LN, Datto M, Roszik J, Ling S, Ravikumar V, Manyam G, Rao A, Shelley S, Liu Y, Ju Z, Hansel D, de Velasco G, Pennathur A, Andersen JB, O'Rourke CJ, Ohshiro K, Jogunoori W, Nguyen BN, Li S, Osmanbeyoglu HU, Ajani JA, Mani SA, Houseman A, Wiznerowicz M, Chen J, Gu S, Ma W, Zhang J, Tong P, Cherniack AD, Deng C, Resar L; Cancer Genome Atlas Research Network, Weinstein JN, Mishra L, Akbani R. A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF-β Superfamily. ***Cell Syst.*** 2018 Oct 24;7(4):422-437.e7. PMID: 30268436

451. Chong LC, Ben-Neriah S, Slack GW, Freeman C, Ennishi D, Mottok A, Collinge B, Abrisqueta P, Farinha P, Boyle M, Meissner B, Kridel R, Gerrie AS, Villa D, Savage KJ, Sehn LH, Siebert R, Morin RD, Gascoyne RD, **Marra MA**, Connors JM, Mungall AJ, Steidl C, Scott DW. High-resolution architecture and partner genes of *MYC* rearrangements in lymphoma with DLBCL morphology. ***Blood Adv***. 2018 Oct 23;2(20):2755-2765. PMID: 30348671

450. Wong H, Zhao EY, Jones MR, Reisle CR, Eirew P, Pleasance E, Grande BM, Karasinska JM, Kalloger SE, Lim HJ, Shen Y, Yip S, Morin RD, Laskin J, **Marra MA,** Jones SJM, Schrader KA, Schaeffer DF, Renouf DJ. Temporal Dynamics of Genomic Alterations in a BRCA1 Germline–Mutated Pancreatic Cancer With Low Genomic Instability Burden but Exceptional Response to Fluorouracil, Oxaliplatin, Leucovorin, and Irinotecan. ***JCO Precis Oncol***. 2018 Oct 19. DOI: 10.1200/PO.18.00057. PMID: 32913994

449. Arthur SE, Jiang A, Grande BM, Alcaide M, Cojocaru R, Rushton CK, Mottok A, Hilton LK, Lat PK, Zhao EY, Culibrk L, Ennishi D, Jessa S, Chong L, Thomas N, Pararajalingam P, Meissner B, Boyle M, Davidson J, Bushell KR, Lai D, Farinha P, Slack GW, Morin GB, Shah S, Sen D, Jones SJM, Mungall AJ, Gascoyne RD, Audas TE, Unrau P, **Marra MA**, Connors JM, Steidl C, Scott DW, Morin RD. Genome-wide discovery of somatic regulatory variants in diffuse large B-cell lymphoma. ***Nat Commun.*** 2018 Oct 1;9(1):4001. doi: 10.1038/s41467-018-06354-3. PMID: 30275490

448. Alexander TB, Gu Z, Iacobucci I, Dickerson K, Choi JK, Xu B, Payne-Turner D, Yoshihara H, Loh ML, Horan J, Buldini B, Basso G, Elitzur S, de Haas V, Zwaan CM, Yeoh A, Reinhardt D, Tomizawa D, Kiyokawa N, Lammens T, De Moerloose B, Catchpoole D, Hori H, Moorman A, Moore AS, Hrusak O, Meshinchi S, Orgel E, Devidas M, Borowitz M, Wood B, Heerema NA, Carrol A, Yang YL, Smith MA, Davidsen TM, Hermida LC, Gesuwan P, **Marra MA**, Ma Y, Mungall AJ, Moore RA, Jones SJM, Valentine M, Janke LJ, Rubnitz JE, Pui CH, Ding L, Liu Y, Zhang J, Nichols KE, Downing JR, Cao X, Shi L, Pounds S, Newman S, Pei D, Guidry Auvil JM, Gerhard DS, Hunger SP, Inaba H, Mullighan CG.

The genetic basis and cell of origin of mixed phenotype acute leukaemia. ***Nature.*** 2018 Oct;562(7727):373-379. PMID: 30209392

447. Yuan AL, Ricks CB, Bohm AK, Lun X, Maxwell L, Safdar S, Bukhari S, Gerber A, Sayeed W, Bering EA, Pedersen H, Chan JA, Shen Y, **Marra M**, Kaplan DR, Mason W, Goodman LD, Ezhilarasan R, Kaufmann AB, Cabral M, Robbins SM, Senger DL, Cahill DP, Sulman EP, Cairncross JG, Blough MD. ABT-888 restores sensitivity in temozolomide resistant glioma cells and xenografts. ***PLoS One***. 2018 Aug 28;13(8):e0202860. doi: 10.1371/journal.pone.0202860 PMID: 30153289

446. Bailey MH, Tokheim C, Porta-Pardo E, Sengupta S, Bertrand D, Weerasinghe A, Colaprico A, Wendl MC, Kim J, Reardon B, Ng PK, Jeong KJ, Cao S, Wang Z, Gao J, Gao Q, Wang F, Liu EM, Mularoni L, Rubio-Perez C, Nagarajan N, Cortés-Ciriano I, Zhou DC, Liang WW, Hess JM, Yellapantula VD, Tamborero D, Gonzalez-Perez A, Suphavilai C, Ko JY, Khurana E, Park PJ, Van Allen EM, Liang H; MC3 Working Group; Cancer Genome Atlas Research Network, Lawrence MS, Godzik A, Lopez-Bigas N, Stuart J, Wheeler D, Getz G, Chen K, Lazar AJ, Mills GB, Karchin R, Ding L. Comprehensive Characterization of Cancer Driver Genes and Mutations. ***Cell***. 2018 Aug 9;174(4):1034-1035. PMID: 29625053

445. Kahles A, Lehmann KV, Toussaint NC, Hüser M, Stark SG, Sachsenberg T, Stegle O, Kohlbacher O, Sander C; Cancer Genome Atlas Research Network, Rätsch G. Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. ***Cancer Cell.*** 2018 Aug 13;34(2):211-224.e6. PMID: 30078747

444. Shen H, Shih J, Hollern DP, Wang L, Bowlby R, Tickoo SK, Thorsson V, Mungall AJ, Newton Y, Hegde AM, Armenia J, Sánchez-Vega F, Pluta J, Pyle LC, Mehra R, Reuter VE, Godoy G, Jones J, Shelley CS, Feldman DR, Vidal DO, Lessel D, Kulis T, Cárcano FM, Leraas KM, Lichtenberg TM, Brooks D, Cherniack AD, Cho J, Heiman DI, Kasaian K, Liu M, Noble MS, Xi L, Zhang H, Zhou W, ZenKlusen JC, Hutter CM, Felau I, Zhang J, Schultz N, Getz G, Meyerson M, Stuart JM; Cancer Genome Atlas Research Network, Akbani R, Wheeler DA, Laird PW, Nathanson KL, Cortessis VK, Hoadley KA. Integrated Molecular Characterization of Testicular Germ Cell Tumors. ***Cell Rep***. 2018 Jun 12;23(11):3392-3406. PMID: 29898407

443. Garzia L, Kijima N, Morrissy AS, Wu X, Wang X, Donovan LK, De Antonellis P, Liu K-W, Luu B, Alamsahebpour A, Thompson YY, Holgado BL, Ramaswamy V, Farooq H, Skowron P, Shih DJH, Li A, Ensan S, Robbins CS, Manno A, Liu J, Qin L, Cybulsky M, Mitra S, Cho Y-J, Weiss WA, Chan JA, Hawkins CE, Massimino M, Jabado N, Bouffet E, Sorensen PHB, Aldape K, **Marra MA**, Wechsler-Reya RJ, Fults DW, Taylor MD. A Hematogenous Route for Medulloblastoma Leptomeningeal Metastases. ***Cell***. 2018 May 31;173(6):1549. PMID: 29856958

442. Waszak SM, Northcott PA, Buchhalter I, Robinson GW, Sutter C, Groebner S, Grund KB, Brugieres L, Jones DTW, Pajtler KW, Morissy S, Kool M, Sturm D, Chavez K, Ernst A, Brabetz S, Hain M, Zichner T, Wang MS, Weischenfeldt J, Rausch T, Mardin BR, Zhou X, Baciu C, Lawerenz C, Chan J, Varlet P, Guerrini-Rousseau L, Fults DW, Grajkowska W, Hauser P, Jabado N, Ra Y-S, Zitterbart K, Shringarpure SS, De La Vega FM, Bustamante CD, Ng H-K, Perry A, MacDonald TJ, Hernaiz-Driever P, Bendel AE, Bowers D, McCowage G, Chintagumpala MM, Cohn R, Hassall T, Fleischhack G, Eggen T, Wesenberg F, Feychting M, Lannering B, Schüz J, Andersen TV, Röösli M, Kuehni CE, Grotzer M, Kjaerheim K, Monoranu CM, Archer TC, Duke E, Pomeroy SL, Shelagh R, Frank S, Sumerauer D, Scheurlen W, Ryzhova MV, Milde T, Kratz CP, Samuel D, Zhang J, Solomon DA, **Marra M**, Eils R, Bartram CR, von Hoff K, Rutkowski S, Ramaswamy V, Korshunov A, Malkin D, Lichter P, Taylor MD, Gajjar A, Korbel JO, Pfister SM. Spectrum and Prevalence of Hereditary Predisposition in Medulloblastoma. ***Lancet Oncol.*** 2018 May 9. pii: S1470-2045(18)30242-0. doi: 10.1016/S1470-2045(18)30242-0. PMID: 29753700

441. Newton Y, Rassekh R, Deyell R, Shen Y, Jones M, Dunham C, Yip S, Leelakumari S, Zhu J, McColl D, Wat S, Salama S, Ng T, Hendson G, Lee AF, Ma Y, Moore R, Mungall A, Haussler D, Stuart J, Jantzen

C, Laskin J, Jones S, **Marra M**, Morozova O. Comparative RNA-Seq analysis benefits a pediatric patient with relapsed cancer. ***JCO PO.*** 2018 Apr 19. http://ascopubs.org/doi/pdf/10.1200/PO.17.00198

440. Liu Y, Sethi NS, Hinoue T, Schneider BG, Cherniack AD, Sanchez-Vega F, Seoane JA, Farshidfar F, Bowlby R, Islam M, Kim J, Chatila W, Akbani R, Kanchi RS, Rabkin CS, Willis JE, Wang KK, McCall SJ, Mishra L, Ojesina AI, Bullman S, Pedamallu CS, Lazar AJ, Sakai R; Cancer Genome Atlas Research Network, Thorsson V, Bass AJ, Laird PW. Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. ***Cancer Cell***. 2018 Apr 9;33(4):721-735.e8. doi: 10.1016/j.ccell.2018.03.010. PMID: 29622466

439. Wang Z, Yang B, Zhang M, Guo W, Wu Z, Wang Y, Jia L, Li S; Cancer Genome Atlas Research Network, Xie W, Yang D. lncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic lncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. ***Cancer Cell.*** 2018 Apr 9;33(4):706-720.e9. doi: 10.1016/j.ccell.2018.03.006. PMID: 29622465

438. Berger AC, Korkut A, Kanchi RS, Hegde AM, Lenoir W, Liu W, Liu Y, Fan H, Shen H, Ravikumar V, Rao A, Schultz A, Li X, Sumazin P, Williams C, Mestdagh P, Gunaratne PH, Yau C, Bowlby R, Robertson AG, Tiezzi DG, Wang C, Cherniack AD, Godwin AK, Kuderer NM, Rader JS, Zuna RE, Sood AK, Lazar AJ, Ojesina AI, Adebamowo C, Adebamowo SN, Baggerly KA, Chen TW, Chiu HS, Lefever S, Liu L, MacKenzie K, Orsulic S, Roszik J, Shelley CS, Song Q, Vellano CP, Wentzensen N; Cancer Genome Atlas Research Network, Weinstein JN, Mills GB, Levine DA, Akbani R. A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. ***Cancer Cell***. 2018 Apr 9;33(4):690-705.e9. doi: 10.1016/j.ccell.2018.03.014. PMID: 29622464

437. Taylor AM, Shih J, Ha G, Gao GF, Zhang X, Berger AC, Schumacher SE, Wang C, Hu H, Liu J, Lazar AJ; Cancer Genome Atlas Research Network, Cherniack AD, Beroukhim R, Meyerson M. Genomic and Functional Approaches to Understanding Cancer Aneuploidy. ***Cancer Cell***. 2018 Apr 9;33(4):676-689.e3. doi: 10.1016/j.ccell.2018.03.007. PMID: 29622463

436. Liu J, Lichtenberg T, Hoadley KA, Poisson LM, Lazar AJ, Cherniack AD, Kovatich AJ, Benz CC, Levine DA, Lee AV, Omberg L, Wolf DM, Shriver CD, Thorsson V; Cancer Genome Atlas Research Network, Hu H. An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. ***Cell.*** 2018 Apr 5;173(2):400-416.e11. doi: 10.1016/j.cell.2018.02.052. PMID: 29625055

435. Chen H, Li C, Peng X, Zhou Z, Weinstein JN; Cancer Genome Atlas Research Network, Liang H. A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. ***Cell***. 2018 Apr 5;173(2):386-399.e12. doi: 10.1016/j.cell.2018.03.027. PMID: 29625054

434. Huang KL, Mashl RJ, Wu Y, Ritter DI, Wang J, Oh C, Paczkowska M, Reynolds S, Wyczalkowski MA, Oak N, Scott AD, Krassowski M, Cherniack AD, Houlahan KE, Jayasinghe R, Wang LB, Zhou DC, Liu D, Cao S, Kim YW, Koire A, McMichael JF, Hucthagowder V, Kim TB, Hahn A, Wang C, McLellan MD, Al-Mulla F, Johnson KJ; Cancer Genome Atlas Research Network, Lichtarge O, Boutros PC, Raphael B, Lazar AJ, Zhang W, Wendl MC, Govindan R, Jain S, Wheeler D, Kulkarni S, Dipersio JF, Reimand J, Meric-Bernstam F, Chen K, Shmulevich I, Plon SE, Chen F, Ding L. Pathogenic Germline Variants in 10,389 Adult Cancers. ***Cell***. 2018 Apr 5;173(2):355-370.e14. doi: 10.1016/j.cell.2018.03.039. PMID: 29625052

433. Malta TM, Sokolov A, Gentles AJ, Burzykowski T, Poisson L, Weinstein JN, Kamińska B, Huelsken J, Omberg L, Gevaert O, Colaprico A, Czerwińska P, Mazurek S, Mishra L, Heyn H, Krasnitz A, Godwin AK, Lazar AJ; Cancer Genome Atlas Research Network, Stuart JM, Hoadley KA, Laird PW, Noushmehr H, Wiznerowicz M. Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. ***Cell.*** 2018 Apr 5;173(2):338-354.e15. doi: 10.1016/j.cell.2018.03.034. PMID: 29625051

432. Sanchez-Vega F, Mina M, Armenia J, Chatila WK, Luna A, La KC, Dimitriadoy S, Liu DL, Kantheti HS, Saghafinia S, Chakravarty D, Daian F, Gao Q, Bailey MH, Liang WW, Foltz SM, Shmulevich I, Ding L,

Heins Z, Ochoa A, Gross B, Gao J, Zhang H, Kundra R, Kandoth C, Bahceci I, Dervishi L, Dogrusoz U, Zhou W, Shen H, Laird PW, Way GP, Greene CS, Liang H, Xiao Y, Wang C, Iavarone A, Berger AH, Bivona TG, Lazar AJ, Hammer GD, Giordano T, Kwong LN, McArthur G, Huang C, Tward AD, Frederick MJ, McCormick F, Meyerson M; Cancer Genome Atlas Research Network, Van Allen EM, Cherniack AD, Ciriello G, Sander C, Schultz N. Oncogenic Signaling Pathways in The Cancer Genome Atlas. ***Cell.*** 2018 Apr 5;173(2):321-337.e10. doi: 10.1016/j.cell.2018.03.035. PMID: 29625050

431. Ding L, Bailey MH, Porta-Pardo E, Thorsson V, Colaprico A, Bertrand D, Gibbs DL, Weerasinghe A, Huang KL, Tokheim C, Cortés-Ciriano I, Jayasinghe R, Chen F, Yu L, Sun S, Olsen C, Kim J, Taylor AM, Cherniack AD, Akbani R, Suphavilai C, Nagarajan N, Stuart JM, Mills GB, Wyczalkowski MA, Vincent BG, Hutter CM, Zenklusen JC, Hoadley KA, Wendl MC, Shmulevich L, Lazar AJ, Wheeler DA, Getz G; Cancer Genome Atlas Research Network. Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. ***Cell.*** 2018 Apr 5;173(2):305-320.e10. doi: 10.1016/j.cell.2018.03.033. PMID: 29625049

430. Hoadley KA, Yau C, Hinoue T, Wolf DM, Lazar AJ, Drill E, Shen R, Taylor AM, Cherniack AD, Thorsson V, Akbani R, Bowlby R, Wong CK, Wiznerowicz M, Sanchez-Vega F, Robertson AG, Schneider BG, Lawrence MS, Noushmehr H, Malta TM; Cancer Genome Atlas Network, Stuart JM, Benz CC, Laird PW. Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. ***Cell.*** 2018 Apr 5;173(2):291-304.e6. doi: 10.1016/j.cell.2018.03.022. PMID: 29625048

429. Ricketts CJ, De Cubas AA, Fan H, Smith CC, Lang M, Reznik E, Bowlby R, Gibb EA, Akbani R, Beroukhim R, Bottaro DP, Choueiri TK, Gibbs RA, Godwin AK, Haake S, Hakimi AA, Henske EP, Hsieh JJ, Ho TH, Kanchi RS, Krishnan B, Kwaitkowski DJ, Lui W, Merino MJ, Mills GB, Myers J, Nickerson ML, Reuter VE, Schmidt LS, Shelley CS, Shen H, Shuch B, Signoretti S, Srinivasan R, Tamboli P, Thomas G, Vincent BG, Vocke CD, Wheeler DA, Yang L, Kim WT, Robertson AG; Cancer Genome Atlas Research Network, Spellman PT, Rathmell WK, Linehan WM. The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. ***Cell Rep***. 2018 Apr 3;23(1):313-326.e5. doi: 10.1016/j.celrep.2018.03.075. PMID: 29617669

428. Chiu HS, Somvanshi S, Patel E, Chen TW, Singh VP, Zorman B, Patil SL, Pan Y, Chatterjee SS; Cancer Genome Atlas Research Network, Sood AK, Gunaratne PH, Sumazin P. Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. ***Cell Rep***. 2018 Apr 3;23(1):297-312.e12. doi: 10.1016/j.celrep.2018.03.064. PMID: 29617668

427. Seiler M, Peng S, Agrawal AA, Palacino J, Teng T, Zhu P, Smith PG; Cancer Genome Atlas Research Network, Buonamici S, Yu L. Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. ***Cell Re****p*. 2018 Apr 3;23(1):282-296.e4. doi: 10.1016/j.celrep.2018.01.088. PMID: 29617667

426. Jayasinghe RG, Cao S, Gao Q, Wendl MC, Vo NS, Reynolds SM, Zhao Y, Climente-González H, Chai S, Wang F, Varghese R, Huang M, Liang WW, Wyczalkowski MA, Sengupta S, Li Z, Payne SH, Fenyö D, Miner JH, Walter MJ; Cancer Genome Atlas Research Network, Vincent B, Eyras E, Chen K, Shmulevich I, Chen F, Ding L. Systematic Analysis of Splice-Site-Creating Mutations in Cancer. ***Cell Rep.*** 2018 Apr 3;23(1):270-281.e3. doi: 10.1016/j.celrep.2018.03.052. PMID: 29617666

425. Peng X, Chen Z, Farshidfar F, Xu X, Lorenzi PL, Wang Y, Cheng F, Tan L, Mojumdar K, Du D, Ge Z, Li J, Thomas GV, Birsoy K, Liu L, Zhang H, Zhao Z, Marchand C, Weinstein JN; Cancer Genome Atlas Research Network, Bathe OF, Liang H. Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. ***Cell Rep***. 2018 Apr 3;23(1):255-269.e4. doi: 10.1016/j.celrep.2018.03.077. PMID: 29617665

424. Knijnenburg TA, Wang L, Zimmermann MT, Chambwe N, Gao GF, Cherniack AD, Fan H, Shen H, Way GP, Greene CS, Liu Y, Akbani R, Feng B, Donehower LA, Miller C, Shen Y, Karimi M, Chen H, Kim P, Jia P, Shinbrot E, Zhang S, Liu J, Hu H, Bailey MH, Yau C, Wolf D, Zhao Z, Weinstein JN, Li L, Ding L,

Mills GB, Laird PW, Wheeler DA, Shmulevich I; Cancer Genome Atlas Research Network, Monnat RJ Jr., Xiao Y, Wang C. Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. ***Cell Rep***. 2018 Apr 3;23(1):239-254.e6. doi: 10.1016/j.celrep.2018.03.076. PMID: 29617664

423. Gao Q, Liang WW, Foltz SM, Mutharasu G, Jayasinghe RG, Cao S, Liao WW, Reynolds SM, Wyczalkowski MA, Yao L, Yu L, Sun SQ; Fusion Analysis Working Group; Cancer Genome Atlas Research Network, Chen K, Lazar AJ, Fields RC, Wendl MC, Van Tine BA, Vij R, Chen F, Nykter M, Shmulevich I, Ding L. Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. ***Cell Rep***. 2018 Apr 3;23(1):227-238.e3. doi: 10.1016/j.celrep.2018.03.050. PMID: 29617662

422. Ge Z, Leighton JS, Wang Y, Peng X, Chen Z, Chen H, Sun Y, Yao F, Li J, Zhang H, Liu J, Shriver CD, Hu H; Cancer Genome Atlas Research Network, Piwnica-Worms H, Ma L, Liang H. Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. ***Cell Rep.*** 2018 Apr 3;23(1):213-226.e3. doi: 10.1016/j.celrep.2018.03.047. PMID: 29617661

421. Campbell JD, Yau C, Bowlby R, Liu Y, Brennan K, Fan H, Taylor AM, Wang C, Walter V, Akbani R, Byers LA, Creighton CJ, Coarfa C, Shih J, Cherniack AD, Gevaert O, Prunello M, Shen H, Anur P, Chen J, Cheng H, Hayes DN, Bullman S, Pedamallu CS, Ojesina AI, Sadeghi S, Mungall KL, Robertson AG, Benz C, Schultz A, Kanchi RS, Gay CM, Hegde A, Diao L, Wang J, Ma W, Sumazin P, Chiu HS, Chen TW, Gunaratne P, Donehower L, Rader JS, Zuna R, Al-Ahmadie H, Lazar AJ, Flores ER, Tsai KY, Zhou JH, Rustgi AK, Drill E, Shen R, Wong CK; Cancer Genome Atlas Research Network, Stuart JM, Laird PW, Hoadley KA, Weinstein JN, Peto M, Pickering CR, Chen Z, Van Waes C. Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. ***Cell Rep.*** 2018 Apr 3;23(1):194-212.e6. doi: 10.1016/j.celrep.2018.03.063. PMID: 29617660

420. Saltz J, Gupta R, Hou L, Kurc T, Singh P, Nguyen V, Samaras D, Shroyer KR, Zhao T, Batiste R, Van Arnam J; Cancer Genome Atlas Research Network, Shmulevich I, Rao AUK, Lazar AJ, Sharma A, Thorsson V. Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. ***Cell Rep***. 2018 Apr 3;23(1):181-193.e7. doi: 10.1016/j.celrep.2018.03.086. PMID: 29617659

419. Way GP, Sanchez-Vega F, La K, Armenia J, Chatila WK, Luna A, Sander C, Cherniack AD, Mina M, Ciriello G, Schultz N; Cancer Genome Atlas Research Network, Sanchez Y, Greene CS. Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. ***Cell Rep***. 2018 Apr 3;23(1):172-180.e3. doi: 10.1016/j.celrep.2018.03.046. PMID: 29617658

418. Chahal M, Pleasance E, Grewal J, Zhao E, Ng T, Chapman E, Jones MR, Shen Y, Mungall KL, Bonakdar M, Taylor GA, Ma Y, Mungall AJ, Moore RA, Lim H, Renouf D, Yip S, Jones SJM, **Marra MA**, Laskin J. Personalized oncogenomic analysis of metastatic adenoid cystic carcinoma: using whole-genome sequencing to inform clinical decision-making. ***Cold Spring Harb Mol Case Stud***. 2018 Apr 2;4(2). pii: a002626. PMID: 29610392

417. Ronsley R, Rassekh R, Shen Y, Lee A, Jantzen C, Halparin J, Albert C, Hawkins D, Amed S, Rothstein R, Mungall AJ, Dix D, Blair G, Jones SJM, Laskin J, **Marra MA**, Deyell R. Application of genomics to identify therapeutic targets in recurrent pediatric papillary thyroid carcinoma. ***Cold Spring Harb Mol Case Stud***. 2018 Apr 2;4(2). pii: a002568. PMID: 29610391

416. Owen DR, Wong HL, Bonakdar M, Jones M, Hughes CS, Morin GB, Jones SJM, Renouf DJ, Lim H, Laskin J, **Marra M**, Yip S, Schaeffer DF. Molecular characterization of ERBB2-amplified colorectal cancer identifies potential mechanisms of resistance to targeted therapies: A report of two instructive cases. ***Cold Spring Harb Mol Case Stud.*** 2018 Apr 2;4(2). pii: a002535. doi: 10.1101/mcs.a002535. PMID: 29438965

415. Schaub FX, Dhankani V, Berger AC, Trivedi M, Richardson AB, Shaw R, Zhao W, Zhang X, Ventura A, Liu Y, Ayer DE, Hurlin PJ, Cherniack AD, Eisenman RN, Bernard B, Grandori C; Cancer Genome Atlas Network. Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. ***Cell Syst.*** 2018 Mar 28;6(3):282-300.e2. doi: 10.1016/j.cels.2018.03.003. PMID: 29596783

414. Ellrott K, Bailey MH, Saksena G, Covington KR, Kandoth C, Stewart C, Hess J, Ma S, Chiotti KE, McLellan M, Sofia HJ, Hutter C, Getz G, Wheeler D, Ding L; MC3 Working Group; Cancer Genome Atlas Research Network. Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. ***Cell Syst***. 2018 Mar 28;6(3):271-281.e7. doi: 10.1016/j.cels.2018.03.002. PMID: 29596782

413 Merk DJ, Ohli J, Merk ND, Thatikonda V, Morrissy S, Schoof M, Schmid SN, Harrison L, Filser S, Ahlfeld J, Erkek S, Raithatha K, Andreska T, Weißhaar M, Launspach M, Neumann JE, Shakarami M, Plenker D, **Marra MA**, Li Y, Mungall AJ, Moore RA, Ma Y, Jones SJM, Lutz B, Ertl-Wagner B, Rossi A, Wagener R, Siebert R, Jung A, Eberhart CG, Lach B, Sendtner M, Pfister SM, Taylor MD, Chavez L, Kool M, Schüller U. Opposing Effects of CREBBP Mutations Govern the Phenotype of Rubinstein-Taybi Syndrome and Adult SHH Medulloblastoma. ***Dev Cell.*** 2018 Mar 26; 44(6):709-724.e6. PMID: 29551561

412. Hung SS, Meissner B, Chavez EA, Ben-Neriah S, Ennishi D, Jones MR, Shulha HP, Chan FC, Boyle M, Kridel R, Gascoyne RD, Mungall AJ, **Marra MA**, Scott DW, Connors JM, Steidl C. Assessment of Capture and Amplicon-based Approaches for the Development of a Targeted Next-generation Sequencing Pipeline to Personalize Lymphoma Management. ***J Mol Diagn.*** 2018 Mar;20(2):203-214. doi: 10.1016/j.jmoldx.2017.11.010. PMID: 29429887

411. Thibodeau ML, Bonakdar M, Mungall KL, Thiessen N, Mungall AJ, Ma YP, Jones M, Renouf D, Lim H, Yip S, Ng T, Ho C, Laskin J, **Marra M**, Schrader KA, Jones SJM. Whole genome and whole transcriptome genomic profiling of metastatic eccrine porocarcinoma. ***NPJ Precis Oncol***. 2018 Mar 19;2(1):8. PMID: 29872726

410. Radovich M, Pickering CR, Felau I, Ha G, Zhang H, Jo H, Hoadley KA, Anur P, Zhang J, McLellan M, Bowlby R, Matthew T, Danilova L, Hegde AM, Kim J, Leiserson MDM, Sethi G, Lu C, Ryan M, Su X, Cherniack AD, Robertson G, Akbani R, Spellman P, Weinstein JN, Hayes DN, Raphael B, Lichtenberg T, Leraas K, Zenklusen JC; Cancer Genome Atlas Network, Fujimoto J, Scapulatempo-Neto C, Moreira AL, Hwang D, Huang J, Marino M, Korst R, Giaccone G, Gokmen-Polar Y, Badve S, Rajan A, Ströbel P, Girard N, Tsao MS, Marx A, Tsao AS, Loehrer PJ. The Integrated Genomic Landscape of Thymic Epithelial Tumors. ***Cancer Cell.*** 2018 Feb 12;33(2):244-258.e10. doi: 10.1016/j.ccell.2018.01.003. PMID: 29438696

409. Wong HL, Yang KC, Shen Y, Zhao EY, Loree JM, Kennecke HF, Kalloger SE, Karasinska JM, Lim HJ, Mungall A, Feng X, Davies JM, Schrader K, Zhou C, Karsan A, Laskin J, **Marra MA,** Schaeffer DF, Gorski SM, Renouf DJ. Molecular characterisation of metastatic pancreatic neuroendocrine tumours (PNETs) using whole genome and transcriptome sequencing. ***Cold Spring Harb Mol Case Stud.*** 2018 Feb 1;4(1). pii: a002329. doi: 10.1101/mcs.a002329. PMID: 29092957

408. Robertson AG, Shih J, Yau C, Gibb EA, Oba J, Mungall KL, Hess JM, Uzunangelov V, Walter V, Danilova L, Lichtenberg TM, Kucherlapati M, Kimes PK, Tang M, Penson A, Babur O, Akbani R, Bristow CA, Hoadley KA, Iype L, Chang MT; TCGA Research Network, Cherniack AD, Benz C, Mills GB, Verhaak RGW, Griewank KG, Felau I, Zenklusen JC, Gershenwald JE, Schoenfield L, Lazar AJ, Abdel-Rahman MH, Roman-Roman S, Stern MH, Cebulla CM, Williams MD, Jager MJ, Coupland SE, Esmaeli B, Kandoth C, Woodman SE. Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. ***Cancer Cell***. 2018 Jan 8;33(1):151. PMID: 28810145

407. Zhao E, Shen Y, Pleasance ED, Kasaian K, Leelakumari S, Jones M, Bose P, Ch’ng C, Reisle C, Eirew P, Corbett R, Mungall KL, Thiessen N, Ma Y, Schein JE, Mungall AJ, Zhao YJ, Moore R, Den Brok W,

Wilson S, Villa D, Shenkier T, Lohrisch C, Chia S, Yip S, Gelmon K, Lim H, Renouf D, Sun S, Schrader KA, Young S, Bosdet I, Karsan A, Laskin J, **Marra MA,** Jones SJM. Homologous Recombination Deficiency and Platinum-based Therapy Outcomes in Advanced Breast Cancer. ***Clin Cancer Res.*** 2017 Dec 15;23(24):7521-7530. PMID: 29246904

406. Jones SJ, Haulena M, Taylor GA, Chan S, Bilobram S, Warren RL, Hammond SA, Mungall KL, Choo C, Kirk H, Pandoh P, Ally A, Dhalla N, Tam AKY, Troussard A, Paulino D, Coope RJN, Mungall AJ, Moore R, Zhao Y, Birol I, Ma Y, **Marra M**, Jones SJM. The genome of the northern sea otter (Enhydra lutris kenyoni). ***Genes*** (Basel). 2017 Dec 11;8(12). pii: E379. doi: 10.3390/genes8120379. PMID: 29232880

405. Jones SJM, Taylor GA, Chan S, Warren RL, Hammond SA, Bilobram S, Mordecai G, Suttle CA, Miller KM, Schulze A, Chan AM, Jones SJ, Tse K, Li I, Cheung D, Mungall KL, Choo C, Ally A, Dhalla N, Tam AKY, Troussard A, Kirk H, Pandoh P, Paulino D, Coope RJN, Mungall AJ, Moore R, Zhao Y, Birol I, Ma Y, **Marra M**, Haulena M. The genome of the beluga whale (Delphinapterus leucas). ***Genes*** (Basel). 2017 Dec 11;8(12). pii: E378. doi: 10.3390/genes8120378. PMID: 29232881

404. Lim EL, Trinh DL, Ries RE, Wang J, Gerbing RB, Ma Y, Topham J, Hughes M, Pleasance E, Mungall AJ, Moore R, Zhao Y, Aplenc R, Sung L, Kolb EA, Gamis A, Smith M, Gerhard DS, Alonzo TA, Meshinchi S, **Marra MA**. MicroRNA Expression-Based Model Indicates Event-Free Survival in Pediatric Acute Myeloid Leukemia. ***J Clin Oncol***. 2017 Dec 10;35(35):3964-3977. PMID: 29068783

403. Jones MR, Lim H, Shen Y, Pleasance E, Ch'ng C, Reisle C, Leelakumari S, Zhao C, Yip S, Ho J, Zhong E, Ng T, Ionescu D, Schaeffer DF, Mungall AJ, Mungall KL, Zhao R, Moore RA, Ma Y, Chia S, Ho C, Renouf DJ, Gelmon K, Jones SJM, **Marra MA**, Laskin J. Successful targeting of the NRG1 pathway indicates novel treatment strategy for metastatic cancer. ***Ann Oncol.*** 2017 Dec 1;28(12):3092-3097. PMID: 28950338

402. Grewal JK, Eirew P, Jones M, Chiu K, Tessier-Cloutier B, Karnezis AN, Karsan A, Mungall A, Zhou C, Yip S, Tinker AV, Laskin J, **Marra M**, Jones SJM. Detection and Genomic Characterization of a mammary-like adenocarcinoma. ***Cold Spring Harb Mol Case Stud.*** 2017 Nov 21;3(6). PMID: 28877932

401. The Cancer Genome Atlas Research Network (Lazar AJ et al). Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. ***Cell***. 2017 Nov 2;171(4):950-965.e28. PMID: 29100075;

400. Siu C, Wiseman S, Gakkhar S, Heravi-Moussavi A, Bilenky M, Carles A, Sierocinski T, Tam A, Zhao E, Kasaian K, Moore R, Mungall A, Walker B, Thomson T, **Marra M**, Hirst M, Jones SJM. Characterization of the human thyroid epigenome. ***J Endocrinol.*** 2017 Nov;235(2):153-165. PMID: 28808080

399. Robertson AG, Kim J, Al-Ahmadie H, Bellmunt J, Guo G, Cherniack AD, Hinoue T, Laird PW, Hoadley KA, Akbani R, Castro MAA, Gibb EA, Kanchi RS, Gordenin DA, Shukla SA, Sanchez-Vega F, Hansel DE, Czerniak BA, Reuter VE, Su X, de Sa Carvalho B, Chagas VS, Mungall KL, Sadeghi S, Pedamallu CS, Lu Y, Klimczak LJ, Zhang J, Choo C, Ojesina AI, Bullman S, Leraas KM, Lichtenberg TM, Wu CJ, Schultz N, Getz G, Meyerson M, Mills GB, McConkey DJ; TCGA Research Network, Weinstein JN, Kwiatkowski DJ, Lerner SP. Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. ***Cell.*** 2017 Oct 19;171(3):540-556.e25. PMID: 28988769

398. Gadd S, Huff V, Walz AL, Ooms A, Armstrong AE, Gerhard DS, Smith MA, Guidry Auvil JM, Meerzaman D, Chen-Q-R, Hsu CH, Yan C, Nguyen C, Hu Y, Hermida LC, Davidson T, Gesuwan P, Ma Y, Zong Z, Mungall AJ, Moore RA, **Marra MA,** Dome JS, Mullighan CG, Ma J, Wheeler DA, Hampton OA, Ross N, Gastier-Foster JM, Arold ST, Perlman EJ. A Children's Oncology Group and TARGET Initiative Exploring the Genetic Landscape of Wilms Tumor. ***Nat Genet.*** 2017 Oct;49(10):1487-1494. PMID: 28825729

397. Mazor T, Chesnelong C, Pankov A, Jalbert L, Hong C, Hayes J, Smirnov I, Marshall R, Souza C, Shen Y, Viswanath P, Noushmehr H, Ronen S, Jones S, **Marra M**, Cairncross JG, Perry A, Nelson S, Chang S, Bollen A, Molinaro A, Bengtsson H, Olshen A, Weiss S, Phillips J, Luchman H, Costello J. Clonal expansion and epigenetic reprogramming following deletion or amplification of mutant *IDH1*. ***Proc Natl Acad Sci U S A.*** 2017 Oct 3;114(40):10743-10748. PMID: 28916733

396. Bosse KR, Raman P, Zhu Z, Lane M, Martinez D, Heitzeneder S, Rathi KW, Kendsersky NM, Randall M, Donovan L, Morrissy S, Sussman RT, Zhelev DV, Feng Y, Wang Y, Hwang J, Lopez Gardia G, Harenza JL, Wei J, Pawel B, Bhatti T, Santi M, Ganguly A, Khan J, **Marra MA,** Taylor MD, Dimitrov DS, Mackall C, Maris JM. Identification of GPC2 as an oncogene and candidate immunotherapeutic target in high-risk neuroblastoma. ***Cancer Cell.*** 2017 Sep 11;32(3):295-309. PMID: 28898695

395. Sloma I, Mitjavila-Garcia M, Feraud O, Griscelli F, Oudrhiri N, El Marsafy S, Gobbo E, Divers D, Proust A, Smadja DM, Desterke C, Carles A, Ma Y, Hirst M, **Marra MA,** Eaves CJ, Bennaceur-Griscelli A, Turhan AG. Whole genome analysis reveals unexpected dynamics of mutant subclone development in a patient with JAK2-V617F-positive chronic myeloid leukemia. ***Exp Hematol.*** 2017 Sep;53:48-58. PMID: 28602946

394. Thibodeau ML, Reisle C, Zhao E, Martin LA, Alwelaie Y, Mungall KL, Ch'ng C, Thomas R, Ng T, Yip S, Lim H, Sun S, Young SS, Karsan A, Zhao Y, Mungall AJ, Moore RA, Renouf D, Gelmon K, Ma YP, Hayes M, Laskin J, **Marra MA**, Schrader KA, Jones SJM. Genomic profiling of pelvic genital type leiomyosarcoma in a woman with a germline CHEK2:c.1100delC mutation and a concomitant diagnosis of metastatic invasive ductal breast carcinoma. ***Cold Spring Harb Mol Case Stud.*** 2017 Sep 1;3(5). PMID: 28514723

393. Cancer Genome Atlas Research Network. Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. ***Cancer Cell.*** 2017 Aug 14;32(2):185-203.e13. PMID: 28810144

392. Northcott PA, Buchhalter I, Morrissy S, Hovestadt V, Groebner S, Ehrenberger T, Segura-Wang M, Zichner T, Weischenfeldt J, Schumacher S, Phillips A, Kleinheinz A, Waszak A, Erkek S, Jones D, Worst B, Kool M, Zapatka M, Jäger N, Chavez L, Hutter B, Bieg M, Paramasivam N, Heinold M, Gu Z, Ishaque N, Jäger-Schmidt C, Warnatz H-J, Risch T, Amstislavskiy V, Weber U, Wolf S, Robinson G, Zhou X, Wu G, Finkelstein D, Cavalli F, Luu B, Ramaswamy V, Wu X, Koster J, Ryzhova M, Cho Y-J, Pomeroy S, Herold-Mende C, Schuhmann M, Ebinger M, Liau L, Mora J, Jabado N, Kumabe T, Witt O, Milde T, von Deimling A, Capper D, Korshunov A, Yaspo M-L, Kriwacki R, Gajjar A, Zhang J, Beroukhim R, Fraenkel E , Korbel J, Schlesner M, Eils R, **Marra M**, Pfister S, Taylor M, Lichter P. The whole genome landscape of medulloblastoma subtypes. ***Nature.*** 2017 Jul 19;547(7663):311-317. PMID: 28726821

391. Haile S, Corbett RD, MacLeod T, Bilobram S, Smailus D, Tsao P, Kirk H, McDonald H, Pandoh P, Bala M, Hirst M, Miller D, Moore R, Mungall AJ, Schein J, Coope R, Ma Y, Zhao YJ, Holt R, Jones S, **Marra M**. Increasing quality, throughput and speed of sample preparation for strand-specific messenger RNA sequencing. ***BMC Genomics.*** 2017 Jul 5;18(1):515. PMID: 28679365

390. Chooback N, Shen Y, Jones M, Kasaian K, Martin M, Ng T, Thomson T, **Marra M**, Laskin J, Ho C. Carcinoma ex pleomorphic adenoma: case report and options for systemic therapy. ***Curr Oncol***. 2017 Jun;24(3):e251-e254. PMID: 28680294

389. Farshidfar F, Zheng S, Gingras MC, Newton Y, Shih J, Robertson AG, Hinoue T, Hoadley KA, Gibb EA, Roszik J, Covington KR, Wu CC, Shinbrot E, Stransky N, Hegde A, Yang JD, Reznik E, Sadeghi S, Pedamallu CS, Ojesina AI, Hess JM, Auman JT, Rhie SK, Bowlby R, Borad MJ; Cancer Genome Atlas Network, Zhu AX, Stuart JM, Sander C, Akbani R, Cherniack AD, Deshpande V, Mounajjed T, Foo WC, Torbenson MS, Kleiner DE, Laird PW, Wheeler DA, McRee AJ, Bathe OF, Andersen JB, Bardeesy N, Roberts LR, Kwong LN. Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. ***Cell Rep.*** 2017 Jun 27;19(13):2878-2880. PMID: 28658632

388. Cancer Genome Atlas Research Network. Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. ***Cell***. 2017 Jun 15;169(7):1327-1341.e23. doi: 10.1016/j.cell.2017.05.046. PMID: 28622513

387. Tech K, Tikunov AP, Farooq H, Morrissy AS, Meidinger J, Fish T, Green SC, Liu H, Li Y, Mungall AJ, Moore RA, Ma Y, Jones SJ, **Marra MA**, Vander Heiden MG, Taylor MD, MacDonald J, Gershon TR. Pyruvate kinase inhibits proliferation during postnatal cerebellar neurogenesis and suppresses medulloblastoma formation. ***Cancer Res***. 2017 Jun 15;77(12):3217-3230. PMID: 28515149

386. Haile S, Pandoh P, McDonald H, Corbett RD, Tsao P, Kirk H, MacLeod T, Jones M, Bilobram S, Brooks D, Smailus D, Steidl C, Scott D, Bala M, Hirst M, Miller D, Moore R, Mungall AJ, Coope R, Ma Y, Zhao YJ, Holt R, Jones S, **Marra MA**. Automated high throughput nucleic acid purification from formalin-fixed paraffin-embedded tissue samples for next generation sequence analysis. ***PLOS ONE***. 2017 Jun 1;12(6):e0178706. PMID: 28570594

385. Wang YK, Bashashati A, Anglesio MS, Cochrane DR, Grewal DS, Ha G, McPherson A, Horlings HM, Senz J, Prentice LM, Karnezis AN, Lai D, Aniba MR, Zhang AW, Shumansky K, Siu C, Wan A, McConechy MK, Li-Chang H, Tone A, Provencher D, de Ladurantaye M, Fleury H, Okamoto A, Yanagida S, Yanaihara N, Saito M, Mungall AJ, Moore R, **Marra MA**, Gilks CB, Mes-Masson AM, McAlpine JN, Aparicio S, Huntsman DG, Shah SP. Genomic consequences of aberrant DNA repair mechanisms stratify ovarian cancer histotypes. ***Nat Genet***. 2017 Jun;49(6):856-865. PMID: 28436987

384. LeBlanc VG, Firme M, Song J, Chan SY, Lee MH, Yip S, Chittaranjan S, **Marra MA**. Comparative transcriptome analysis of isogenic cell line models and primary cancers links CIC loss to activation of the MAPK signalling cascade. ***J Pathol.*** 2017 Jun;242(2):206-220. PMID: 28295365

383. Zahir FR, Mwenifumbo JC, Chun HE, Lim EL, Van Karnebeek CDM, Couse M, Mungall KL, Lee L, Makela N, Armstrong L, Boerkoel CF, Langlois SL, McGillivray BM, Jones SJM, Friedman JM, **Marra MA**. Comprehensive whole genome sequence analyses yields novel genetic and structural insights for Intellectual Disability. ***BMC Genomics.*** 2017 May 24;18(1):403. doi: 10.1186/s12864-017-3671-0. PMID: 28539120

382. Ennishi D, Mottok A, Ben-Neriah S, Shulha HP, Farinha P, Chan FC, Meissner B, Boyle M, Hother C, Kridel R, Lai D, Saberi S, Bashashati A, Shah SP, Morin RD, **Marra MA**, Savage KJ, Sehn LH, Steidl C, Connors JM, Gascoyne RD, Scott DW. Genetic profiling of *MYC* and *BCL2* in diffuse large B-cell lymphoma determines cell of origin-specific clinical impact. ***Blood***. 2017 May 18;129(20):2760-2770. PMID: 28351934

381. Morrissy AS, Cavalli FM, Remke M, Ramaswamy V, Shih DJ, Holgado BL, Farooq H, Donovan LK, Garzia L, Agnihotri S, Kiehna EN, Mercier E, Mayoh C, Papillon-Cavanagh S, Nikbakht H, Gayden T, Torchia J, Picard D, Merino DM, Vladoiu M, Luu B, Wu X, Daniels C, Horswell S, Thompson YY, Hovestadt V, Northcott PA, Jones DT, Peacock J, Wang X, Mack SC, Reimand J, Albrecht S, Fontebasso AM, Thiessen N, Li Y, Schein JE, Lee D, Carlsen R, Mayo M, Tse K, Tam A, Dhalla N, Ally A, Chuah E, Cheng Y, Plettner P, Li HI, Corbett RD, Wong T, Long W, Loukides J, Buczkowicz P, Hawkins CE, Tabori U, Rood BR, Myseros JS, Packer RJ, Korshunov A, Lichter P, Kool M, Pfister SM, Schüller U, Dirks P, Huang A, Bouffet E, Rutka JT, Bader GD, Swanton C, Ma Y, Moore RA, Mungall AJ, Majewski J, Jones SJ, Das S, Malkin D, Jabado N, **Marra MA**, Taylor MD. Spatial heterogeneity in medulloblastoma. ***Nat Genet***. 2017 May;49(5):780-788. PMID: 28394352

380. Cancer Genome Atlas Research Network. Integrated genomic and molecular characterization of cervical cancer. ***Nature.*** 2017 Mar 16;543(7645):378-384. PMID: 28112728

379. Cherniack AD, Shen H, Walter V, Stewart C, Murray BA, Bowlby R, Hu X, Ling S, Soslow RA, Broaddus RR, Zuna RE, Robertson G, Laird PW, Kucherlapati R, Mills GB; Cancer Genome Atlas Research Network, Weinstein JN, Zhang J, Akbani R, Levine DA. Integrated Molecular Characterization of Uterine Carcinosarcoma. ***Cancer Cell***. 2017 Mar 13;31(3):411-423. PMID: 28292439

378 Weymann D, Laskin J, Roscoe R, Schader KA, Chia S, Yip S, Cheung WY, Gelmon KA, Karsan A, Renouf DJ, **Marra M,** Regier DA. The cost and cost trajectory of whole-genome analysis guiding treatment of patients with advanced cancers. ***Mol Genet Genomic Med***. 2017 Mar 12;5(3):251-260. PMID: 28546995

377. Fishbein L, Leshchiner I, Walter V, Danilova L, Robertson AG, Johnson AR, Lichtenberg TM, Murray BA, Ghayee HK, Else T, Ling S, Jefferys SR, de Cubas AA, Wenz B, Korpershoek E, Amelio AL, Makowski L, Rathmell WK, Gimenez-Roqueplo AP, Giordano TJ, Asa SL, Tischler AS; Cancer Genome Atlas Research Network, Pacak K, Nathanson KL, Wilkerson MD. Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. ***Cancer Cell***. 2017 Feb 13;31(2):181-193. PMID: 28162975

376. Cancer Genome Atlas Research Network. Integrated genomic characterization of oesophageal carcinoma. ***Nature.*** 2017 Jan 12;541(7636):169-175. PMID: 28052061

375. Sheffield BS, Tessier-Cloutier B, Li-Chang H, Shen Y, Pleasance E, Kasaian K, Li Y, Jones SJM, Lim HJ, Renouf DJ, Huntsman DG, Yip S, Laskin J, **Marra M**, Schaeffer DF. Personalized oncogenomics in the management of gastrointestinal carcinomas - Early experiences from a pilot study. ***Curr Oncol.*** 2016 Dec;23(6):e571-e575. PMID: 28050146

374. Kridel R, Fong FC, Mottok A, Boyle M, Farinha P, Tan K, Meissner B, Bashashati A, McPherson A, Roth R, Shumansky K, Yap D, Ben-Neriah S, Rosner J, Smith MA, Nielsen C, Gine E, Telenius A, Ennishi D, Mungall A, Moore R, Morin RD, Johnson NA, Sehn LH, Tousseyn T, Dogan A, Connors JM, Scott DW, Steidl C, **Marra MA**, Gascoyne RD, Shah SP. Histological Transformation and Progression in Follicular Lymphoma: A Clonal Evolution Study. ***PLoS Med***. 2016 Dec 13;13(12):e1002197. PMID: 27959929

373. Topham JT, **Marra MA**. Sequencing Strategies to Guide Decision Making in Cancer Treatment. ***PLoS Med***. 2016 Dec 6;13(12):e1002189. PMID: 27923042

372. Chan CK, Pan Y, Nyberg K, **Marra MA**, Lim EL, Jones SJM, Maar D, Gibb EA, Robertson AG, Gunaratne PH, Rowat AC. Tumour-suppressor microRNAs regulate ovarian cancer cell physical properties and invasive behaviour. ***Open Biol***. 2016 Nov;6(11). PMID: 27906134

371. Stunnenberg HG; International Human Epigenome Consortium, Hirst M. The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. ***Cell.*** 2016 Nov 17;167(5):1145-1149. PMID: 27863232

370. Pellacani D, Bilenky M, Kannan N, Heravi-Moussavi A, Knapp DJ, Gakkhar S, Moksa M, Carles A, Moore R, Mungall AJ, **Marra MA,** Jones SJ, Aparicio S, Hirst M, Eaves CJ. Analysis of Normal Human Mammary Epigenomes Reveals Cell-Specific Active Enhancer States and Associated Transcription Factor Networks. ***Cell Rep.*** 2016 Nov 15;17(8):2060-2074. PMID: 27851968

369. Ooms AH, Gadd S, Gerhard DS, Smith MA, Guidry Auvil JM, Meerzaman D, Chen QR, Hsu CH, Yan C, Nguyen C, Hu Y, Ma Y, Zong Z, Mungall AJ, Moore RA, **Marra MA**, Huff V, Dome JS, Chi YY, Tian J, Geller JI, Mullighan CG, Ma J, Wheeler DA, Hampton OA, Walz AL, van den Heuvel-Eibrink MM, de Krijger RR, Ross N, Gastier-Foster JM, Perlman EJ. Significance of TP53 Mutation in Wilms Tumors with Diffuse Anaplasia: A Report from the Children's Oncology Group. ***Clin Cancer Res.*** 2016 Nov 15;22(22):5582-5591. PMID: 27702824

368. Gu Z, Churchman M, Roberts K, Li Y, Liu Y, Harvey RC, McCastlain K, Reshmi SC, Payne-Turner D, Iacobucci I, Shao Y, Chen IM, Valentine M, Pei D, Mungall KL, Mungall AJ, Ma Y, Moore R, **Marra M**, Stonerock E, Gastier-Foster JM, Devidas M, Dai Y, Wood B, Borowitz M, Larsen EE, Maloney K, Mattano LA Jr, Angiolillo A, Salzer WL, Burke MJ, Gianni F, Spinelli O, Radich JP, Minden MD, Moorman AV, Patel B, Fielding AK, Rowe JM, Luger SM, Bhatia R, Aldoss I, Forman SJ, Kohlschmidt J, Mrózek K, Marcucci G, Bloomfield CD, Stock W, Kornblau S, Kantarjian HM, Konopleva M, Paietta

E, Willman CL, L Loh M, P Hunger S, Mullighan CG. Genomic analyses identify recurrent MEF2D fusions in acute lymphoblastic leukaemia. ***Nat Commun***. 2016 Nov 8;7:13331. PMID: 27824051

367. Zahir FR, Tucker T, Mayo S, Brown CJ, Lim EL, Taylor J, **Marra MA**, Hamdan FF, Michaud JL, Friedman JM. Intragenic CNVs for epigenetic regulatory genes in intellectual disability: Survey identifies pathogenic and benign single exon changes. ***Am J Med Genet A***. 2016 Nov;170(11):2916-2926. PMID: 27748065

366. LeBlanc VG and **Marra MA**. DNA methylation in adult diffuse gliomas. ***Brief Funct Genomics.*** 2016 Nov;15(6):491-500. (Review) PMID: 27288434

365. Costa S, Regier DA, Meissner B, Cromwell I, Ben-Neriah S, Chavez E, Hung S, Steidl C, Scott DW, **Marra MA**, Peacock SJ, Connors JM. A time-and-motion approach to micro-costing of high-throughput genomic assays. ***Curr Oncol.*** 2016 Oct;23(5):304-313. PMID: 27803594

364. Sheffield BS, Fulton R, Kalloger SE, Milne K, Geller G, Jones M, Jacquemont C, Zachara S, Zhao E, Pleasance E, Laskin J, Jones SJM, **Marra MA**, Yip S, Nelson BH, Gown AM, Ho C, Ionescu DN. Investigation of PD-L1 Biomarker Testing Methods for PD-1 Axis Inhibition in Non-squamous Non–small Cell Lung Cancer. ***J Histochem Cytochem.*** 2016 Oct;64(10):587-600. PMID: 27591097

363. Grinshtein N, Rioseco CC, Marcellus R, Uehling D, Aman A, Lun X, Muto O, Podmore L, Lever J, Shen Y, Blough MD, Cairncross GJ, Robbins SM, Jones SJ, **Marra MA**, Al-Awar R, Senger DL, Kaplan DR. Small molecule epigenetic screen identifies novel EZH2 and HDAC inhibitors that target glioblastoma brain tumor-initiating cells. ***Oncotarget***. 2016 Sep 13;7(37):59360-59376. PMID: 27449082

362. Chong LC, Twa DD, Mottok A, Ben-Neriah S, Woolcock BW, Zhao Y, Savage KJ, **Marra MA,** Scott DW, Gascoyne RD, Morin RD, Mungall AJ, Steidl C. Comprehensive characterization of programmed death ligand structural rearrangements in B-cell non-Hodgkin lymphomas. ***Blood.*** 2016 Sep 1;128(9):1206-1213. PMID: 27268263

361. Zipeto MA, Court AC, Sadarangani A, Delos Santos NP, Balaian L, Chun HJ, Pineda G, Morris SR, Mason CN, Geron I, Barrett C, Goff DJ, Wall R, Pellecchia M, Minden M, Frazer KA, **Marra MA**, Crews LA, Jiang Q, Jamieson CH. ADAR1 Activation Drives Leukemia Stem Cell Self-Renewal by Impairing Let-7 Biogenesis. ***Cell Stem Cell.*** 2016 Aug 4;19(2):177-191. PMID: 27292188

360. Alassiri AH, Ali RH, Shen Y, Lum A, Strahlendorf C, Deyell R, Rassekh R, Sorensen PH, Laskin J, **Marra M**, Yip S, Lee C-H, Ng TL. ETV6-NTRK3 is expressed in a subset of ALK-negative inflammatory myofibroblastic tumors: case series of 20 patients. ***Am J Surg Pathol.*** 2016 Aug;40(8):1051-1061. PMID: 27259007

359. McPherson A, Roth A, Laks E, Masud T, Bashashati A, Zhang AW, Ha G, Biele J, Yap D, Wan A, Prentice LM, Khattra J, Smith MA, Nielsen CB, Mullaly SC, Kalloger S, Karnezis A, Shumansky K, Siu C, Rosner J, Chan HL, Ho J, Melnyk N, Senz J, Yang W, Moore R, Mungall AJ, **Marra MA**, Bouchard-Côté A, Gilks CB, Huntsman DG, McAlpine JN, Aparicio S, Shah SP. Divergent modes of clonal spread and intraperitoneal mixing in high-grade serous ovarian cancer. ***Nat Genet***. 2016 Jul;48(7):758-767. PMID: 27182968

358 Campbell JD, Alexandrov A, Kim J, Wala J, Berger AH, Pedamallu CS, Shukla SA, Guo G, Brooks AN, Murray BA, Imielinski M, Hu X, Ling S, Akbani R, Rosenberg M, Cibulskis C, Ramachandran A, Collisson EA, Kwiatkowski DJ, Lawrence MS, Weinstein JN, Verhaak RGW, Wu CJ, Hammerman PS, Cherniack AD, Getz G, Cancer Genome Atlas Research Network, Artyomov MN, Schreiber R, Govindan R, Meyerson M. Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. ***Nat Genet.*** 2016 Jun;48(6):607-616. PMID: 27158780

357. Oh S, Flynn RA, Floor SN, Purzner J, Martin L, Do BT, Schubert S, Vaka D, Morrissy S, Li Y, Kool M, Hovestadt V, Jones DT, Northcott PA, Risch T, Warnatz HJ, Yaspo ML, Adams CM, Leib RD, Breese M, **Marra MA**, Malkin D, Lichter P, Doudna JA, Pfister SM, Taylor MD, Chang HY, Cho YJ.

Medulloblastoma-associated DDX3 variant selectively alters the translational response to stress. ***Oncotarget.*** 2016 May 10;7(19):28169-28182. PMID: 27058758

356. Zheng S, Cherniack AD, Dewal N, Moffitt RA, Danilova L, Murray BA, Lerario AM, Else T, Knijnenburg TA, Ciriello G, Kim S, Assie G, Morozova O, Akbani R, Shih J, Hoadley KA, Choueiri TK, Waldmann J, Mete O, Robertson AG, Wu HT, Raphael BJ, Shao L, Meyerson M, Demeure MJ, Beuschlein F, Gill AJ, Sidhu SB, Almeida MQ, Fragoso MC, Cope LM, Kebebew E, Habra MA, Whitsett TG, Bussey KJ, Rainey WE, Asa SL, Bertherat J, Fassnacht M, Wheeler DA; Cancer Genome Atlas Research Network, Hammer GD, Giordano TJ, Verhaak RG. Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. ***Cancer Cell***. 2016 May 9;29(5):723-736. PMID: 27165744

355. Maxson JE, Ries RE, Wang YC, Gerbing RB, Kolb EA, Thompson SL, Guidry Auvil JM, **Marra MA**, Ma Y, Zong Z, Mungall AJ, Moore R, Long W, Gesuwan P, Davidsen TM, Hermida LC, Hughes SB, Farrar JE, Radich JP, Smith MA, Gerhard DS, Gamis AS, Alonzo TA, Meshinchi S. CSF3R mutations have a high degree of overlap with CEBPA mutations in pediatric AML. ***Blood***. 2016 Jun 16;127(24):3094-3098. PMID: 27143256

354. Pan Y, Robertson AG, Pedersen L, Lim E, Hernandez-Herrera A, Rowat A, Chan C, Wen Y, Zhang X, Patil S, Basu-Roy U, Mansukhani A, Chu A, Sipahimalani P, Bowlby R, Brooks D, Thiessen N, Ma Y, Moore R, Schein J, Mungall A, Pecot C, Sood A, Jones S, **Marra M**, Gunaratne P. miR-509-3p is clinically significant and strongly attenuates cellular migration and multi-cellular spheroids in ovarian cancer. ***Oncotarget.*** 2016 May 3;7(18):25930-25948. PMID: 27036018

353. Jones MR, Schrader KA, Shen Y, Pleasance E, Ch'ng C, Dar N, Yip S, Renouf DJ, Schein JE, Mungall AJ, Zhao Y, Moore R, Ma Y, Sheffield BS, Ng T, Jones SJM, **Marra M**, Laskin J, Lim H. Response to Angiotensin Blockade with Irbesartan in a Patient with Metastatic Colorectal Cancer. ***Ann Oncol.*** 2016 May;27(5):801-806. PMID: 27022066

352. Nielsen JS, Sedgwick C, Shahid A, Zong Z, Brumme ZL, Yu S, Liu L, Kroeger DR, Treon SP, Connors JM, Gascoyne RD, Berry BR, **Marra MA**, Morin RD, Macpherson N, Nelson BH. Toward personalized lymphoma immunotherapy: Identification of common driver mutations recognized by patient CD8+ T cells. ***Clin Cancer Res.*** 2016 May 1;22(9):2226-2236. PMID: 26631611

351. Craig DW, Nasser S, Corbett R, Chan SK, Murray L, Legendre C, Tembe W, Adkins J, Kim N, Wong S, Baker A, Enriquez D, Pond S, Pleasance E, Mungall AJ, Moore RA, McDaniel T, Ma Y, Jones SJ, **Marra MA**, Carpten JD, Liang WS. A somatic reference standard for cancer genome sequencing. ***Sci Rep***. 2016 Apr 20;6:24607. PMID: 27094764

350. Pineda G, Lennon KM, Delos Santos NP, Lambert-Fliszar F, Riso GL, Lazzari E, **Marra MA**, Morris S, Sakaue-Sawano A, Miyawaki A, Jamieson CH. Tracking of Normal and Malignant Progenitor Cell Cycle Transit in a Defined Niche. ***Sci Rep***. 2016 Apr 4;6:23885. PMID: 27041210

349. Chun H-J, Lim EL, Heravi-Moussavi A, Saberi S, Mungall KL, Bilenky M, Carles A, Tse K, Shlafman I, Zhu K, Qian JQ, Harvey D, He An, Long W, Goya R, Ng M, LeBlanc VG, Pleasance E, Thiessen N, Wong T, Chuah E, Zhao YJ, Schein JE, Gerhard DS, Taylor MD, Mungall AJ, Moore RA, Ma Y, Jones SJM, Perlman EJ, Hirst M, **Marra MA**. Genome-wide profiles of extra-cranial malignant rhabdoid tumors reveal heterogeneity and dysregulated developmental pathways. ***Cancer Cell.*** 2016 Mar 14; 29(3): 394-406. PMID: 26977886

348. Kasaian K, Wiseman SM, Walker BA, Schein JE, Hirst M, Moore RA, Mungall AJ, **Marra MA**, Jones SJ. Putative BRAF activating fusion in a medullary thyroid cancer. ***Cold Spring Harb Mol Case Stud.*** 2016 Mar; 2(2): a000729. PMID: 27148585

347. Parker JD, Shen Y, Pleasance E, Li Y, Schein JE, Zhao YJ, Moore R, Wegrzyn-Woltosz J, Savage KJ, Weng AP, Gascoyne RD, Jones S, **Marra M**, Laskin J, Karsan A. Molecular etiology of an indolent

lymphoproliferative disorder determined by whole-genome sequencing. ***Cold Spring Harb Mol Case Stud.*** 2016 Mar;2(2):a000679. PMID: 27148583

346. Davis B, Shen Y, Poon CC, Luchman HA, Stechishin OD, Pontifex CS, Wu W, Kelly JJ, Blough MD; Terry Fox Research Institute Glioblastoma Consortium. Comparative genomic and genetic analysis of glioblastoma-derived brain tumor-initiating cells and their parent tumors. ***Neuro Oncol.*** 2016 Mar;18(3):350-360. PMID: 26245525

345. Ceccarelli M, Barthel FP, Malta TM, Sabedot TS, Salama SR, Murray BA, Morozova O, Newton Y, Radenbaugh A, Pagnotta SM, Anjum S, Wang J, Manyam G, Zoppoli P, Ling S, Rao AA, Grifford M, Cherniack AD, Zhang H, Poisson L, Carlotti CG Jr, Tirapelli DP, Rao A, Mikkelsen T, Lau CC, Yung WK, Rabadan R, Huse J, Brat DJ, Lehman NL, Barnholtz-Sloan JS, Zheng S, Hess K, Rao G, Meyerson M, Beroukhim R, Cooper L, Akbani R, Wrensch M, Haussler D, Aldape KD, Laird PW, Gutmann DH; TCGA Research Network, Noushmehr H, Iavarone A, Verhaak RG. Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. ***Cell.*** 2016 Jan 28;164(3):550-563. PMID: 26824661

344. Morrissy AS, Garzia L, Shih DJ, Zuyderduyn S, Huang X, Skowron P, Remke M, Cavalli FM, Ramaswamy V, Lindsay PE, Jelveh S, Donovan LK, Wang X, Luu B, Zayne K, Li Y, Mayoh C, Thiessen N, Mercier E, Mungall KL, Ma Y, Tse K, Zeng T, Shumansky K, Roth AJ, Shah S, Farooq H, Kijima N, Holgado BL, Lee JJ, Matan-Lithwick S, Liu J, Mack SC, Manno A, Michealraj KA, Nor C, Peacock J, Qin L, Reimand J, Rolider A, Thompson YY, Wu X, Pugh T, Ally A, Bilenky M, Butterfield YS, Carlsen R, Cheng Y, Chuah E, Corbett RD, Dhalla N, He A, Lee D, Li HI, Long W, Mayo M, Plettner P, Qian JQ, Schein JE, Tam A, Wong T, Birol I, Zhao Y, Faria CC, Pimentel J, Nunes S, Shalaby T, Grotzer M, Pollack IF, Hamilton RL, Li XN, Bendel AE, Fults DW, Walter AW, Kumabe T, Tominaga T, Collins VP, Cho YJ, Hoffman C, Lyden D, Wisoff JH, Garvin JH Jr, Stearns DS, Massimi L, Schüller U, Sterba J, Zitterbart K, Puget S, Ayrault O, Dunn SE, Tirapelli DP, Carlotti CG, Wheeler H, Hallahan AR, Ingram W, MacDonald TJ, Olson JJ, Van Meir EG, Lee JY, Wang KC, Kim SK, Cho BK, Pietsch T, Fleischhack G, Tippelt S, Ra YS, Bailey S, Lindsey JC, Clifford SC, Eberhart CG, Cooper MK, Packer RJ, Massimino M, Garre ML, Bartels U, Tabori U, Hawkins CE, Dirks P, Bouffet E, Rutka JT, Wechsler-Reya RJ, Weiss WA, Collier LS, Dupuy AJ, Korshunov A, Jones DT, Kool M, Northcott PA, Pfister SM, Largaespada DA, Mungall AJ, Moore RA, Jabado N, Bader GD, Jones SJ, Malkin D, **Marra MA**, Taylor MD. Divergent Clonal Selection Dominates Medulloblastoma at Recurrence. ***Nature.*** 2016 Jan 21;529(7586):351-357. PMID: 26760213

343. <u>Pon JR</u> and **Marra MA**. MEF2 transcription factors: developmental regulators and emerging cancer genes. ***Oncotarget.*** 2016 Jan 19;7(3):2297-2312. (Review) PMID: 26506234;

342. Cancer Genome Atlas Research Network, Linehan WM, Spellman PT, Ricketts CJ, Creighton CJ, Fei SS, Davis C, Wheeler DA, Murray BA, Schmidt L, Vocke CD, Peto M, Al Mamun AA, Shinbrot E, Sethi A, Brooks S, Rathmell WK, Brooks AN, Hoadley KA, Robertson AG, Brooks D, Bowlby R, Sadeghi S, Shen H, Weisenberger DJ, Bootwalla M, Baylin SB, Laird PW, Cherniack AD, Saksena G, Haake S, Li J, Liang H, Lu Y, Mills GB, Akbani R, Leiserson MD, Raphael BJ, Anur P, Bottaro D, Albiges L, Barnabas N, Choueiri TK, Czerniak B, Godwin AK, Hakimi AA, Ho TH, Hsieh J, Ittmann M, Kim WY, Krishnan B, Merino MJ, Mills Shaw KR, Reuter VE, Reznik E, Shelley CS, Shuch B, Signoretti S, Srinivasan R, Tamboli P, Thomas G, Tickoo S, Burnett K, Crain D, Gardner J, Lau K, Mallery D, Morris S, Paulauskis JD, Penny RJ, Shelton C, Shelton WT, Sherman M, Thompson E, Yena P, Avedon MT, Bowen J, Gastier-Foster JM, Gerken M, Leraas KM, Lichtenberg TM, Ramirez NC, Santos T, Wise L, Zmuda E, Demchok JA, Felau I, Hutter CM, Sheth M, Sofia HJ, Tarnuzzer R, Wang Z, Yang L, Zenklusen JC, Zhang J, Ayala B, Baboud J, Chudamani S, Liu J, Lolla L, Naresh R, Pihl T, Sun Q, Wan Y, Wu Y, Ally A, Balasundaram M, Balu S, Beroukhim R, Bodenheimer T, Buhay C, Butterfield YS, Carlsen R, Carter SL, Chao H, Chuah E, Clarke A, Covington KR, Dahdouli M, Dewal N, Dhalla N, Doddapaneni HV, Drummond JA, Gabriel SB, Gibbs RA, Guin R, Hale W, Hawes A, Hayes DN, Holt RA, Hoyle AP, Jefferys SR, Jones SJ, Jones CD, Kalra D, Kovar C, Lewis L, Li J, Ma Y, **Marra MA**, Mayo M, Meng S,

Meyerson M, Mieczkowski PA, Moore RA, Morton D, Mose LE, Mungall AJ, Muzny D, Parker JS, Perou CM, Roach J, Schein JE, Schumacher SE, Shi Y, Simons JV, Sipahimalani P, Skelly T, Soloway MG, Sougnez C, Tam A, Tan D, Thiessen N, Veluvolu U, Wang M, Wilkerson MD, Wong T, Wu J, Xi L, Zhou J, Bedford J, Chen F, Fu Y, Gerstein M, Haussler D, Kasaian K, Lai P, Ling S, Radenbaugh A, Van Den Berg D, Weinstein JN, Zhu J, Albert M, Alexopoulou I, Andersen JJ, Auman JT, Bartlett J, Bastacky S, Bergsten J, Blute ML, Boice L, Bollag RJ, Boyd J, Castle E, Chen YB, Cheville JC, Curley E, Davies B, DeVolk A, Dhir R, Dike L, Eckman J, Engel J, Harr J, Hrebinko R, Huang M, Huelsenbeck-Dill L, Iacocca M, Jacobs B, Lobis M, Maranchie JK, McMeekin S, Myers J, Nelson J, Parfitt J, Parwani A, Petrelli N, Rabeno B, Roy S, Salner AL, Slaton J, Stanton M, Thompson RH, Thorne L, Tucker K, Weinberger PM, Winemiller C, Zach LA, Zuna R. Comprehensive Molecular Characterization of Papillary Renal- Cell Carcinoma. ***N Engl J Med.*** 2016 Jan 14;374(2):135-145. PMID: 26536169

341. Pon JR, **Marra MA**. Clinical impact of molecular features in diffuse large B-cell lymphoma and follicular lymphoma. ***Blood***. 2016 Jan 14;127(2):181-186. PMID: 26447189

340. Chu A, Robertson G, Brooks D, Mungall AJ, Birol İ, Coope R, Ma Y, Jones S, **Marra M.** Large-scale profiling of microRNAs for The Cancer Genome Atlas. ***Nucleic Acids Res.*** 2016 Jan 8;44(1):e3. doi: 10.1093/nar/gkv808. PMID: 26271990

339. Kasaian K, Wiseman SM, Walker BA, Schein JE, Zhao YJ, Hirst M, Moore RA, Mungall AJ, **Marra MA**, Jones SJM. The genomic and transcriptomic landscape of anaplastic thyroid cancer: implications for therapy. ***BMC Cancer***. 2015 Dec 18;15(1):984. PMID: 26680454

338. Holm F, Hellqvist E, Mason CN, Ali SA, Delos-Santos N, Barrett CL, Chun HJ, Minden MD, Moore RA, **Marra MA**, Runza V, Frazer KA, Sadarangani A, Jamieson CH. Reversion to an embryonic alternative splicing program enhances leukemia stem cell self-renewal. ***Proc Natl Acad Sci U S A***. 2015 Dec 15;112(50):15444-15449. PMID: 26621726

337. Garside VC, Cullum R, Alder O, Lu DY, Vander Werff R, Bilenky M, Zhao Y, Jones SJ, **Marra MA**, Underhill TM, Hoodless PA. SOX9 modulates the expression of key transcription factors required for heart valve development. ***Development***. 2015 Dec 15;142(24):4340-4350. PMID: 26525672

336. Perlman EJ, Gadd S, Gerhard DS, Jennings LJ, Arold ST, Huff V, Guidry Auvil JM, Davidsen TM, Dome JS, Meerzaman D, Hsu CH, Nguyen C, Anderson JR, Ma Y, Mungall AJ, Moore RA, **Marra MA**, Mullighan CG, Ma J, Gastier-Foster JM, Ross N, Smith M. MLLT1 YEATS domain mutations in clinically distinctive Favourable Histology Wilms tumours. ***Nat Commun***. 2015 Dec 4;6:10013. doi: 10.1038/ncomms10013. PMID: 26635203

335. Cancer Genome Atlas Research Network (Abeshouse A et al). The Molecular Taxonomy of Primary Prostate Cancer. ***Cell.*** 2015 Nov 5;163(4):1011-1025. PMID: 26544944

334. Kridel R, Mottok A, Farinha P, Ben-Neriah S, Ennishi D, Zheng Y, Chavez EA, Shulha HP, Tan K, Chan FC, Boyle M, Meissner B, Telenius A, Sehn LH, **Marra MA**, Shah SP, Steidl C, Connors JM, Scott DW, Gascoyne RD. Cell-of-origin of transformed follicular lymphoma. ***Blood.*** 2015 Oct 29;126(18):2118-2127. PMID: 26307535

333. Laskin J, Jones S, Aparicio S, Chia S, Ch'ng C, Deyell R, Eirew P, Fok A, Gelmon K, Ho C, Huntsman D, Jones M, Kasaian K, Karsan A, Leelakumari S, Li V, Lim H, Ma Y, Mar C, Martin M, Moore R, Mungall A, Mungall K, Pleasance E, Rassekh S, Renouf D, Shen YQ, Schein J, Schrader K, Tinker A, Zhao E, Yip S, **Marra M**. Lessons learned from the application of whole genome analysis to the treatment of patients with advanced cancers. ***Cold Spring Harb Mol Case Stud.*** 2015 Oct;1(1):a000570. PMID: 27148575

332. Ciriello G, Gatza ML, Beck AH, Wilkerson MD, Rhie SK, Pastore A, Zhang H, McLellan M, Yau C, Kandoth C, Bowlby R, Shen H, Hayat S, Fieldhouse R, Lester SC, Tse GM, Factor RE, Collins LC, Allison KH, Chen YY, Jensen K, Johnson NB, Oesterreich S, Mills GB, Cherniack AD, Robertson G,

Benz C, Sander C, Laird PW, Hoadley KA, King TA; TCGA Research Network, Perou CM. Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. ***Cell.*** 2015 Oct 8;163(2):506-519. PMID: 26451490

331. LeBlanc VG, **Marra MA**. Next-Generation Sequencing Approaches in Cancer: Where Have They Brought Us and Where Will They Take Us? ***Cancers*** (Basel). 2015 Sep 23;7(3):1925-1958. (Review). PMID: 26404381

330. Bose P, Pleasance ED, Jones M, Shen Y, Ch'ng C, Reisle C, Schein JE, Mungall AJ, Moore R, Ma Y, Sheffield BS, Thomson T, Rasmussen S, Ng T, Yip S, Lee CW, Ho C, Laskin J, **Marra MA**, Jones SJ. Integrative genomic analysis of ghost cell odontogenic carcinoma. ***Oral Oncol.*** 2015 Sep;51(9):e71-5. PMID: 26173781

329. Pon J, Wong J, Saberi S, Moksa M, Hirst M, **Marra M**. MEF2B Mutations in Non-Hodgkin Lymphoma Dysregulate Cell Migration by Decreasing MEF2B Target Gene Activation. ***Nat Commun.*** 2015 Aug 6;6:7953. doi: 10.1038/ncomms8953. PMID: 26245647

328. Schmouth JF, Arenillas D, Corso-Diaz X, Xie YY, Bohacec S, Banks KG, Bonaguro RJ, Wong SH, Jones SJ, **Marra MA**, Simpson EM, Wasserman WW. Combined serial analysis of gene expression and transcription factor binding site prediction identifies novel-candidate-target genes of Nr2e1 in neocortex development. ***BMC Genomics.*** 2015 Jul 24;16:545. PMID: 26204903

327. Lebovitz CB, Robertson G, Goya R, Jones S, Morin RD, **Marra MA**, Gorski SM. Cross-cancer profiling of molecular alterations within the human autophagy interaction network. ***Autophagy.*** 2015;11(9):1668-1687. PMID: 26208877

326. Cusulin C, Chesnelong C, Bose P, Bilenky M, Kopciuk K, Chan JA, Cairncross JG, Jones SJ, **Marra MA**, Luchman HA, Weiss S. Precursor States of Brain Tumor Initiating Cell Lines are Predictive of Survival in Xenografts and Associated with Glioblastoma Subtypes. ***Stem Cell Rep.*** 2015 Jul 14;5(1):1-9. PMID: 26095605

325. Cancer Genome Atlas Network (Brat DJ et al). Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. ***New Eng J Med***. 2015 Jun 25;372(26):2481-2498. PMID: 26061751

324. Cancer Genome Atlas Research Network (Akbani R et al). Genomic Classification of Cutaneous Melanoma. ***Cell.*** 2015 Jun 18;161(7):1681-1696. PMID: 26091043

323. Twa DD, Mottok A, Chan FC, Ben-Neriah S, Woolcock BW, Tan KL, Mungall AJ, McDonald H, Zhao Y, Lim RS, Nelson BH, Milne K, Shah SP, Morin RD, **Marra MA**, Scott DW, Gascoyne RD, Steidl C. Recurrent genomic rearrangements in primary testicular lymphoma. ***J Pathol.*** 2015 Jun;236(2):136-141. PMID: 25712539.

322. Anglesio MS, Bashashati A, Wang YK, Senz J, Ha G, Yang W, Aniba MR, Prentice LM, Farahani H, Chang HL, Karnezis AN, **Marra MA**, Yong PJ, Hirst M, Gilks B, Shah SP, Huntsman DG. Multifocal endometriotic lesions associated with cancer are clonal and carry a high mutation burden. ***J Pathol.*** 2015 Jun;236(2):201-209. PMID: 25692284

321. Chittaranjan S, Xu J, Kuzyk M, Dullat HK, Wilton J, De Vorkin L, Lebovitz C, Morin GB, **Marra MA**, Gorski S. The Drosophila TIPE family member Sigmar interacts with the Ste20-like kinase Misshapen and modulates JNK signaling, cytoskeletal remodeling and autophagy. ***Biol Open.*** 2015 Apr 2 ;4(5):672-684. PMID: 25836674

320. Kasaian K, Chindris A-M, Wiseman SM, Mungall KL, Zeng T, Tse K, Schein JE, Rivera M, Necela BM, Kachergus JM, Casler JD, Mungall AJ, Moore RA, **Marra MA**, Copland JA, Thompson EA, Smallridge RC, Jones SJM. *MEN1* Mutations in Hürthle Cell (Oncocytic) Thyroid Carcinoma. ***J Clin Endocrinol Metab.*** 2015 Apr; 100(4): E611-E615. PMID: 25625803

319. Sadarangani A, Pineda G, Lennon KM, Chun HJ, Shih A, Schairer AE, Court AC, Goff DJ, Prashad SL, Geron I, Wall R, McPherson JD, Moore RA, Pu M, Bao L, Jackson-Fisher A, Munchhof M, VanArsdale T, Reya T, Morris SR, Minden MD, Messer K, Mikkola HK, **Marra MA**, Hudson TJ, Jamieson CH. GLI2 inhibition abrogates human leukemia stem cell dormancy. ***J Transl Med.*** 2015 Mar 21;13(1):98. PMID: 25889765

318. Sheffield BS, Tinker AV, Shen Y, Hwang H, Li-Chang HH, Pleasance E, Ch'ng C, Lum A, Lorette J, McConnell YJ, Sun S, Jones SJM, Gown AM, Huntsman DG, Schaeffer DF, Churg A, Yip S, Laskin J, **Marra MA**, Churg A. Personalized Oncogenomics: Clinical Experience with Malignant Peritoneal Mesothelioma Using Whole Genome Sequencing. ***PLoS ONE.*** 2015 Mar 23;10(3):e0119689. doi: 10.1371/journal.pone.0119689. eCollection 2015. PMID: 25798586

317. Hoskins RA, Carlson JW, Wan KH, Park S, Mendez I, Galle SE, Booth BW, Pfeiffer BD, George RA, Svirskas R, Krzywinski M, Schein J, Accardo MC, Damia E, Messina G, Méndez-Lago M, de Pablos B, Demakova OV, Andreyeva EN, Boldyreva LV, **Marra M**, Carvalho AB, Dimitri P, Villasante A, Zhimulev IF, Rubin GM, Karpen GH, Celniker SE. The release 6 reference sequence of the Drosophila melanogaster genome. ***Genome Res***. 2015 Mar;2 5(3):445-458. PMID: 25589440

316. Roadmap Epigenomics Consortium, Kundaje A, Meuleman W, Ernst J, Bilenky M, Yen A, Wang J, Sarkar A, Quon G, Kheradpour P, Zhang Z, Heravi-Moussavi A, Wang X, Ward LD, Liu Y, Wu Y-C, Eaton ML, Claussnitzer M, Schultz MD, Ziller MJ, Sandstrom RS, Whitaker JW, Amin V, Coarfa C, Harris RA, Shoresh N, Epstein CB, Leung D, Xie W, Hawkins RD, Lister R, Hong C, Gascard P, Mungall AJ, Moore R, Chuah E, Carles A, Eaton ML, Elliott G, Farh K-HFeizi S, Gjoneska E, Karlic R, Kim A-R, Kulkarni A, Li D, Lowdon R, Mercer TR, Neph SJ, Onuchic V, Pfenning A, Polak P, Rajagopal N, Ray P, Sallari RC, Siebenthall KT, Sinnott-Armstrong N, Stevens M, Thurman RE, Wu J, Zhang B, Zhou X, Beaudet AE, Boyer L, De Jager P, Farnham PJ, Fisher SJ, Haussler D, Jones S, Li W, **Marra M**, McManus MT, Sunyaev S, Thomson JA, Tlsty TD, Tsai L-H, Wang W, Waterland RA, Zhang M, Chadwick LH, Bernstein BE, Costello JF, Ecker JR, Hirst M, Meissner A, Milosavljevic A, Ren B, Stamatoyannopoulos JA, Wang T, Kellis M. Integrative analysis of 111 reference human epigenomes. ***Nature.*** 2015 Feb 19;518(7539):317-330. PMID: 25693563

315. Eirew P, Ha G, Khattra J, Steif A, Yap D, Gelmon K, Chia S, Wan A, Shumansky K, Rosner J, McPherson A, Nielsen C, Roth AJL, Lefebre C, Bashashati Al, Edward J, Oloumi A, Osako T, Bruna A, Sandoval J, Algara T, Greenwood W, Leung K, Cheng H, Xue H, Wang Y, Lin D, Mungall A, Moore R, Zhao YJ, Lorette J, Nguyen L, Huntsman D, Eaves C, Hansen C, **Marra M**, Caldas C, Shah SP, Aparicio S. Dynamics of genomic clones in breast cancer patient xenografts at single-cell resolution. ***Nature***. 2015 Feb 19;518(7539):422-426. PMID: 25470049

314. Elliott G, Hong C, Xing X, Zhou X, Li D, Coarfa C, Bell RJ, Maire CL, Ligon KL, Sigaroudinia M, Gascard P, Tlsty TD, Harris RA, Schalkwyk LC, Bilenky M, Mill J, Farnham PJ, Kellis M, **Marra MA**, Milosavljevic A, Hirst M, Stormo GD, Wang T, Costello JF. Intermediate DNA methylation is a conserved signature of genome regulation. ***Nat Commun***. 2015 Feb 18;6:6363. doi: 10.1038/ncomms7363. PMID: 25691127

313. Gascard P, Bilenky M, Sigaroudinia M, Zhao J, Li L, Carles A, Delaney A, Tam A, Kamoh B, Cho S, Griffith M, Chu A, Robertson G, Cheung D, Li I, Heravi-Moussavi A, Moksa M, Mingay M, Hussainkhel A, Davis B, Nagarajan RP, Hong C, Echipare L, O'Geen H, Hangauer MJ, Cheng JB, Neel D, Hu D, McManus MT, Moore R, Mungall A, Ma Y, Plettner P, Ziv E, Wang T, Farnham PJ, Jones SJ, **Marra MA**, Tlsty TD, Costello JF, Hirst M. Epigenetic and transcriptional determinants of the human breast. ***Nat Commun***. 2015 Feb 18;6:6351. doi: 10.1038/ncomms7351.

312. Walz AL, Ooms A, Gadd S, Gerhard DS, Smith MA, Guidry Auvil JM, Meerzaman D, Chen QR, Hsu CH, Yan C, Nguyen C, Hu Y, Bowlby R, Brooks D, Ma Y, Mungall AJ, Moore RA, Schein J, **Marra MA**, Huff V, Dome JS, Chi YY, Mullighan CG, Ma J, Wheeler DA, Hampton OA, Jafari N, Ross N, Gastier-Foster JM, Perlman EJ. Recurrent DGCR8, DROSHA, and SIX Homeodomain Mutations in

Favorable Histology Wilms Tumors. ***Cancer Cell***. 2015 Feb 9;27(2):286-297. doi: 10.1016/j.ccell.2015.01.003. PMID: 25670082

311. Chan FC, Telenius A, Healy S, Ben-Neriah S, Mottok A, Lim R, Drake M, Hu S, Ding J, Ha G, Scott DW, Kridel R, Bashashati A, Rogic S, Johnson N, Morin RD, Rimsza LM, Sehn L, Connors JM, **Marra MA**, Gascoyne RD, Shah SP, Steidl C. An RCOR1 loss-associated gene expression signature identifies a prognostically significant DLBCL subgroup. ***Blood.*** 2015 Feb 5;125(6):959-966.

310. Lim EL, Trinh DL, Scott DW, Chu A, Krzywinski M, Zhao YJ, Robertson AG, Mungall AJ, Schein J, Boyle M, Mottok A, Ennishi D, Johnson NA, Steidl C, Connors JM, Morin RD, Gascoyne RD, **Marra MA**. Comprehensive miRNA Sequence Analysis Reveals Survival Differences in Diffuse Large B-cell Lymphoma Patients. ***Genome Biol***. 2015 Jan 29;16(1):18. **(This article was featured on the cover of the journal.)** PMID: 25723320

309. The Cancer Genome Atlas Network (Lawrence MS et al). Comprehensive genomic characterization of head and neck squamous cell carcinomas. ***Nature.*** 2015 Jan 29;517(7536):576-582. PMID: 25631445

308. Kulic I, Robertson G, Chang L, Baker JH, Lockwood WW, Mok W, Fuller M, Fournier M, Wong N, Chou V, Robinson MD, <u>Chun HJ</u>, Gilks B, Kempkes B, Thomson TA, Hirst M, Minchinton AI, Lam WL, Jones S, **Marra M**, Karsan A. Loss of the Notch effector RBPJ promotes tumorigenesis. ***J Exp Med.*** 2015 Jan 12;212(1):37-52. PMID: 25512468

307. Lowdon RF, Zhang B, Bilenky M, Mauro T, Li D, Gascard P, Sigaroudinia M, Farnham PJ, Bastian BC, Tlsty TD, **Marra MA**, Hirst M, Costello JF, Wang T, Cheng JB. Regulatory network decoded from epigenomes of surface ectoderm-derived cell types. ***Nat Commun.*** 2014 Nov 25;5:5442. PMID: 25421844

306. Cancer Genome Atlas Research Network (Agrawal N et al). Integrated genomic characterization of papillary thyroid carcinoma. ***Cell.*** 2014 Oct 23;159(3):676-690. PMID: 25417114

305. Ha G, Roth A, Khattra J, Ho J, Yap D, Prentice LM, Melnyk N, McPherson A, Bashashati A, Laks E, Biele J, Ding J, Le A, Rosner J, Shumansky K, **Marra MA**, Gilks CB, Huntsman DG, McAlpine JN, Aparicio S, Shah SP. TITAN: Inference of copy number architectures in clonal cell populations from tumor whole genome sequence data. ***Genome Res.*** 2014 Nov;24(11):1881-1893. PMID: 25060187

304. Parfenov M, Pedamallu CS, Gehlenborg N, Freeman SS, Danilova L, Bristow CA, Lee S, Hadjipanayis AG, Ivanova EV, Wilkerson MD, Protopopov A, Yang L, Seth S, Song X, Tang J, Ren X, Zhang J, Pantazi A, Santoso N, Xu AW, Mahadeshwar H, Wheeler DA, Haddad RI, Jung J, Ojesina AI, Issaeva N, Yarbrough WG, Hayes DN, Grandis JR, El-Naggar AK, Meyerson M, Park PJ, Chin L, Seidman JG, Hammerman PS, Kucherlapati R; the Cancer Genome Atlas Network. Characterization of HPV and host genome interactions in primary head and neck cancers. ***Proc Natl Acad Sci U S A.*** 2014 Oct 28;111(43):15544-15549. PMID: 25313082

303. Alder O, Cullum R, Lee S, Kan AC, Wei W, Yi Y, Garside V, Bilenky M, Griffith M, Morrissy AS, Robertson G, Thiessen N, Zhao YJ, Chen Q, Pan D, Jones SJM, **Marra MA**, Hoodless PA. Hippo Signalling Influences HNF4 and FOXA2 Enhancer Switching During Hepatocyte Differentiation. ***Cell Rep***. 2014 Oct 9;9(1):261-271. PMID: 25263553

302. Chittaranjan S, Chan S, <u>Yang C</u>, <u>Yang KC</u>, Chen V, Moradian A, <u>Firme M</u>, <u>Song J</u>, Go NE, Blough MD, Chan JA, JG Cairncross, Gorski SM, Morin GB, Yip S, **Marra MA**. Mutations in CIC and IDH1 cooperatively regulate 2-hydroxyglutarate levels and cell clonogenicity. ***Oncotarget.*** 2014 Sep 15;5(17):7960-7979. **(This article was featured on the cover of the journal.)** PMID: 25277207

301. Cancer Genome Atlas Research Network (Bass AJ et al). Comprehensive molecular characterization of gastric adenocarcinoma. ***Nature.*** 2014 Sep 11;513(7517):202-209. PMID: 25079317

300. Davis CF, Ricketts CJ, Wang M, Yang L, Cherniack AD, Shen H, Buhay C, Kang H, Kim SC, Fahey CC, Hacker KE, Bhanot G, Gordenin DA, Chu A, Gunaratne PH, Biehl M, Seth S, Kaipparettu BA, Bristow CA, Donehower LA, Wallen EM, Smith AB, Tickoo SK, Tamboli P, Reuter V, Schmidt LS, Hsieh JJ, Choueiri TK, Hakimi AA; The Cancer Genome Atlas Research Network, Chin L, Meyerson M, Kucherlapati R, Park WY, Robertson AG, Laird PW, Henske EP, Kwiatkowski DJ, Park PJ, Morgan M, Shuch B, Muzny D, Wheeler DA, Linehan WM, Gibbs RA, Rathmell WK, Creighton CJ; The Cancer Genome Atlas Research Network. The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. ***Cancer Cell.*** 2014 Sep 8;26(3):319-330. PMID: 25155756

299. Firme M and **Marra MA**. The Molecular Landscape of Pediatric Brain Tumours in the Next-generation Sequencing Era. (Review article) ***Curr Neurol Neurosci Rep***. 2014 Sep;14(9):474. PMID: 25037717

298. Hoadley KA, Yau C, Wolf DM, Cherniack AD, Tamborero D, Ng Sam, Leiserson MDM, Niu B, McLellan MD, Uzunangelov, V, Zhang J, Kandoth C, Akbani R, Shen H, Omberg L, Chu A, Margolin AA, van't Veer LJ, Lopel-Bigas N, Laird PW, Raphael BJ, Ling L, Robertson AG, Byers LA, Mills GB, Weinstein JN, Van Waes C, Chen Z, Collisson EA, The Cancer Genome Atlas Research Network, Benz CC, Perou CN, Stuart JM. Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. ***Cell***. 2014 Aug 14;158(4):929-944. PMID: 25109877

297. Cancer Genome Atlas Research Network (Collisson EA et al). Comprehensive Molecular Profiling of Lung Adenocarcinoma. ***Nature***. 2014 Jul 31;511(7511):543-550. PMID: 25079552

296. Vanner RJ, Remke M, Gallo M, Selvadurai H, Coutinho F, Lee L, Kushida M, Head R, Morrissy S, Zhu X, Aviv T, Voisin V, Clarke ID, Li Y, Mungall AJ, Moore RA, Ma Y, Jones SJM, **Marra MA**, Malkin D, Northcott PA, Kool M, Pfister SM, Bader G, Hochedlinger K, Korshunov A, Taylor MD, Dirks PB. Quiescent Sox2+ cells drive hierarchical growth and relapse in Sonic hedgehog subgroup medulloblastoma. ***Cancer Cell.*** 2014 Jul 14;26(1):33-47. PMID: 24954133

295. Chang AC, Garside VC, Fournier M, Smrz J, Vrljicak P, Umlandt P, Fuller M, Robertson G, Zhao Y, Tam A, Jones SJ, **Marra MA**, Hoodless PA, Karsan A. A Notch-dependent transcriptional hierarchy promotes mesenchymal transdifferentiation in the cardiac cushion. ***Dev Dyn***. 2014 Jul;243(7):894-905. PMID: 24633789

294. Dias C, Rupps R, Millar B, Choi K, **Marra M**, Demos M, Kratz LE, Boerkoel CF. Desmosterolosis: An illustration of diagnostic ambiguity of cholesterol synthesis disorders. ***Orphanet J Rare Dis***. 2014 Jun 25;9(1):94. PMID: 24961299

293. Jamshidi F, Pleasance E, Li Y, Shen Y, Kasaian K, Corbett R, Eirew P, Lum A, Pandoh P, Zhao YJ, Schein JE, Moore RA, Rassekh R, Huntsman DG, Knowling M, Lim H, Renouf DJ, Jones SJM, **Marra MA**, Nielsen TO, Laskin J, Yip S. Diagnostic Value of Next-Generation Sequencing in an Unusual Sphenoid Tumor. ***The Oncologis****t*. 2014 Jun;19(6):623-630. PMID: 24807916

292. Tucker T, Zahir F, Griffith M, Delaney A, Chai D, Tsang E, Lemyre E, Dobrzeniecka S, **Marra M**, Eydoux P, Langlois S, Hamdan F, Michaud J, Friedman J. Single-exon-resolution targeted chromosomal microarray analysis of known and candidate intellectual disability genes. ***Eur J Hum Genet***. 2014 Jun;22(6):792-800. PMID: 24253858

291. Berg T, Thoene S, Yap D, Wee T, Schoeler N, Rosten P, Lim E, Bilenky M, Mungall AJ, Oellerich T, Lee S, Lai CK, Umlandt P, Salmi A, Chang H, Yue L, Lai D, Cheng G, Morin RD, Hirst M, Serve SS, **Marra MA**, Morin GB, Gascoyne RD, Aparicio SA, Humphries RK. A transgenic mouse model demonstrating the oncogenic role of mutations in the polycomb-group gene EZH2 in lymphomagenesis. ***Blood.*** 2014 Jun 19;123(25):3914-3924. PMID: 24802772

290. Ramos P, Karnezis AN, Craig DW, Sekulic A, Russell ML, Hendricks WP, Corneveaux JJ, Barrett MT, Shumansky K, Yang Y, Shah SP, Prentice LM, **Marra MA**, Kiefer J, Zismann VL, McEachron TA, Salhia B, Prat J, D'Angelo E, Clarke BA, Pressey JG, Farley JH, Anthony SP, Roden RB, Cunliffe HE,

Huntsman DG, Trent JM. Small cell carcinoma of the ovary, hypercalcemic type, displays frequent inactivating germline and somatic mutations in SMARCA4. ***Nat Genet***. 2014 May;46(5):427-429. PMID: 24658001

289. Janbon G, Ormerod KL, Paulet D, Byrnes III EJ, Chatterjee G, Yadav V, Hon C-C, Billmyre RB, Brunel F, Bahn Y-S, Chen W, Chen Y, Chow EWL, Coppée Y-J, Floyd-Averette A, Gaillardin C, Gerik KJ, Goebels C, Goldberg J, Gonzalez-Hilarion S, Gujja S, Hamlin JL, Hsueh Y-P, Ianiri1 G, Jones S, Kodira CD, Lam W, **Marra M**, Mesner LD, Mieczkowski PA, Moyrand F, Nielsen K, Proux C, Rossignol T, Schein JE, Sun S, Wood IA, Zeng Q, Neuvéglise C, Newlon CS, Perfect JR, Lodge JL, Idnurm A, Stajich JE, Kronstad JW, Sanyal K, Heitman J, Fraser JA, Cuomo CA, Dietrich FS. Analysis of the genome and transcriptome of Cryptococcus neoformans var. grubii reveals complex RNA expression and microevolution leading to virulence attenuation. ***PLoS Genet*.** 2014 Apr 17;10(4):e1004261. PMID: 24743168

288. Gunawardana J, Telenius A, Woolcock B, Tan KL, Ben-Neriah S, Chan FC, Lim R, Rogic S, Boyle M, Kridel R, Guiter C, Haioun C, Leroy K, Rimsza LM, Gaulard P, Savage KJ, Connors JM, **Marra MA**, Shah SP, Gascoyne RD, Steidl C. Recurrent Somatic Mutations of PTPN1 in Primary Mediastinal B cell lymphoma and Hodgkin Lymphoma. ***Nat Genet***. 2014 Apr;46(4):329-335. PMID: 24531327

287. Zovoilis A, Mungall A, Moore R, Varhol R, Chu A, Wong T, **Marra M,** Jones S. The expression level of small non-coding RNAs derived from the first exon of protein coding genes is predictive of cancer status. ***EMBO Rep***. 2014 Apr 1;15(4):402-410. PMID: 24534129

286. Cancer Genome Atlas Research Network (Weinstein JN et al). Comprehensive molecular characterization of urothelial bladder carcinoma. ***Nature***. 2014 Mar 20;507(7492):315-322. PMID: 24476821

285. Shlush LI, Zandi S, Mitchell A, Chen WC, Brandwein JM, Gupta V, Kennedy JA, Schimmer AD, Schuh AC, Yee KW, McLeod JL, Doedens M, Medeiros JJ, Marke R, Kim HJ, Lee K, McPherson JD, Hudson TJ; HALT Pan-Leukemia Gene Panel Consortium, Brown AM, Trinh QM, Stein LD, Minden MD, Wang JC, Dick JE. Identification of pre-leukaemic haematopoietic stem cells in acute leukaemia. ***Nature***. 2014 Feb 20;506(7488):328-333. PMID: 24522528

284. Mack S, Witt H, Piro RM, Gu L, Zuyderduyn S, Stütz AM, Wang X, Gallo M, Garzia L, Zayne K, Zhang X, Ramaswamy V, Jäger N, Jones DT, Sill M, Pugh TJ, Ryzhova M, Wani KM, Shih DJ, Head R, Remke M, Bailey SD, Zichner T, Faria CC, Barszczyk M, Stark S, Seker-Cin H, Hutter S, Johann P, Bender S, Hovestadt V, Tzaridis T, Dubuc AM, Northcott PA, Peacock J, Bertrand KC, Agnihotri S, Cavalli FM, Clarke I, Nethery-Brokx K, Creasy CL, Verma SK, Koster J, Wu X, Yao Y, Milde T, Sin-Chan P, Zuccaro J, Lau L, Pereira S, Castelo-Branco P, Hirst M, **Marra MA,** Roberts SS, Fults D, Massimi L, Cho YJ, Van Meter T, Grajkowska W, Lach B, Kulozik AE, von Deimling A, Witt O, Scherer SW, Fan X, Muraszko KM, Kool M, Pomeroy SL, Gupta N, Phillips J, Huang A, Tabori U, Hawkins C, Malkin D, Kongkham PN, Weiss WA, Jabado N, Rutka JT, Bouffet E, Korbel JO, Lupien M, Aldape KD, Bader GD, Eils R, Lichter P, Dirks PB, Pfister SM, Korshunov A, Taylor MD. Epigenomic Alterations define lethal CIMP positive ependymomas of infancy. ***Nature.*** 2014 Feb 27;506(7489):445-450. PMID: 24553142

283. Johnson BE, Mazor T, Hong C, Barnes M, McLean CY, Fouse SD, Yamamoto S, Ueda H, Tatsuno K, Aihara J, Asthana S, Jalbert LE, Nelson SJ, Bollen AW, Gustafson WC, Charron E, Weiss WA, Smirnov IV, Song JS, Olshen AB, Cha S, Zhao YJ, Moore RA, Mungall AJ, Jones SJM, Hirst M, **Marra MA**, Mukasa A, Saito N, Aburatani H, Berger MS, Chang SM, Taylor BS, Costello JF. Mutational Analysis Reveals the Origin and Therapy-driven Evolution of Recurrent Glioma. ***Science.*** 2014 Jan 10;343(6167):189-193. doi: 10.1126/science.1239947. PMID: 24336570

282. Vojvodic M, Hansford LM, Morozova O, Blakely KM, Taylor P, Fathers KE, Moffat J, **Marra M**, Smith KM, Moran MF, Kaplan DR. A Phosphoproteomics Approach to Identify Candidate Kinase Inhibitor Pathway Targets in Lymphoma-Like Primary Cell Lines. ***Curr Drug Discov Technol***. 2013 Dec;10(4):283-304. PMID: 23701117

281. Bosdet IE, Docking TR, Butterfield YS, Mungall AJ, Zeng T, Coope RJ, Yorida E, Chow K, Bala M, Young SS, Hirst M, Birol I, Moore RA, Jones SJ, **Marra MA**, Holt R, Karsan A. A clinically validated diagnostic second-generation sequencing assay for detection of hereditary BRCA1 and BRCA2 mutations. ***J Mol Diagn.*** 2013 Nov;15(6):796-809. PMID: 24094589

280. Najafzadeh M, Johnston KM, Peacock SJ, Connors JM, **Marra MA**, Lynd LD, Marra CA. Genomic testing to determine drug response: measuring preferences of the public and patients using Discrete Choice Experiment (DCE). ***BMC Health Serv Res***. 2013 Oct 31;13(1):454. PMID: 24176050

279. Brennan CW, Verhaak RGW, McKenna A, Campos B, Noushmehr H, Salama S, Zheng S, Chakravarty D, Sanborn JZ, Berman HS, Beroukhim R, Bernard B, Wu CJ, Genovese G, Shmulevich I, Barnholtz-Sloan J, Zou L, Vegesna R, Shukla SA, Ciriello G, WK Yung, Zhang W, Sougnez C, Mikkelsen T, Aldape K, Bigner DD, Van Meir EG, Prados M, Sloan A, Black KL, Eschbacher J, Finocchiaro G, Friedman W, Andrews DW, Guha A, Iacocca M, O'Neill BP, Foltz G, Myers J, Weisenberger DJ, Penny R, Kucherlapati R, Perou CM, Hayes DN, Gibbs R, **Marra M**, Mills GB, Lander E, Spellman P, Wilson R, Sander C, Weinstein J, Meyerson M, Gabriel S, Laird PW, Haussler D, Getz G, Chin L, TCGA Research Network. The Somatic Genomic Landscape of Glioblastoma. ***Cell.*** 2013 Oct 10;155(2):462-477. PMID: 24120142

278. Cancer Genome Atlas Research Network, Weinstein JN, Collisson EA, Mills GB, Shaw KR, Ozenberger BA, Ellrott K, Shmulevich I, Sander C, Stuart JM. The Cancer Genome Atlas Pan-Cancer analysis project. ***Nat Genet.*** 2013 Oct;45(10):1113-1120. PMID: 24071849

277. Stevens M, Cheng JB, Li D, Xie M, Hong C, Maire CL, Ligon KL, Hirst M, **Marra MA**, Costello JF, Wang T. Estimating absolute methylation levels at single CpG resolution from methylation enrichment and restriction enzyme sequencing methods. ***Genome Res.*** 2013 Sep;23(9):1541-1553. PMID: 23804401

276. Zhang B, Zhou Y, Lin N, Lowdon RF, Hong C, Nagarajan RP, Cheng JB, Li D, Stevens M, Lee HJ, Xing X, Zhou J, Sundaram V, Elliott G, Gu J, Gascard P, Sigaroudinia M, Tlsty TD, Kadlecek T, Weiss A, O'Geen H, Farnham PJ, Maire CL, Ligon KL, Madden PA, Tam A, Moore R, Hirst M, **Marra MA**, Zhang B, Costello JF, Wang T. Functional DNA methylation differences between tissues, cell types, and across individuals discovered using the M&M algorithm. ***Genome Res***. 2013 Sep;23(9):1522-1540. PMID: 23804400

275. Bashashati A, Ha G, Tone A, Ding J, Prentice L, Roth A, Rosner J, Shumansky R, Kalloger S, Senz J, Yang W, McConechy M, Melnyk N, Anglesio M, Luk M, Tse K, Zeng T, Moore R, Zhao YJ, **Marra M**, Gilks B, Yip S, Huntsman D, Sohrab S. Distinct evolutionary trajectories of primary high-grade serous ovarian cancers revealed through spatial mutational profiling. ***J Pathol.*** 2013 Sep;231(1):21-34. PMID: 23780408

274. Morin RD, Mungall K, Pleasance E, Mungall AJ, Goya R, Huff R, Scott D, Ding J, Roth A, Chiu R, Corbett RD, Chan FC, Mendez-Lago M, Trinh D, Bolger-Munro M, Taylor G, Khodabakhshi AH, Ben-Neriah S, Pon J, Meissner B, Woolcock B, Farnoud N, Rogic S, Lim E, Johnson NA, Shah S, Jones S, Steidl C, Holt R, Birol I, Moore R, Connors JM, Gascoyne RD, **Marra MA**. Mutational and Structural Analysis of Diffuse Large B-cell Lymphoma using Whole Genome Sequencing. ***Blood.*** 2013 Aug 15;122(7):1256-1265. PMID: 23699601

273. Cancer Genome Atlas Research Network (Creighton CJ et al, including Chun H-J). Comprehensive molecular characterization of clear cell renal cell carcinoma. ***Nature***. 2013 Jul 4;499(7456):43-49. PMID: 23792563

272. Xie M, Hong C, Zhang B, Lowdon RF, Xing X, Li D, Zhou X, Lee HJ, Maire CL, Ligon KL, Gascard P, Sigaroudinia M, Tlsty TD, Kadlecek T, Weiss A, O'Geen H, Farnham PJ, Madden PA, Mungall AJ, Tam A, Kamoh B, Cho S, Moore R, Hirst M, **Marra MA**, Costello JF, Wang T. DNA hypomethylation within specific transposable element families associates with tissue-specific enhancer landscape. ***Nat Genet.*** 2013 Jul;45(7):836-841. PMID: 23708189

271. Kasaian K, Wiseman SM, Thiessen NT, Mungall KL, Corbett RD, Qian JQ, Nip KM, He A, Tse K, Chuah E, Varhol RJ, McDonald H, Zeng T, Tam A, Schein J, Birol I, Mungall AJ, Moore RA, Zhao YJ, Hirst M, **Marra MA**, Walker BA, Jones SJM. Complete Genomic Landscape of a Recurring Sporadic Parathyroid Carcinoma Tumor. ***J Pathol.*** 2013 Jul;230(3):249-260. PMID: 23616356

270. Wei W, Hou J, Alder O, Ye X Lee S, Cullum R, Chu A, Zhao YJ, Warner SM, Knight DA, Yang D, Jones SJM, **Marra MA**, Hoodless PA**.** Genome-wide microRNA and mRNA profiling in mouse liver development implicates mir302b and mir20a in repressing TGFβ signaling. ***Hepatology***. 2013 Jun;57(6):2491-2501. PMID: 23315977

269. Cancer Genome Atlas Research Network (Ley TJ et al, including <u>Chun H-J)</u>. Genomic and epigenomic landscape of adult *de novo* Acute Myeloid Leukemia. ***N J Engl Med.*** 2013 May 30;368(22):2059-2074. PMID: 23634996

268. Mwenifumbo JC and **Marra MA**. Cancer genome sequencing study design. (Invited review article). ***Nat Rev Genet***. 2013 May;14(5):321-332. PMID: 23594910

267. Lim E, **Marra M**. MicroRNA dysregulation in B-cell non-Hodgkin lymphoma. ***Blood Lymphat Cancer: Targets and Therapy***. 2013 May; 3: 25-40.

266. Cancer Genome Atlas Research Network, (including <u>Chun H-J</u>), Kandoth C, Schultz N, Cherniack AD, Akbani R, Liu Y, Shen H, Robertson AG, Pashtan I, Shen R, Benz CC, Yau C, Laird PW, Ding L, Zhang W, Mills GB, Kucherlapati R, Mardis ER, Levine DA. Integrated genomic characterization of endometrial carcinoma. ***Nature***. 2013 May 2;497(7447):67-73. PMID: 25417114

265. Trinh DL, Scott DW, <u>Morin RD</u>, <u>Mendez-Lago M</u>, An J, Jones SJM, Mungall AJ, Zhao YJ, Schein J, Steidl C, Connors JM, Gascoyne RD, **Marra MA**. Analysis of *FOXO1* mutations in Diffuse Large B-Cell Lymphoma. ***Blood.*** 2013 May 2;121(18):3666-3674. PMID: 23460611

264. Meissner B, Kridel R, Lim RS, Rogic S, Tse K, Scott DW, Moore R, Mungall AJ, **Marra MA**, Connors JM, Steidl C, Gascoyne RD. The E3 ubiquitin ligase UBR5 is recurrently mutated in mantle cell lymphoma. (Brief Report) ***Blood.*** 2013 Apr 18;121(16):3161-3164. PMID: 23407552

263. Nolte SM, Venugopal C, McFarlane N, <u>Morozova O</u>, Hallett RM, O'Farrell E, Manoranjan B, Murty NK, Klurfan P, Kachur E, Provias JP, Hassell JA, **Marra M**, Singh SK. A cancer stem cell model for studying brain metastases from primary lung cancer. ***J Natl Cancer Inst.*** 2013 Apr 17;105(8):551-562. PMID: 23418195

262. <u>Griffith M</u>, <u>Mwenifumbo JC</u>, <u>Cheung PY</u>, <u>Paul JE</u>, <u>Pugh TJ,</u> Tang MJ, <u>Chittaranjan S</u>, <u>Morin RD</u>, Asano JK, Ally AA, Miao L, Lee A, Chan SY,Taylor G, Severson T, <u>Hou Y-C</u>, Griffith OL, Cheng GSW, Novik K, Moore R, Luk M, Owen D, Brown CJ, Morin GB, Gill S, Tai IT, **Marra MA**. Novel mRNA isoforms and mutations of uridine monophosphate synthetase are associated with fluorouracil resistance in colorectal cancer. ***Pharmacogenomics J.*** 2013 Apr;13(2):148-158. PMID: 22249354

261. Dubuc AM, Remke M, Korshunov A, Northcott PA, Zhan S, <u>Mendez-Lago M</u>, Kool M, Jones DTW, Unterberger A, Morrissy AS, Shih D, Peacock J, Ramaswamy V, Rolider A, Witt H, Hielscher T, Hawkins C, Vibhakar R, Croul S, Rutka JT, Weiss WA, Jones SJM, Eberhart CG, **Marra MA,** Pfister SM, Taylor MD. Aberrant Patterns of H3K4 and H3K27 Histone Lysine Methylation Occur Across Subgroups in Medulloblastoma. ***Acta Neuropathol***. 2013 Mar;125(3):373-384. PMID: 23184418

260. Tennant BR, Robertson AG, Beach M, Li L, Zhang X, Zhan SH, Whiting CJ, Kim A, Gottardo R, **Marra MA**, Jones SJM, Hoodless PA, Hoffman BG. Identification and analysis of murine pancreatic islet enhancers. ***Diabetologia***. 2013 Mar;56(3):542-552. PMID: 23238790

259. Pugh TJ, <u>Morozova O</u>, Attiyeh EF, Asgharzadeh S, Wei JS, Auclair D, Carter SL, Cibulskis K, Hanna M, Kiezun A, Kim J, Lawrence MS, Lichenstein L, McKenna A, Pedamallu CS, Ramos AH, Shefler E, Sivachenko A, Sougnez C, Stewart C, Ally A, Birol I, Chiu R, Corbett RD, Hirst M, Jackman SD, Kamoh

B, Khodabakshi AH, Krzywinski M, Lo A, Moore RA, Mungall KL, Qian J, Tam A, Thiessen N, Zhao YJ, Cole KA, Diamond M, Diskin SJ, Mosse YP, Wood AC, Ji L, Sposto R, Badgett T, London WB, Moyer Y, Gastier-Foster JM, Smith MA, Auvil JM, Gerhard DS, Hogarty MD, Jones SJ, Lander ES, Gabriel SB, Getz G, Seeger RC, Khan J**, Marra MA**, Meyerson M, Maris JM. The genetic landscape of high-risk neuroblastoma. ***Nat Genet.*** 2013 Mar;45(3):279-284. **(This paper got included in the Faculty of 1000's. F1000 is composed of faculty members and only selects and rates the best articles in biology and medicine)** PMID: 23334666

258. Goff DJ, Recart AC, Sadarangani A, Chun H-J, Barrett CL, Krajewska M, Leu H, Low-Marchelli J, Ma W, Shih AY, Wei J, Zhai D, Geron I, Pu M, Bao L, Chuang R, Balaian L, Gotlib J, Minden M, Martinelli G, Rusert J, Dao KH, Shazand K, Wentworth P, Smith KM, Jamieson CA, Morris SR, Goldstein LS, Hudson TJ, **Marra M**, Frazer KA, Pellecchia M, Reed JC, Jamieson CH. A Pan-BCL2 Inhibitor Renders Bone-Marrow-Resident Human Leukemia Stem Cells Sensitive to Tyrosine Kinase Inhibition. ***Cell Stem Cell.*** 2013 Mar 7;12(3):316-328. PMID: 23333150

257. Chand D, Yamazaki Y, Ruuth K, Schönherr C, Martinsson T, Kogner P, Attiyeh EF, Maris J, Morozova O, **Marra MA**, Ohira M, Nakagawara A, Sandström P-E, Palmer RH, Hallberg B. Cell culture and Drosophila model systems define three classes of anaplastic lymphoma kinase mutations in neuroblastoma. ***Dis Models Mech.*** 2013 Mar;6(2):373-382. PMID: 23104988

256. Jiang Q, Crews LA, Barrett CL, Chun H-J, Court AC, Isquith JM, Zipeto MA, Goff DJ, Minden M, Sadarangani A, Rusert JM, Dao K-HT, Morris SR, Goldstein LSB, **Marra MA**, Frazer KA, Jamieson CHM. ADAR1 Promotes Malignant Progenitor Reprogramming in Chronic Myeloid Leukemia. ***Proc Natl Acad Sci USA.*** 2013 Jan 15;110(3):1041-1046. PMID: 23275297

255. Wu C, Wyatt AW, McPherson A, Lin D, McConeghy BJ, Mo F, Shukin R, Lapuk AV, Jones SJM, Zhao YJ, **Marra MA**, Gleave ME, Volik SV, Wang Y, Sahinalp SC, Collins CC. Poly-gene Fusion Transcripts and Chromothripsis in Prostate Cancer. ***Gene Chromosome Canc***. 2012 Dec;51(12):1144-1153. PMID: 22927308

254. Cheng SWG, Kuzyk MA, Moradian A, Ichu T-A, Chang VCD, Tien JF, Vollett SE, Griffith M, **Marra MA**, Morin GB. The interaction of CDK12/CrkRS with CYCLIN K1 is required for the phosphorylation of the C-terminal domain of RNA Pol II. ***Mol Cell Biol.*** 2012 Nov;32(22):4691-4704. PMID: 22988298

253. Khodabakhshi AH, Morin RD, Fejes AP, Mungall AJ, Mungall KL, Bolger-Munro M, Johnson NA, Connors JM, Gascoyne RD, **Marra MA**, Birol I, Jones SJM. Recurrent targets of aberrant somatic hypermutation in lymphoma. ***Oncotarget.*** 2012 Nov;3(11):1308-1319. PMID: 23131835

252. Cancer Genome Atlas Network (Koboldt DC et al, including Chun H-J). Comprehensive molecular portraits of human breast tumors. ***Nature***. 2012 Oct 4;490(7418):61-70. PMID: 23000897

251. Tsang E, Rupps R, Friedman JM, McGillivray B, Eydoux P, **Marra M**, Zahir F. Life-history Chronicle for a Patient with the Recently Described Chromosome 4q21 Microdeletion Syndrome. ***Am J Med Genet A.*** 2012 Oct;158A(10):2606-2609. PMID: 22903878

250. Ha G, Roth A, Lai D, Bashashati A, Ding J, Goya R, Giuliany R, Rosner J, Oloumi A, Shumansky K, Chin S-F, Turashvili G, Hirst M, Caldas C, **Marra MA**, Aparicio S, Shah SP. Integrative analysis of genome-wide loss of heterozygosity and mono-allelic expression at nucleotide resolution reveals disrupted pathways in triple negative breast cancer. ***Genome Res.*** 2012 Oct;22(10):1995-2007. PMID: 22637570

249. Astanehe A, Finkbeiner MR**,** Krzywinski M, Fotovati A, Dhillon J, Berquin IM, Mills GB, **Marra MA**, Dunn SE. MKNK1 is a YB-1 target gene responsible for imparting trastuzumab resistance and can be blocked by RSK inhibition. ***Oncogene***. 2012 Oct 11;31(41):4434-4446. PMID: 22249268

248. Cancer Genome Atlas Research Network (Hammerman PS et al, including Chun H-J). Comprehensive genomic characterization of squamous cell lung cancers. ***Nature***. 2012 Sep 27;489(7417):519-525. PMID: 22960745

247. Krzywinski M, Birol I, Jones S, **Marra M**. Hive Plots – Rational Approach to Visualizing Networks. ***Brief Bioinform.*** 2012 Sep;13(5):627-644. PMID: 22155641

246. Crisan A, Goya R, Ha G, Ding J, Prentice LM, Oloumi A, Senz J, Zeng T, Tse K, Delaney A, Marra MA, Huntsman DG, Hirst M, Aparicio S, Shah S. Mutation Discovery in Regions of Segmental Cancer Genome Amplifications with CoNAn-SNV: A Mixture Model for Next Generation Sequencing of Tumors. ***PLoS One***. 2012;7(8):e41551. PMID: 22916110

245. Roberts KG, Morin R, Zhang J, Hirst M, Zhao YJ, Su X, Chen S-C, Payne-Turner D, Churchman M, Chen X, Harvey R, Kasap C, Yan C, Becksfort J, Finney R, Teachey D, Maude S, Tse K, Moore R, Jones S, Mungall K, Birol I, Edmonson M, Hu Y, Buetow K, Chen I-M, Carol W, Wei L, Ma J, Kleppe M, Levine R, Garcia-Manero G, Larsen E, Shah N, Devidas M, Reaman G, Smith M, Paugh S, Evans W, Grupp S, Jeha S, Pui C-H, Gerhard D, Downing J, Willman C, Loh M, Hunger S, **Marra M**, Mullighan C. Genetic alterations activating kinase and cytokine receptor signaling in high risk acute lymphoblastic leukemia. ***Cancer Cell***. 2012 Aug 14;22(2):153-166. PMID: 22897847

244. Northcott PA, Shih DJH, Peacock J, Garzia L, Morrissy S, Stütz AM, Zichner T, Korshunov A, Reimand J, Schumacher SE, Beroukhim R, Ellison DE, Marshall CR, Lionel AC, Mack S, Dubuc A, Yao Y, Ramaswamy V, Luu B, Rolider A, Cavalli F, Wang X, Remke M, Wu X, Chiu RYB, Chu A, Chuah E, Corbett RD, Hoad GR, Jackman SD, Li Y, Lo A, Mungall KL, Nip KM, Qian JQ, Raymond AGR, Thiessen N, Varhol RJ, Birol I, Moore RA, Mungall AJ, Holt R, Kawauchi D, Roussel MF, Kool M, Jones DTW, Witt H, Fernandez A, Kenney AM, Wechsler-Reya R, Dirks P, Aviv T, Grajkowska WA, Perek-Polnik M, Haberler CC, Delattre OO, Reynaud SS, Doz FF, Pernet-Fattet SS, Cho B-K, Kim S-K, Wang K-C, Scheurlen W, Eberhart CG, Fèvre-Montange M, Jouvet A, Pollack IF, Fan X, Muraszko KM, Gillespie YG, Di Rocco C, Massimi L, Michiels EMC, Kloosterhof NK, French PJ, Kros JM, Olson JM, Ellenbogen RG, Zitterbart K, Thompson RC, Cooper MK, Lach B, McLendon RE, Bigner DD, Fontebasso A, Albrecht S, Jabado N, Gupta N, Weiss WA, Bognár L, Klekner A, Van Meter TE, Kumabe T, Tominaga T, Elbabaa SK, Leonard JR, Rubin JB, Liau L, Van Meir EG, Fouladi M, Cinalli G, Garami M, Hauser P, Saad A, Iolascon A, Zollo M, Jung S, Carlotti CG, Vibhakar R, Ra YS, Robinson S, Faria CF, Chan J, Levy ML, Sorensen PHB, Meyerson M, Pomeroy SL, Cho Y-J, Bader GD, Tabori U, Hawkins CE, Bouffet E, Scherer SW, Rutka JT, Malkin D, Clifford SC, Jones SJM, Korbel JO, Pfister SM, **Marra MA**, Taylor MD. Subgroup specific structural variation across 1,000 medulloblastoma genomes. ***Nature.*** 2012 Aug 2;488(7409):49-56. PMID: 22832581

243. Vrljicak P, Cullum R, Xu E, Chang AC, Wederell ED, Bilenky M, Jones SJ, **Marra MA**, Karsan A, Hoodless PA. Twist1 transcriptional targets in the developing atrio-ventricular canal of the mouse. ***PLoS One.*** 7(7):e40815, 2012. PMID: 22815831

242. Cancer Genome Atlas Network (Muzny DM et al, including Marra M, Chun H-J). Comprehensive molecular characterization of human colon and rectal cancer. ***Nature***. 2012 July 18;487(7407):330-337. PMID: 22810696

241. Chen K, Wallis JW, Kandoth C, Kalicki-Veizer JM, Mungall KL, Mungall AJ, Jones SJ, **Marra MA**, Ley TJ, Mardis ER, Wilson RK, Weinstein JN, Ding L. BreakFusion: Targeted Assembly-based Identification of Gene Fusions in Whole Transcriptome Paired-end Sequencing Data. ***Bioinformatics***. 2012 Jul 15;28(14):1923-1924. PMID: 22563071

240. Lapuk AV, Wu C, Wyatt AW, McPherson A, McConeghy BJ, Brahmbhatt S, Mo F, Zoubeidi A, Anderson S, Bell RH, Haegert A, Shukin R, Wang Y, Fazli L, Hurtado-Coll A, Jones EC, Hach F, Hormozdiari F, Hajiresouliha I, Boutros PC, Bristow RG, Zhao YJ, **Marra MA**, Fanjul A, Maher CA, Chinnaiyan AM, Rubin MA, Beltran H, Sahinalp SC, Gleave ME, Volik SV, Collins CC. From sequence

to molecular pathology, and a mechanism driving the neuroendocrine phenotype in prostate cancer. ***J Pathol.*** 2012 Jul;227(3):286-297. PMID: 22553170

239. Blough MD, Al-Najjar M, Chesnelong C, Binding CE, Rogers AD, Luchman HA, Kelly JJ, Fliegel L, Morozova O, Yip S, **Marra M**, Weiss S, Chan JA, Cairncross JG. DNA hypermethylation and 1p Loss silence NHE-1 in oligodendroglioma. ***Ann Neurol***. 2012 Jun; 71(6):845-849. PMID: 22718548

238. Baradaran-Heravi A, Cho KS, Tolhuis B, Sanyal M, Morozova O, Morimoto M, Elizondo LI, Bridgewater D, Lubieniecka J, Beirnes K, Myung C, Leung D, Fam HK, Choi K, Huang Y, Dionis KY, Zonana J, Keller K, Stenzel P, Mayfield C, Lücke1 T, Bokenkamp A, **Marra MA**, van Lohuizen M, Lewis DB, Shaw C, Boerkoel CF. Penetrance of biallelic *SMARCAL1* mutations is associated with environmental and genetic disturbances of gene expression. ***Hum Mol Genet.*** 2012 Jun 1;21(11):2572-2587. PMID: 22378147

237. Schuetz JM, Johnson NA, Morin RD, Scott DW, Tan K, Ben-Nierah S, Boyle M, Slack GW, **Marra MA**, Connors JM, Brooks-Wilson AR, Gascoyne RD. BCL2 mutations in diffuse large B-cell lymphoma. ***Leukemia.*** 2012 Jun;26(6):1383-1390. PMID: 22189900

236. Scott DW, Mungall KL, Ben-Neriah S, Rogic S, Morin RD, Slack GW, Tan KL, Chan FC, Lim RS, Connors JM, **Marra MA**, Mungall AJ, Steidl C, Gascoyne RD. *TBL1XR1/TP63* – a novel recurrent gene fusion in B-cell non-Hodgkin lymphoma. ***Blood.*** 2012 May 24;119(21):4949-4952. PMID: 22496164

235. Wu C, Wyatt AW, Lapuk AV, McPherson A, McConeghy BJ, Bell RH, Anderson S, Haegert A, Brahmbhatt S, Shukin R, Fazli L, Hurtado-Coll A, Butterfield YS, Boutros PC, Bristow RG, Jones SJ, Hirst M, **Marra MA**, Maher CA, Chinnaiyan AM, Sahinalp SC, Gleave ME, Volik SV, Collins CC. Integrated genome and transcriptome sequencing identifies a novel case of hybrid and aggressive prostate cancer. ***J Pathol.*** 2012 May;227(1):53-61. PMID: 22294438

234. Najafzadeh M, Lynd LD, Davis JC, Bryan S, Anis A, **Marra M**, Marra CA. Barriers to integrating personalized medicine into clinical practice: a best-worst scaling choice experiment. ***Genet Med***. 2012 May;14(5):520-526. PMID: 22241089

233. Shah SP, Roth A, Goya R, Oloumi A, Ha G, Zhao YJ, Turashvili G, Ding J, Tse K, Haffari G, Bashashati A, Prentice L, Khattra J, Burleigh A, Yap D, Bernard V, McPherson A, Shumansky K, Crisan A, Giuliany R, Heravi-Moussavi A, Rosner J, Lai D, Birol I, Varhol R, Tam A, Dhalla N, Zeng T, Ma K, Chan S, Griffith M, Moradian A, Cheng SWG, Morin G, Watson P, Gelmon K, Chia S, Chin S-F, Curtis C, Rueda O, Pharoah P, Damaraju S, Mackey J, Hoon K, Harkins T, Tadigotla V, Sigaroudinia M, Gascard P, Tlsty T, Costello J, Meyer IM, Eaves CE, Wasserman WW, Jones S, Huntsman D, Hirst M, Caldas C, **Marra MA**, Aparicio S. The clonal and mutational evolution spectrum of primary triple-negative breast cancers. ***Nature.*** 2012 Apr 4;486(7403):395-399. PMID: 22495314

232. Roth A, Ding J, Morin RD, Crisan A, Ha G, Giuliany R, Bashashati A, Hirst M, Turashvili G, Oloumi A, **Marra MA**, Aparicio S, Shah SP. JointSNVMix : a probabilistic model for accurate detection of somatic mutations in normal/tumour paired next generation sequencing data**.** ***Bioinformatics***. 2012 Apr 1;28(7):907-913. PMID: 22285562

231. Chu JS, Johnsen RC, Chua SY, Tu D, Dennison M, **Marra M,** Jones SJ, Baillie DL, Rose AM. Allelic ratios and the mutational landscape reveal biologically significant heterozygous SNVs. ***Genetics.*** 2012 Apr;190(4):1225-1233. PMID: 22267497

230. Dubuc AM, Morrissy AS, Kloosterhof NK, Northcott PA, Yu EP, Shih D, Peacock J, Grajkowska W, van Meter T, Eberhart CG, Pfister S, **Marra MA,** Weiss WA, Scherer SW, Rutka JT, French PJ, Taylor MD. Subgroup-specific alternative splicing in medulloblastoma. ***Acta Neuropathol***. 2012 Apr;123(4):485-499. PMID: 22358458

229. Northcott PA, Shih DJH, Remke M, Cho Y-J, Kool M, Hawkins C, Eberhart CG, Dubuc A, Guettouche T, Cardentey Y, Bouffet E, Pomeroy SL, **Marra M**, Malkin D, Rutka JT, Korshunov A, Pfister S, Taylor

MD. Rapid, reliable, and reproducible molecular sub-grouping of clinical medulloblastoma samples. ***Acta Neuropathol***. 2012 Apr;123(4):615-626. PMID: 22057785

228. Collins CC, Volik SV, Lapuk A, Wang Y, Gout PW, Wu C, Xue H, Cheng H, Haegert A, Bell RH, Brahmbhatt S, Anderson S, Fazli L, Hurtado-Coll A, Rubin MA, Demichelis F, Beltran H, Hirst M, **Marra MA**, Maher CA, Chinnaiyan AM, Gleave ME, Bertino JR, Lubin M, Wang Y. Next Generation Sequencing of Prostate Cancer from a Patient Identifies a Deficiency of Methylthioadenine Phosphorylase (MTAP), an Exploitable Tumor Target. ***Mol Cancer Ther.*** 2012 Mar;11(3):775-783. PMID: 22252602

227. Kridel R, Meissner B, Rogic S, Boyle M, Telenius A, Woolcock B, Gunawardana J, Jenkins C, Cochrane C, Ben-Neriah S, Tan K, Morin RD, Opat S, Sehn LH, Connors JM, **Marra MA**, Weng AP, Steidl C, Gascoyne RD. Whole transcriptome sequencing reveals recurrent NOTCH1 mutations in mantle cell lymphoma. ***Blood.*** 2012 Mar 1;119(9):1963-1971. PMID: 22210878

226. Mo F, Wyatt A, Wu C, Lapuk A, **Marra M,** Gleave M, Volik S, Collins C. Next generation sequencing of prostate tumours provides independent evidence of XMRV contamination. ***J Clin Microbiol.*** 2012 Feb;50(2):536-537. PMID: 22162557

225. Heravi-Moussavi A, Anglesio MS, Cheng S-WG, Senz J, Yang W, Prentice L, Fejes A, Chow C, Tone A, Kalloger SE, Hamel N, Roth A, Ha G, Wan ANC, Maines-Bandiera S, Salamanca C, Pasini B, Clarke BA, Lee AF, Lee C-H, Zhou C, Young RH, Aparicio AS, Sorensen PHB, Woo MMM, Boyd N, Jones SJM, Hirst M, **Marra MA**, Gilks B, Shah SP, Foulkes WD, Morin GB, Huntsman DG. Recurrent Somatic DICER1 Mutations in Non-Epithelial Ovarian Tumors. ***N Engl J Med.*** 2012 Jan 19;366(3):234-242. PMID: 22187960

224. Lee CH, Ou WB, Mariño-Enriquez A, Zhu M, Mayeda M, Wang Y, Guo X, Brunner AL, Amant F, French CA, West RB, McAlpine JN, Gilks CB, Yaffe MB, Prentice LM, McPherson A, Jones SJ, **Marra MA**, Shah SP, van de Rijn M, Huntsman DG, Dal Cin P, Debiec-Rychter M, Nucci MR, Fletcher JA. 14-3-3 Fusion Oncogenes in High-grade Endometrial Stromal Sarcoma. ***Proc Natl Acad Sci U S A***. 2012 Jan 17;109(3):929-934. PMID: 22223660

223. Ding J, Bashashati A, Roth A, Oloumi A, Tse K, Zeng T, Haffari G, Hirst M, **Marra MA**, Condon A, Aparicio S, Shah SP. Feature based classifiers for somatic mutation detection in tumour-normal paired sequencing data. ***Bioinformatics.*** 2012 Jan 15;28(2):167-175. PMID: 22084253

222. Gibson WT, Hood RL, Zhan SH, Bulman DE, Fejes AP, Moore R, Mungall AJ, Eydoux P, Babul-Hirji R, Chitayat D, An J**, Marra MA**, FORGE Canada Consortium, Boycott KM, Weaver DD, Jones SJ. Mutations in EZH2 cause Weaver syndrome. ***Am J Hum Genet.*** 2012 Jan 13;90(1):110-118. PMID: 22177091

221. Yip S, Butterfield YS, Morozova O, Chittaranjan S, Blough MD, An J, Birol I, Chesnelong C, Chiu R, Chuah E, Corbett R, Docking R, Firme M, Hirst M, Jackman S, Karsan A, Li H, Louis DN, Maslova A, Moore R, Moradian A, Mungall KL, Perizzolo M, Qian J, Roldan G, Smith EE, Tamura-Wells J, Thiessen N, Varhol R, Weiss S, Wu W, Young S, Zhao YJ, Mungall AJ, Jones SJM, Morin GB, Chan JA, Cairncross JG, **Marra MA**. Concurrent CIC mutations, IDH mutations and 1p/19q loss distinguish oligodendrogliomas from other cancers. ***J Pathol.*** 2012 Jan;226(1):7-16. **This paper was awarded the *The Journal of Pathology* 2012 Jeremy Jass Prize for Research Excellence in Pathology**) PMID: 22072542

220. Kuchenbauer F, Mah SM, Heuser M, McPherson A, Ruschmann J, Rouhi A, Berg T, Bullinger L, Argiropoulos B, Morin RD, Lai D, Starczynowski DT, Karsan A, Eaves CJ, Watahiki A, Wang Y, Aparicio SA, Ganser A, Krauter J, Döhner H, Döhner K, **Marra MA**, Camargo FD, Palmqvist L, Buske C, Humphries RK. Comprehensive analysis of mammalian miRNA* species and their role in myeloid cells. ***Blood***. 2011 Sep 22;118(12):3350-3358. PMID: 21628414

219. Schrader KA, Heravi-Moussavi A, Waters PJ, Senz J, Whelan J, Ha G, Eydoux P, Nielsen T, Gallagher B, Oloumi A, Boyd N, Fernandez BA, Young TL, Jones SJ, Hirst M, Shah SP, **Marra MA**, Green J, Huntsman DG. Using next-generation sequencing for the diagnosis of rare disorders: a family with retinitis pigmentosa and skeletal abnormalities. ***J Pathol***. 2011 Sep;225(1):12-18. PMID: 21792934

218. Chang ACY, Fu Y, Garside VC, Niessen K, Chang L, Fuller M, Setiadi A, Smrz J, Kyle A, Minchinton A, **Marra M**, Hoodless PA, Karsan A. Notch initiates endothelial-to-mesenchymal transition in the atrioventricular canal through autocrine activation of soluble guanylyl cyclase. ***Dev Cell.*** 2011 Aug 16;21(2):288-300. PMID: 21839921

217. Morrissy AS, Griffith M, **Marra MA**. Extensive relationship between antisense transcription and alternative splicing in the human genome. ***Genome Res.*** 2011 Aug;21(8):1203-1212. PMID: 21719572

216. O'Connor MD, Wederell E, Robertson G, Delaney A, Morozova O, Poon SS, Yap D, Fee J, Zhao Y, McDonald H, Zeng T, Hirst M**, Marra MA**, Aparicio SA, Eaves CJ. Retinoblastoma-binding proteins 4 and 9 are important for human pluripotent stem cell maintenance. ***Exp Hematol.*** 2011 Aug;39(8):866-879.e1. PMID: 21689726

215. White AK, Vaninsberghe M, Petriv OI, Hamidi M, Sikorski D, **Marra MA,** Piret J, Aparicio S, Hansen CL. High-Throughput Microfluidic single-cell RT-qPCR. ***Proc Natl Acad Sci U SA.*** 2011 Aug 23;108(34):13999-14004. PMID: 21808033

214. Morin RD, Mendez-Lago M, Mungall AJ, Goya R, Mungall KL, Corbett RD, Johnson NA, Severson TM, Chiu R, Field M, Jackman S, Krzywinski M, Scott DW, Trinh DL, Tamura-Wells J, Li S, Firme MR, Rogic S, Griffith M, Chan S, Yakovenko O, Meyer IM, Zhao EY, Smailus D, Moksa M, Chittaranjan S, Rimsza L, Brooks-Wilson A, Spinelli JJ, Ben-Neriah S, Meissner B, Woolcock B, Boyle M, McDonald H, Tam A, Zhao Y, Delaney A, Zeng T, Tse K, Butterfield Y, Birol I, Holt R, Schein J, Horsman DE, Moore R, Jones SJ, Connors JM, Hirst M, Gascoyne RD, **Marra MA**. Frequent mutation of histone-modifying genes in non-Hodgkin lymphoma. ***Nature***. 2011 Jul 27; 476(7360):298-303. PMID: 21796119

213. Heuser M, Yun H, Berg T, Yung E, Argiropoulos B, Kuchenbauer F, Park G, Hamwi I, Palmqvist L, Lai CK, Leung M, Lin G, Chaturvedi A, Thakur BK, Iwasaki M, Bilenky M, Thiessen N, Robertson G, Hirst M, Kent D, Wilson NK, Göttgens B, Eaves C, Cleary ML, **Marra M**, Ganser A, Humphries RK. Cell of Origin in AML: Susceptibility to MN1-Induced Transformation Is Regulated by the MEIS1/AbdB-like HOX Protein Complex. ***Cancer Cell***. 2011 Jul 12;20(1):39-52. PMID: 21741595

212. McPherson AW, Hormozdiari F, Zayed A, Giuliany R, Ha G, Sun MGF, Griffith M, Heravi-Moussavi A, Senz J, Melnyk N, Pacheco M, **Marra MA**, Hirst M, Nielsen TO, Sahinalp SC, Huntsman D, Shah S. deFuse: an algorithm for gene fusion discovery in tumor RNA-Seq data. ***PLOS Comput Biol.*** 2011 May;7(5):e1001138. PMID: 21625565

211. Tucker T, Montpetit A, Chai D, Chan S, Chénier S, Coe BP, Delaney A, Eydoux P, Lam WL Langlois S, Lemyre E, **Marra M**, Qian H, Rouleau GA, Vincent D, Michaud JL, Friedman JM. Comparison of genome-wide array genomic hybridization platforms for the detection of copy number variants in idiopathic mental retardation. ***BMC Med Genomics***. 2011 Mar 25;4(1):25. PMID: 21439053

210. Slobodan J, Corbett R, Wye N, Schein JE, **Marra MA**, Coope RJN. High performance gel imaging with a commercial single lens reflex camera***.*** ***Rev Sci Instrum***. 2011 Mar;82(3):034301. PMID: 21456768

209. Steidl C, Shah SP, Woolcock BW, Rui L, Kawahara M, Farinha P, Johnson NA, Zhao Y, Telenius A, Ben-Neriah S, McPherson A, Meissner B, Okoye UC, Diepstra A, van den Berg A, Sun M, Leung G, Jones SJ, Connors JM, Huntsman DG, Savage KJ, Rimsza LM, Horsman DE, Staudt LM, Steidl U**, Marra MA**, Gascoyne RD. MHC Class II Transactivator CIITA is a Recurrent Gene Fusion Partner in Lymphoid Cancers. ***Nature***. 2011 Mar 17;471(7338):377-381. PMID: 21368758

208. Yap DB, Chu J, Berg T, Schapira M, Cheng SW, Moradian A, Morin RD, Mungall AJ, Meissner B, Boyle M, Marquez VE, **Marra MA**, Gascoyne RD, Humphries RK, Arrowsmith CH, Morin GB, Aparicio SA.

Somatic mutations at EZH2 Y641 act dominantly through a mechanism of selectively altered PRC2 catalytic activity, to increase H3K27 trimethylation. ***Blood***. 2011 Feb 24;117(8):2451-2459. PMID: 21190999

207. Berezikov E, Robine N, Samsonova A, Westholm JO, Naqvi A, Hung JH, Okamura K, Dai Q, Bortolamiol-Becet D, Martin R, Zhao YJ, Zamore PD, Hannon GJ, **Marra MA**, Weng Z, Perrimon N, Lai EC. Deep annotation of Drosophila melanogaster microRNAs yields insights into their processing, modification, and emergence. ***Genome Res***. 2011 Feb;21(2):203-215. PMID: 21177969

206. Blahnik KR, Dou L, Echipare L, Iyengar S, O'Geen H, Sanchez E, Zhao YJ, **Marra MA**, Hirst M, Costello JF, Korf I, Farnham PJ. Characterization of the contradictory chromatin signatures at the 3' exons of zinc finger genes**. *PLoS One.*** 2011 Feb 15;6(2):e17121. PMID: 21347206

205. D'Souza C, Kronstad J, Taylor G, Warren R, Yuen M, Hu G, Jung WH, Sham A, Kidd S, Tangen K, Lee N, Zeilmaker T, Sawkins J, McVicker G, Shah S, Gnerre S, Griggs A, Zeng Q, Bartlett K, Li W, Wang X, Heitman J, Stajich J, Fraser J, Meyer W, Carter D, Schein J, Krzywinski M, Kwon-Chung KJ, Varma A, Wang J, Brunham R, Fyfe M, Ouellette BFF, Siddiqui A, **Marra M**, Jones S, Holt R, Birren B, Galagan J, Cuomo C. Genome variation in *Cryptococcus gattii*, an emerging pathogen of immunocompetent hosts**. *MBio***. 2011 Feb 8;2(1). pii: e00342-10. PMID: 21304167

204. DiGuistini S, Wang Y, Liao NY, Taylor G, Tanguay P, Feau N, Henrissat B, Chan SK, Hesse-Orce U, Alamouti SM, Tsui CK, Docking R, Levasseur A, Haridas S, Robertson G, Birol I, Holt R, **Marra M**, Hamelin RC, Hirst M, Jones SJM, Bohlmann J, Breuil C. Genome and transcriptome analyses of the mountain pine beetle-fungal symbiont *Grosmannia clavigera*, a lodgepole pine pathogen. ***Proc Natl Acad Sci U SA.*** 2011 Feb 8;108(6):2504-2509. PMID: 21262841

203. Starczynowski D, <u>Morin RD</u>, McPherson A, Kuchenbauer F, Tohyama K, Hirst M, Humphries K, **Marra M,** Lam W, Karsan A. Genome-wide identification of human microRNAs located in leukemia-associated genomic alterations. ***Blood.*** 2011 Jan 13;117(2):595-607. PMID: 20962326

202. Hirst M, **Marra MA**. Next Generation Sequencing Based Approaches to Epigenomics. ***Brief Funct Genomics***. 2010 Dec;9(5-6):455-465. PMID: 21266347

201. The modENCODE Consortium. Identification of Functional Elements and Regulatory Circuits by Drosophila modENCODE**. *Science***. 2010 Dec 24;330(6012):1787-1797. PMID: 21177974

200. McLarren KW, Severson T, du Souich C, Stockton DW, Kratz LE, Cunningham D, Hendson G, <u>Morin RD, Wu D</u>, <u>Paul JE</u>, An J, Nelson TN, Chou A, DeBarber AE, Merkens LS, Michaud JL, Waters PJ, Yin J, McGillivray B, Demos M, Rouleau GA, Grzeschik K-H, Smith R, Tarpey PS, Kini U, Schwartz CE, Gecz J, Stratton MR, Arbour L, Hurlburt J, Van Allen MI, Herman GE, Zhao YJ, Moore R, Kelley RI, Jones SJ, Steiner RD, Raymond L, **Marra MA**, Boerkoel CF. Hypomorphic temperature-sensitive alleles of NSDHL cause CK syndrome**. *Am J Hum Genet*.** 2010 Dec 10;87(6):905-914. PMID: 21129721

199. Cheung KJ, Johnson NA, Affleck JG, Severson T, Steidl C, Ben-Neriah S, Schein J, <u>Morin RD</u>, Moore R, Shah SP, Qian H, Paul JE, Telenius A, Relander T, Lam W, Savage K, Connors JM, Brown C, **Marra MA**, Gascoyne RD, Horsman DE. Acquired TNFRSF14 mutations in follicular lymphoma are associated with worse prognosis. ***Cancer Res***. 2010 Nov 15;70(22):9166-9174. PMID: 20884631

198. Cerchietti LC, Hatzi K, Caldas-Lopes E, Yang SN, Figueroa ME, <u>Morin RD</u>, Hirst M, Mendez L, Shaknovich R, Cole P, Bhalla K, Gascoyne RD, **Marra M**, Chiosis G, Melnick A. BCL6 repression of *EP300* provides a basis for rational combinatorial therapy in diffuse large B cell lymphomas. ***J Clin Invest.*** 2010 Nov 1. pii: 42869. PMID: 21041953

197. Robertson G, Schein J, Chiu R, Field M, Jackman SD, Mungall K, Lee S, Okada SM, Corbett R, Qian JQ, <u>Griffith M</u>, Raymond A, Thiessen N, Cezard T, Butterfield Y, Newsome R, Chan SK, Varhol R, Kamoh B, Prabhu A-L, Tam A, Zhao YJ, Moore R, Hirst M, **Marra MA**, Jones SJM, Hoodless PA, Birol I. De

Novo Assembly and Analysis of RNA-Seq Data. ***Nat Methods***. 2010 Nov;7(11):909-912. PMID: 20935650

196. Jinno H, Morozova O, Jones KL, Biernaskie JA, Paris M, Hosokawa R, Rudnicki M, Chai Y, Rossi F, **Marra MA,** Miller FD. Convergent genesis of an adult neural crest-like dermal stem cell from distinct developmental origins. ***Stem Cells***. 2010 Nov;28(11):2027-2040.

195. Law MJ, Lower KM, Voon HP, Hughes JR, Garrick D, Viprakasit V, Mitson M, De Gobbi M, **Marra M**, Morris A, Abbott A, Wilder SP, Taylor S, Santos GM, Cross J, Ayyub H, Jones S, Ragoussis J, Rhodes D, Dunham I, Higgs DR, Gibbons RJ. ATR-X syndrome protein targets tandem repeats and influences allele-specific expression in a size-dependent manner. ***Cell.*** 2010 Oct 29;143(3):367-378. PMID: 21029860

194. Bernstein BE, Stamatoyannopoulos JA, Costello JF, Ren B, Milosavljevic A, Meissner A, Kellis M, **Marra MA**, Beaudet AL, Ecker JR, Farnham PJ, Hirst M, Lander ES, Mikkelsen TS, Thomson JA. The NIH Roadmap Epigenomics Mapping Consortium. ***Nat Biotechnol***. 2010 Oct;28(10):1045-1048. PMID: 20944595

193. Wiegand KC, Shah SP, Al-Agha OM, Zhao Y, Tse K, Zeng T, Senz J, McConechy MK, Anglesio MS, Kalloger SE, Yang W, Heravi-Moussavi A, Giuliany R, Chow C, Fee J, Zayed A, Prentice L, Melnyk N, Turashvili G, Delaney AD, Madore J, Yip S, McPherson AW, Ha G, Bell L, Fereday S, Tam A, Galletta L, Tonin PN, Provencher D, Miller D, Jones SJ, Moore RA, Morin GB, Oloumi A, Boyd N, Aparicio SA, Shih IeM, Mes-Masson AM, Bowtell DD, Hirst M, Gilks B, **Marra MA**, Huntsman DG. ARID1A mutations in endometriosis-associated ovarian carcinomas. ***N Engl J Med.*** 2010 Oct 14;363(16):1532-1543. PMID: 20942669

192. Griffith M, Griffith OL, Mwenifumbo J, Morin RD, Goya R, Tang MJ, Hou Y-C, Pugh TJ, Robertson G, Chittaranjan S, Ally A, Asano JK, Chan SY, Li HI, McDonald H, Teague K, Zhao YJ, Zeng T, Delaney A, Hirst M, Morin GB, Jones SJM, Tai IT, **Marra MA**. Alternative expression analysis by RNA sequencing. ***Nat Methods.*** 2010 Oct;7(10):843-847. PMID: 20835245

191. Harris RA, Wang T, Coarfa C, Zhou X, Xi Y, Nagarajan RP, Hong C, Downey S, Johnson BE, Delaney A, Zhao YJ, Olshen A, Ballinger T, Schillebeeckx M, Echipare L, O'Geen H, Lister R, Pelizzola M, Chung W-Y, Gu H, Bock C, Gnirke A, Zhang MQ, Haussler D, Ecker J, Li W, Farnham PJ, Waterland RA, Meissner A, **Marra MA**, Hirst M, Milosavljevic A, Costello JF. Comparison of sequencing-based methods to profile DNA methylation and identification of monoallelic epigenetic modifications. ***Nat Biotechnol***. 2010 Oct;28(10):1097-1105. PMID: 20852635

190. Romanuik TL, Wang G, Morozova O, Delaney A, **Marra MA**, Sadar MD. LNCaP Atlas: Gene expression associated with in vivo progression to castration-recurrent prostate cancer. ***BMC Med Genomics***. 2010 Sep 24;3(1):43. PMID: 20868494

189. Smith KM, Datti A, Fujitani M, Grinshtein N, Zhang L, Morozova O, Blakely KM, Rotenberg SA, Hansford LM, Miller FD, Yeger H, Irwin MS, Moffat J, **Marra MA**, Baruchel S, Wrana JL, Kaplan DR. Selective targeting of neuroblastoma tumour-initiating cells by compounds identified in stem cell-based small molecule screens. ***EMBO Mol Med.*** 2010 Sep;2(9):371-384. PMID: 20721990

188. Petriv OI, Kuchenbauer F, Delaney AD, Lecault V, White A, Kent D, Marmolejo L, Heuser M, Berg T, Copley M, Ruschmann J, Sekulovic S, Antignano F, Kuroda E, Ho V, Benz C, Halim T, Giambra V, Krystal G, Takei CJF, Weng AP, Eaves C, Piret J, **Marra MA**, Humphries RK, Hansen CL. Comprehensive microRNA Expression Profiling of the Hematopoietic Hierarchy. ***Proc Natl Acad Sci USA***. 2010 Aug 31;107(35):15443-15448. PMID: 20702766

187. Jones SJM, Laskin J, Li YY, Griffith OL, An J, Bilenky M, Butterfield YS, Cezard T, Chuah E, Corbett R, Fejes A, Griffith M, Yee J, Montgomery M, Mayo M, Melnyk N, Morin RD, Pugh TJ, Severson T, Shah SP, Sutcliffe M, Tam A, Terry J, Thiessen N, Thomson T, Varhol R, Zeng T, Zhao YJ, Moore RA, Huntsman DG, Birol I, Hirst M, Holt RA, **Marra MA**. Evolution of an adenocarcinoma in response to

selection by targeted kinase inhibitors. ***Genome Biol***. 2010 Aug 9;11(8):R82. **(Mentioned in "*Genomes on Prescription*", by Brendan Maher, Nature 478,22-24; 5 Oct 2011).** PMID: 20696054

186. Morozova O, Vojvodic M, Grinshtein N, Hansford L, Blakely K, Maslova A, Hirst M, Cezard T, Morin R, Moore R, Smith K, Miller F, Taylor P, Thiessen N, Varhol R, Zhao YJ, Jones S, Moffat J, Kislinger T, Moran M, Kaplan D, **Marra M**. Systems-level analysis of neuroblastoma tumor-initiating cells implicates AURKB as a novel drug target for neuroblastoma. ***Clin Cancer Res.*** 2010 Sep 15;16(18):4572-4582. PMID: 20651058

185. Hoffman BG, Robertson G, Zavaglia B, Beach M, Cullum R, Lee S, Soukhatcheva G, Li L, Wederell ED, Thiessen N, Bilenky M, Cezard T, Tam A, Kamoh B, Birol I, Dai D, Zhao YJ, Hirst M, Verchere B, Helgason CD, **Marra MA**, Jones SJM, Hoodless PA. Locus co-occupancy, nucleosome positioning, and H3K4me1 regulate the functionality of FOXA2-, HNF4A-, and PDX1-bound loci in islets and liver. ***Genome Res.*** 2010 Aug;20(8):1037-1051. PMID: 20551221

184. Cheung KJ, Delaney A, Ben-Neriah S, Schein J, Lee T, Shah SP, Cheung D, Johnson NA, Mungall AJ, Telenius A, Lai B, Boyle M, Connors JM, Gascoyne RD, **Marra MA**, Horsman DE. High resolution analysis of follicular lymphoma genomes reveals somatic recurrent sites of copy-neutral loss of heterozygosity and copy number alterations that target single genes. ***Gene Chromosome Canc***. 2010 Aug;49(8):669-681. PMID: 20544841

183. Wong RTF, Flibotte S, Corbett R, Saeedi P, Jones SJM, **Marra MA**, Schein JE, Birol I. LaneRuler: Automated Lane Tracking for DNA Electrophoresis Gel Images. ***IEEE T Autom Sci Eng***. 2010 Jul; 7(3): 706-708.

182. Maunakea AK, Nagarajan RP, Bilenky M, Ballinger TJ, D'Souza C, Fouse1 SD, Johnson BE, Hong C, Nielsen C, Zhao YJ, Turecki G, Delaney A, Varhol R, Thiessen N, Shchors K, Heine VM, Rowitch DH, Xing X, Fiore C, Schillebeeckx M, Jones SJ, Haussler D, **Marra MA**, Hirst M, Wang T, Costello JF. Conserved Role of Intragenic DNA Methylation in Regulating Alternative Promoters. ***Nature***. 2010 Jul 8;466(7303):253-257. PMID: 20613842

181. Ahn HW, Morin RD, Zhao H, Harris RA, Coarfa C, Chen ZJ, Milosavljevic A, **Marra MA**, Rajkovic A. MicroRNA transcriptome in the newborn mouse ovaries determined by massive parallel sequencing. ***Mol Hum Reprod***. 2010 Jul;16(7):463-471. PMID: 20215419

180. Flibotte S ,Edgley ML, Chaudhry I,Taylor J, Neil SE, Rogula A, Zapf R, Hirst M, Butterfield Y, Jones SJ, Marra MA, Barstead RJ, Moerman DG. Whole-genome profiling of mutagenesis in *Caenorhabditis elegans*. **Genetics.** 2010 Jun;185(2):431-441. PMID: 20439774

179. International Cancer Genome Consortium (Hudson TJ et al). International network of cancer genome projects. ***Nature***. 2010 Apr 15;464(7291): 993-998. PMID: 20393554

178. Goya R, Sun MGF, Morin RD, Leung G, Ha G, Wiegand K, Senz J, Crisan A, **Marra MA**, Hirst M, Huntsman D, Murphy KP, Aparicio S, Shah SP. SNVMix: predicting single nucleotide variants from next generation sequencing of tumors. ***Bioinformatics.*** 2010 Mar 15;26(6):730-736. PMID: 20130035

177. Rose AM, O'Neil NJ, Bilenky M, Butterfield YS, Malhis N, Flibotte S, Jones MR, **Marra M**, Baillie DL, Jones SJ. Genomic sequence of a mutant strain of *Caenorhabditis elegans* with an altered recombination pattern. ***BMC Genomics***. 2010 Feb 23;11(1):131. PMID: 20178641

176. Morin RD, Johnson NA, Severson TM, Mungall AJ, An J, Goya R, Paul JE, Boyle M, Woolcock BW, Kuchenbauer F, Yap D, Humphries RK, Griffith OL, Shah S, Zhu H, Kimbara M, Shashkin P, Charlot JF, Tcherpakov M, Corbett R, Tam A, Varhol R, Smailus D, Moksa M, Zhao YJ, Delaney A, Qian H, Birol I, Schein J, Moore R, Holt R, Horsman DE, Connors JM, Jones S, Aparicio S, Hirst M, Gascoyne RD, **Marra MA**. Somatic mutations altering EZH2 (Tyr641) in follicular and diffuse large B-cell lymphomas of germinal-center origin. ***Nat Genet***. 2010 Feb ;42(2):181-185. **(Commentary published in *Nat Genet*. 2010 Feb;42(2):100-101.)** PMID: 20081860

175. Vrljicak P, Chang A, Morozova O, Wederell E, Niessen K, **Marra M**, Karsan A, Hoodless P. Genomic Analysis Distinguishes Phases of Early Development of the Mouse Atrio-Ventricular Canal. ***Physiol Genomics***. 2010 Feb 4;40(3):150-157. PMID: 19952280

174. Starczynowski DT, Kuchenbauer F, Argiropoulos B, Sung S, Morin R, Muranyi A, Hirst M, Hogge D, **Marra M**, Wells RA, Buckstein R, Lam W, Humphries RK, Karsan A. Identification of miR-145 and miR-146a as mediators of the 5q- syndrome phenotype. ***Nat Med***. 2010 Jan;16(1):49-58. PMID: 19898489

173. Costello JF, Krzywinski M, **Marra MA**. A first look at the entire human methylomes. ***Nat Biotechnol.*** 2009 Dec;27(12):1130-1132. PMID: 20010593

172. The MGC Project Teams (Temple G et al). The Completion of the Mammalian Gene Collection (MGC). ***Genome Res***. 2009 Dec;19(12):2324-2333. PMID: 19767417

171. Biernaskie J, Paris M, Morozova O, Fagan BM, **Marra M**, Pevny L, Miller FD. SKPs derive from hair follicle precursors and exhibit properties of adult dermal stem cells. ***Cell Stem Cell***. 2009 Dec 4;5(6):610-623. PMID: 19951689

170. Lehman AM, Friedman JM, Zahir FH, Eydoux P, **Marra MA**, Prisman L, Tsang E, Armstrong L. A characteristic syndrome associated with microduplication of 8q12, inclusive of *CHD7*. ***Eur J Med Genet***. 2009 Nov-Dec;52(6):436-439. PMID: 19772954

169. Birol I, Jackman S, Nielsen C, Qian J, Varhol R, Stazyk G, Zhao YJ, Hirst M, Schein J, Horsman D, Connors J, Gascoyne R, **Marra M**, Jones S. De novo Transcriptome Assembly with AbySS. ***Bioinformatics.*** 2009 Nov 1;25(21):2872-2877. PMID: 19528083

168. Friedman JM, Adam S, Arbour L, Armstrong L, Baross A, Birch P, Boerkoel C, Chan S, Chai D, Delaney AD, Flibotte S, Gibson WT, Langlois S, Lemyre E, Li HI, MacLeod P, Mathers J, Michaud JL, McGillivray BC, Patel MS, Qian H, Rouleau GA, Van Allen MI, Yong S-L, Zahir FR, Eydoux P, **Marra MA.** Detection of pathogenic copy number variants in children with idiopathic intellectual disability using 500K SNP array genomic hybridization. ***BMC Genomics.*** 2009 Nov 16;10:526. PMID: 19917086

167. Romanuik TL, Wang G, Holt RA, Jones SJM, **Marra MA**, Sadar MD. Identification of novel androgen-responsive genes by deep sequencing of LongSAGE libraries. ***BMC Genomics***. 2009 Oct 15;10(1):476. PMID: 19832994

166. Morrissy AS, Morin RD, Delaney A, Zeng T, McDonald H, Zhao YJ, Hirst M, Jones S, **Marra MA**. Next generation tag sequencing for cancer gene expression profiling. ***Genome Res.*** 2009 Oct;19(10):1825-1835. PMID: 19541910

165. Shah SP, Morin R, Khattra J, Prentice L, Pugh T, Burleigh A, Delaney A, Gelmon K, Guliany R, Senz J, Steidl C, Holt RA, Jones S, Sun M, Leung G, Moore R, Severson T, Taylor G, Teschendorff AE, Tse K, Turashvili G, Varhol R, Warren RL, Watson P, Zhao YJ, Caldas C, Huntsman D, Hirst M, **Marra MA**, Aparicio S. Mutational evolution in a lobular breast tumour profiled at single nucleotide resolution. ***Nature***. 2009 Oct 8;461(7265):809-813. PMID: 19812674 **(Featured as Research Highlight in Nature Reviews Cancer 9, 770-771 (Nov 2009)**.

164. DiGuistini S, Liao NY, Platt D, Robertson G, Seidel M, Chan SK, Birol I, Holt RA, Hirst M, Mardis E, **Marra MA**, Hamelin RC, Bohlmann J, Breuil C, Jones SJM. De novo genome sequence assembly of a filamentous fungus using Sanger, 454 and Illumina sequence data. ***Genome Biol.*** 2009 Sep 11;10(9):R94. PMID: 19747388

163. Krzywinski M, Schein J, Birol I, Connors J, Gascoyne R, Horsman D, Jones SJ, **Marra M**. Circos: an Information Aesthetic for Comparative Genomics. ***Genome Res.*** 2009 Sep;19(9):1639-1645. PMID: 19541911

162. Halaschek-Wiener J, Amirabbasi-Beik M, Monfared N, Pieczyk M, Sailer C, Kollar A, Turnbull R, Agalaridis G, Yamada S, Oliveira L, Collins J, Meneilly G, **Marra MA**, Madden KM, Le ND, Connors JM, Brooks-Wilson AR. Genetic variation in healthy oldest-old. ***PloS One.*** 2009 Aug 14;4(8):e6641. PMID: 19680556

161. Morozova O, Hirst M, **Marra MA**. Applications of new sequencing technologies for transcriptome analysis. ***Annu Rev Genomics Hum Genet***. 2009;10:135-151. PMID: 19715439

160. Pugh TJ, Keyes M, Barclay L, Delaney A, Krzywinski M, Thomas D, Novik K, Yang C, Agranovich A, McKenzie M, Morris WJ, Olive PL, **Marra MA**, Moore RA. Sequence variant discovery in DNA repair genes from radiosensitive and radiotolerant prostate brachytherapy patients. ***Clin Cancer Res.*** 2009 Aug 1;15(15):5008-5016. PMID: 19638463

159. Tucker T, **Marra M**, Friedman JM. Massively Parallel Sequencing: The Next Big Thing in Genetic Medicine. ***Am J Hum Genet.*** 14 Aug 2009;85(2):142-154. (Review) PMID: 19679224

158. Friedländer MR, Adamidi C, Han T, Lebedeva S, Isenbarger TA, Hirst M, **Marra M**, Nusbaum C, Lee WL, Jenkin JC, Alvarado AS, Kim JK, Rajewsky N. High-resolution profiling and discovery of planarian small RNAs. ***Proc Natl Acad Sci U S A***. 2009 Jul 14;106(28):11546-11551. PMID: 19564616

157. Meissner B, Warner A, Wong K, Dube N, Lorch A, McKay SJ, Khattra J, Rogalski T, Somasiri A, Chaudhry I, Fox RM, Miller DM, Baillie DL, Holt RA, Jones SJM, **Marra MA**, Moerman DG. An integrated strategy to study muscle development and myofilament structure in *Caenorhabditis elegans*. ***PLoS Genet***. 2009 Jun;5(6):e1000537. PMID: 19557190

156. Shah S, Köbel M, Senz J, Morin RD, Clarke BA, Wiegand K, Leung G, Zayed A, Mehl E, Kalloger S, Sun M, Guiliany R, Yorida E, Jones S, Varhol R, Swenerton KD, Miller D, Clement PB, Crane C, Madore J, Provencher D, Leung P, DeFazio A, Khattra J, Turashvili G, Zhao YJ, Zeng T, Glover JNM, Vanderhyden B, Zhao C, Parkinson CA, Jimenez-Linan M, Mes-Masson AM, Brenton JD, Aparicio SA, Boyd N, Hirst M, Gilks CB, **Marra MA**, Huntsman DG. Mutation of the FOXL2 gene in granulosa cell tumors of the ovary. ***N Engl J Med***. 2009 Jun 25;360(26):2719-2729. PMID: 19516027

155. Kent DG, Copley MR, Benz C, Wöhrer S, Dykstra BJ, Ma E, Cheyne J, Zhao YJ, Bowie M, Zhao YJ, Gasparetto M, Delaney A, Smith C, **Marra M**, Eaves CJ. Prospective isolation and molecular characterization of hematopoietic stem cells with durable self-renewal potential. ***Blood***. 2009 Jun 18;113(25):6342-6350. PMID: 19377048

154. Zahir FR, Langlois S, Gall K, Eydoux P, **Marra MA**, Friedman JM. A novel de novo 1.1 Mb duplication of 17q21.33 associated with cognitive impairment and other anomalies. ***Am J Med Genet A***. 2009 Jun;149A(6):1257-1262. PMID: 19449402

153. Wang X, Zhao JY, Wong K, Ehlers P, Kohara Y, Jones SJ, **Marra MA**, Holt RA, Moerman DG, Hansen D. Identification of genes expressed in the hermaphrodite germ line of *C. elegans* using SAGE. ***BMC Genomics.*** 2009 May 9;10:213. PMID: 19426519

152. Bovine Genome Sequencing and Analysis Consortium, Elsik CG, Tellam RL, Worley KC, Gibbs RA, Muzny DM, Weinstock GM, Adelson DL, Eichler EE, Elnitski L, Guigó R, Hamernik DL, Kappes SM, Lewin HA, Lynn DJ, Nicholas FW, Reymond A, Rijnkels M, Skow LC, Zdobnov EM, Schook L, Womack J, Alioto T, Antonarakis SE, Astashyn A, Chapple CE, Chen HC, Chrast J, Câmara F, Ermolaeva O, Henrichsen CN, Hlavina W, Kapustin Y, Kiryutin B, Kitts P, Kokocinski F, Landrum M, Maglott D, Pruitt K, Sapojnikov V, Searle SM, Solovyev V, Souvorov A, Ucla C, Wyss C, Anzola JM, Gerlach D, Elhaik E, Graur D, Reese JT, Edgar RC, McEwan JC, Payne GM, Raison JM, Junier T, Kriventseva EV, Eyras E, Plass M, Donthu R, Larkin DM, Reecy J, Yang MQ, Chen L, Cheng Z, Chitko-McKown CG, Liu GE, Matukumalli LK, Song J, Zhu B, Bradley DG, Brinkman FS, Lau LP, Whiteside MD, Walker A, Wheeler TT, Casey T, German JB, Lemay DG, Maqbool NJ, Molenaar AJ, Seo S, Stothard P, Baldwin CL, Baxter R, Brinkmeyer-Langford CL, Brown WC, Childers CP, Connelley T,

Ellis SA, Fritz K, Glass EJ, Herzig CT, Iivanainen A, Lahmers KK, Bennett AK, Dickens CM, Gilbert JG, Hagen DE, Salih H, Aerts J, Caetano AR, Dalrymple B, Garcia JF, Gill CA, Hiendleder SG, Memili E, Spurlock D, Williams JL, Alexander L, Brownstein MJ, Guan L, Holt RA, Jones SJ, **Marra MA,** Moore R, Moore SS, Roberts A, Taniguchi M, Waterman RC, Chacko J, Chandrabose MM, Cree A, Dao MD, Dinh HH, Gabisi RA, Hines S, Hume J, Jhangiani SN, Joshi V, Kovar CL, Lewis LR, Liu YS, Lopez J, Morgan MB, Nguyen NB, Okwuonu GO, Ruiz SJ, Santibanez J, Wright RA, Buhay C, Ding Y, Dugan-Rocha S, Herdandez J, Holder M, Sabo A, Egan A, Goodell J, Wilczek-Boney K, Fowler GR, Hitchens ME, Lozado RJ, Moen C, Steffen D, Warren JT, Zhang J, Chiu R, Schein JE, Durbin KJ, Havlak P, Jiang H, Liu Y, Qin X, Ren Y, Shen Y, Song H, Bell SN, Davis C, Johnson AJ, Lee S, Nazareth LV, Patel BM, Pu LL, Vattathil S, Williams RL Jr, Curry S, Hamilton C, Sodergren E, Wheeler DA, Barris W, Bennett GL, Eggen A, Green RD, Harhay GP, Hobbs M, Jann O, Keele JW, Kent MP, Lien S, McKay SD, McWilliam S, Ratnakumar A, Schnabel RD, Smith T, Snelling WM, Sonstegard TS, Stone RT, Sugimoto Y, Takasuga A, Taylor JF, Van Tassell CP, Macneil MD, Abatepaulo AR, Abbey CA, Ahola V, Almeida IG, Amadio AF, Anatriello E, Bahadue SM, Biase FH, Boldt CR, Carroll JA, Carvalho WA, Cervelatti EP, Chacko E, Chapin JE, Cheng Y, Choi J, Colley AJ, de Campos TA, De Donato M, Santos IK, de Oliveira CJ, Deobald H, Devinoy E, Donohue KE, Dovc P, Eberlein A, Fitzsimmons CJ, Franzin AM, Garcia GR, Genini S, Gladney CJ, Grant JR, Greaser ML, Green JA, Hadsell DL, Hakimov HA, Halgren R, Harrow JL, Hart EA, Hastings N, Hernandez M, Hu ZL, Ingham A, Iso-Touru T, Jamis C, Jensen K, Kapetis D, Kerr T, Khalil SS, Khatib H, Kolbehdari D, Kumar CG, Kumar D, Leach R, Lee JC, Li C, Logan KM, Malinverni R, Marques E, Martin WF, Martins NF, Maruyama SR, Mazza R, McLean KL, Medrano JF, Moreno BT, Moré DD, Muntean CT, Nandakumar HP, Nogueira MF, Olsaker I, Pant SD, Panzitta F, Pastor RC, Poli MA, Poslusny N, Rachagani S, Ranganathan S, Razpet A, Riggs PK, Rincon G, Rodriguez-Osorio N, Rodriguez-Zas SL, Romero NE, Rosenwald A, Sando L, Schmutz SM, Shen L, Sherman L, Southey BR, Lutzow YS, Sweedler JV, Tammen I, Telugu BP, Urbanski JM, Utsunomiya YT, Verschoor CP, Waardenberg AJ, Wang Z, Ward R, Weikard R, Welsh TH Jr, White SN, Wilming LG, Wunderlich KR, Yang J, Zhao FQ. The Genome Sequence of Taurine Cattle: A window to ruminant biology and evolution. ***Science***. 2009 Apr 24;324(5926):522-528. PMID: 19390049

151. Hillier LH, Reinke V, Green P, Hirst M, **Marra MA**, Waterston RH. Massively parallel sequencing of the poly-adenylated transcriptome of *C. elegans.* ***Genome Res.*** 2009 Apr;19(4):657-666. PMID: 19181841

150. McGhee JD, Fukushige T, Krause MW, Minnema SE, Goszczynski B, Gaudet J, Kohara Y, Bossinger O, Zhao Y, Khattra J, Hirst M, Jones SJ, **Marra MA**, Ruzanov P, Warner A, Zapf R, Moerman DG, Kalb JM. ELT-2 is the predominant transcription factor controlling differentiation and function of the *C. elegans* intestine, from embryo to adult. ***Dev Biol.*** 2009 Mar 15;327(2):551-565. PMID: 19111532

149. Hirst M and **Marra MA**. Epigenetics and Human Disease. ***Int J Biochem Cell Biol.*** 2009 Jan;41(1):136-146. (Review) PMID: 18852064

148. Robertson AG, Bilenky M, Tam A, Zhao YJ, Zeng T, Thiessen N, Cezard T, Fejes AP, Wederell ED, Cullum R, Euskirchen G, Krzywinski M, Birol I, Snyder M, Hoodless PA, Hirst M, **Marra MA**, Jones SJM. (first two are first co-authors) Genome wide relationship between histone H3 lysine 4 mono-methylation and transcription factor binding. ***Genome Res.*** 2008 Dec;18(12):1906-1917. PMID: 18787082

147. <u>Morozova O</u> and **Marra MA**. Applications of next-generation sequencing technologies in functional genomics. ***Genomics.*** 2008 Nov;92(5):255-264. (Review) **(#1 most downloaded article from Genomics for 2008).** PMID: 18703132

146. Kuchenbauer F, <u>Morin RD</u>, Argiropoulos B, Petriv OI, <u>Griffith M</u>, Heuser M, Yung E, Piper J, Delaney A, Prabhu A-L, Zhao YJ, McDonald H, Zeng T, Hirst M, Hansen CL, **Marra MA**, Humphries RK. In depth characterization of the microRNA transcriptome in a leukemia progression model. ***Genome Res.*** 2008 Nov;18(11):1787-1797. PMID: 18849523

145. Salvagiotto G, Zhao Y, Vodyanik M, Ruotti V, Stewart R, **Marra M**, Thomson J, Eaves C, and Slukvin I. Molecular profiling reveals similarities and differences between primitive subsets of hematopoietic cells generated in vitro from human embryonic stem cells and in vivo during embryogenesis. ***Exp Hematol.*** 2008 Oct;36(10):1377-1389. PMID: 18922365

144. Ralph SG, Chun H-J, Kolosova N, Cooper D, Oddy C, Ritland CE, Kirkpatrick R, Moore R, Barber S, Holt RA, Jones SJM, **Marra MA**, Douglas CJ, Ritland K, Bohlmann J. A conifer genomics resource of 200,000 spruce (*Picea spp.*) ESTs and 6,464 high-quality, sequence-finished full-length cDNAs for Sitka spruce (*Picea sitchensis*). ***BMC Genomics.*** 2008 Oct 14;9(1):484. PMID: 18854048

143. Morozova O, Morozov V, Hoffman B, Helgason CD, **Marra MA**. A Seriation Approach for Visualization-Driven Discovery of Co-Expression Patterns in Serial Analysis of Gene Expression (SAGE) Data. ***PLoS ONE***. 2008 Sep 12;3(9): e3205. PMID: 18787709

142. Pugh TJ, Delaney AD, Farnoud N, Flibotte S, Griffith M, Li I, Qian H, Farinha P, Gascoyne RD, **Marra MA**. Impact of Whole Genome Amplification on Analysis of Copy Number Variants. ***Nucleic Acids Res.*** 2008 Aug;36(13):e80. PMID: 18559357

141. Wederell ED, Bilenky M, Cullum R, Thiessen N, Dagpinar M, Delaney A, Varhol R, Zhao YJ, Zeng T, Bernier B, Ingham M, Hirst M, Robertson G, **Marra MA**, Jones S, Hoodless PA. Global Analysis of *In Vivo* FoxA2 Binding Sites in Mouse Adult Liver Using Massively Parallel Sequencing. ***Nucleic Acids Res.*** 2008 Aug;36(14):4549-4564. PMID: 18611952

140. D'Souza CA, Chopra V, Varhol R, Xie Y, Bohacec S, Zhao Y, Lee LLC, Bilenky M, Portales-Casamar E, He A, Wasserman WW, Goldowitz D, **Marra MA,** Holt RA, Simpson EM, Jones SJM. Identification of a set of genes showing regionally enriched expression in the mouse brain. ***BMC Neurosci.*** 2008 Jul 14;9(1):66. PMID: 18625066

139. Shin H, Hirst M, Bainbridge M, Magrini V, Mardis E, Moerman DG, **Marra MA**, Baillie DL, Jones SJM. Transcriptome Analysis for *Caenorhabditis elegans* based on Novel Expressed Sequence Tags (ESTs). ***BMC Biol.*** 2008 Jul 8;6(1):30. PMID: 18611272

138. Morin RD, Bainbridge M, Fejes A, Hirst M, Krzywinski M, Pugh TJ, McDonald H, Varhol R, Jones SJM, **Marra MA.** (first 2 are first co-authors) Profiling the HeLa S3 transcriptome using randomly primed cDNA and massively parallel short-read sequencing. ***BioTechniques.*** 2008 Jul; 45(1): 81-94. PubMed PMID: 18611170

137. Raouf A, Zhao Y, To K, Stingl HJ, Delaney A, Barbara M, Iscove N, Jones S, McKinney S, Emerman J, Aparicio S, **Marra M**, Eaves C. Transcriptome analysis of the normal human mammary cell commitment and differentiation process. ***Cell Stem Cell.*** 2008 Jul 3;3(1):109-118. PMID: 18593563

136. Hoffman BG, Zavaglia B, Witzsche J, Ruiz de Algara T, Hoodless PA, Jones S, **Marra MA**, Helgason CD. Identification of transcripts with enriched expression in the developing and adult pancreas. ***Genome Biol.*** 2008 Jun 14;9(6):R99. PMID: 18554416

135. Morozova O and Marra MA. From cytogenetics to next-generation sequencing technologies: advances in the detection of genome rearrangements in tumors. ***Biochem Cell Biol.*** 2008 Apr; 86(2): 81-91. (Review) PMID: 18443621

134. Zahir F, Baross A, Delaney AD, Eydoux P, Fernandez ND, **Marra M**, Friedman JM. A patient with vertebral, cognitive and behavioural abnormalities and a *de novo* deletion of *NRXN1a*. ***J Med Genet.*** 2008 Apr;45(4):239-243. PMID: 18057082

133. Morin RD, O'Connor MD, Griffith M, Kuchenbauer F, Delaney A, Prabhu A-L, Zhao YJ, McDonald H, Zeng T, Hirst M, Eaves CJ, **Marra MA**. Application of massively parallel sequencing to microRNA profiling and discovery in human embryonic stem cells. ***Genome Res.*** 2008 Apr;18(4):610-621. PMID: 18285502

132. Griffith M. Tang MJ, Griffith OL, Chan SY, Asano JK, Zeng T, Flibotte S, Ally A, Baross A, Morin RD, Hirst M, Jones SJM, Morin GB, Tai IT. **Marra M**. ALEXA – A microarray design platform for alternative expression analysis. ***Nat Methods.*** 2008 Feb; 5(2):118. PMID: 18235430

131. Ralph SG, Chun HJE, Cooper D, Kirkpatrick R, Kolosova N, Gunter L, Tuskan GA, Douglas CJ, Holt RA, Jones SJM, **Marra MA**, Bohlmann J. Analysis of 4, 664 high-quality sequence-finished poplar full-length cDNA clones and their utility for the discovery of genes responding to insect feeding. ***BMC Genomics.*** 2008 Jan 29;9(1):57. PMID: 18230180

130. Kneller JM, Ehlen T, Matisic JP, Miller D, Van Niekerk D, Lam WL, **Marra M**, Richards-Kortum R, Follen M, MacAulay C, Jones SJM. Using longSAGE to detect biomarkers of cervical cancer potentially amenable to optical contrast agent labeling. ***Biomedical Insights*** 2007:2 447-461. PMID: 19662225

129. Peng FY, Reid KE, Liao N, Schlosser J, Lijavetzky D, Holt R, Martínez Zapater JM, Jones S, **Marra M**, Bohlmann J, Lund ST. Generation of ESTs in *Vitis vinifera* wine grape (Cabernet Sauvignon) and table Grape (Muscat Hamburg) and discovery of new candidate genes with possible roles in berry development. ***Gene.*** 2007 Nov 1;402(1-2):40-50. PMID: 17761391

128. Krzywinski M, Bosdet I, Mathewson C, Wye N, Brebner J, Chiu R, Corbett R, Field M, Lee D, Pugh T, Volik S, Siddiqui A, Jones S, Schein J, Collins C, **Marra MA**. A BAC clone fingerprinting approach to the detection of human genome rearrangements. ***Genome Biol.*** 2007 Oct 22;8(10):R224. PMID: 17953769

127. Baross A, Delaney AD, Li HI, Nayar T, Flibotte S, Qian H, Chan SY, Asano J, Ally A, Cao M, Birch P, Brown-John M, Fernandes N, Go A, Kennedy G, Langlois S, Eydoux P, Friedman JM, **Marra MA**. Assessment of algorithms for high throughput detection of genomic copy number variation in oligonucleotide microarray data. ***BMC Bioinformatics.*** 2007 Oct 2;8(1):368. PMID: 17910767

126. Huang P, Pleasance ED, Maydan JS, Hunt-Newbury R, O’Neil NJ, Mah A, Baillie DL, **Marra MA**, Moerman DG, Jones SJ. Identification and analysis of internal promoters in *Caenorhabditis elegans* operons. ***Genome Res*.** 2007 Oct;17(10):1478-1485. PMID: 17712020

125. Stratford AL, Habibi G, Astanehe A, Jiang H, Hu K, Park E, Shadeo A, Buys TP, Lam W, Pugh T, **Marra M**, Nielsen TO, Klinge U, Mertens PR, Aparicio S, Dunn SE. Epidermal growth factor receptor (EGFR) is transcriptionally induced by the Y-box binding protein-1 (YB-1) and can be inhibited with Iressa in basal-like breast cancer providing a potential target for therapy. ***Breast Cancer Res.*** 2007 Sep 17;9(5):R61. PMID: 17875215

124. Hunt-Newbury R, Viveiros R, Johnsen R, Mah A, Anastis D, Fang L, Halfnight E, Lee D, Lin J, Lorch A, Mckay S, Okada HM, Pan J, Shultz AK, Tu D, Wong K, Zhao Z, Alexeyenko A, Burglin T, Sonnhammer E, Schnabel R, Jones SJ, **Marra MA**, Baillie DL, Moerman DG. High Throughput In Vivo Analysis of Gene Expression in *C. Elegans*. ***PloS Biology***. 2007 Sep;5(9):e237. PMID: 17850180

123. Zahir F, Firth HV, Baross A, Delaney AD, Eydoux P, Gibson WT, Langlois S, Martin H, Willat L, **Marra M**, Friedman JM. Novel deletions of 14q11.2 associated with developmental delay, cognitive impairment and similar minor anomalies in three children. ***J Med Genet.*** 2007 Sep;44(9):556-561. PMID: 17545556

122. Snelling WM, Chiu R, Schein JE, Hobbs M, Abbey CA, Adelson DL, Bennett GL, Bosdet IE, Boussaha M, Brauning R, Caetano AR, Costa MM, Crawford AM, Dalrymple BP, Eggen A, Everts-van der Wind A, Floriot S, Gautier M, Gill CA, Green RD, Holt R, Jones SJM, Kappes SM, Keele JW, de Jong PJ, Larkin DM, Lewin HA, McEwan JC, McKay S, McWilliam S, **Marra MA**, Mathewson CA, Matukumalli LK, Moore SS, Murdoch B, Nicholas F, Osoegawa K, Roy A, Salih H, Schibler L, Schnabel R, Silveri L, Skow LC, Smith TPL, Sonstegard TS, Taylor J, Tellam R, Van Tassell CP, Williams JL, Womack JE, Wye NH, Yang G, Zhao S. A physical map of the bovine genome. ***Genome Biol.*** 2007 Aug 14;8(8):R165. PMID: 17697342

121. Hou J, Charters AM, Lee SC, Zhao Y, Wu MK, Jones SJM, **Marra MA**, Hoodless PA. A systematic screen for genes expressed in definitive endoderm by Serial Analysis of Gene Expression (SAGE). ***BMC Dev. Biol.*** 2007 Aug 2;7(1):92. PMID: 17683524

120. Ruzanov P, Riddle DL, **Marra MA**, McKay SJ, Jones SM. Genes that may modulate longevity in *C. elegans* in both dauer larvae and long-lived *daf-2* adults. ***Exp Gerontol.*** 2007 Aug;42(8):825-839. PMID: 17543485

119. Robertson G, Hirst M, Bainbridge M, Bilenky M, Zhao YJ, Zeng T, Euskirchen G, Bernier B, Varhol R, Delaney A, Thiessen N, Griffith OL, He A, **Marra M**, Snyder M, Jones S. Genome-wide profiles of STAT1 DNA association using chromatin immunoprecipitation and massively parallel sequencing. ***Nat Methods.*** 2007 Aug;4(8):651-657. PMID: 17558387

118. Pugh TJ, Bebb G, Barclay L, Sutcliffe M, Fee J, Salski C, O'Connor R, Ho C, Murray N, Melosky B, English J, Vielkind J, Horsman D, Laskin JJ, **Marra MA.** Correlations of EGFR mutations and increases in EGFR and HER2 copy number to gefitinib response in a retrospective analysis of lung cancer patients. ***BMC Cancer.*** 2007 Jul 13;7(1):128. PMID: 17626639

117. Etchberger JF, Lorch A, Sleumer M, Zapf R, Jones SJ, **Marra MA**, Holt RA, Moerman DG, Hobert O. The molecular signature and *cis*-regulatory architecture of a *C. elegans* gustatory neuron. ***Genes Dev.*** 2007 Jul 1; 21(13): 1653-1674. PMID: 17606643

116. Hu G, Linning R, Joseph C, McCallum B, Banks T, Cloutier S, Butterfield Y, Liu J, Kirkpatrick R, Stott J, Yang G, Smailus D, Jones S, **Marra M**, Schein J, Bakkeren G. Generation of a wheat leaf rust, *Puccinia triticina*, EST database from stage-specific cDNA libraries. ***Mol Plant Pathol.*** 2007 Jul;8(4):451-467. PMID: 20507513

115. Zhao Y, Raouf A, Kent D, Khattra J, Delaney A, Schnerch A, Asano J, MacDonald H, Chan C, Jones S, **Marra MA**, Eaves CJ. A modified polymerase chain reaction-long serial analysis of gene expression protocol identifies novel novel transcripts in human CD34+ bone marrow cells. ***Stem Cells.*** 2007 Jul;25(7):1681-1689. PMID: 17412892

114. Hirst M, Delaney A, Rogers SA, Schnerch A, Persaud DR, O'Connor MD, Zeng T, Moksa M, Fichter K, Mah D, Go A, Morin RD, Baross A, Zhao YJ, Khattra J, Prabhu A-L, Pandoh P, McDonald H, Asano J, Dhalla N, Ma K, Lee S, Ally A, Chahal N, Menzies S, Siddiqui A, Holt R, Jones S, Gerhard DS, Thomson JA, Eaves CJ, **Marra MA.** LongSAGE profiling of 9 human embryonic stem cell lines**. *Genome Biol.*** 2007 Jun 14;8(6):R113. PMID: 17570852

113. Margulies EH, Coope GM, Asimenos G, Thomas DJ, Dewey CN, Siepe A, Birney E, Keepe D, Schwart AS, Hou M, Taylot J, Nikolaev S, Montoya-Burgos JI, Loytynoja A, Whelan S, Pardi F, Massingham T, Brown JB, Bickel P, Holmes I, Mullikin JC, Ureta-Vidal A, Paten B, Schuler G, Church D, Rosenbloom KR, Kent J, NISC Comparative Sequencing Program, Baylor College of Medicine Human Genome Sequencing Center, Washington University Genome Sequencing Center, Broad Institute. UCSC Genome Browser Team, British Columbia Cancer Agency Genome Sciences Centre (Field MA, Moore RA, Mathewson CA, Schein JE, and **Marra MA**), et al. Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. ***Genome Res.*** 2007 Jun;17(6):760-774. PMID: 17567995

112. Kelleher CT, Chiu R. Shin H, Bosdet IE, Krzywinski MI, Fjell CD, Wilkin J, Yin TM, DiFazio SP, Ali J, Asano JK, Chan S, Cloutier A, Girn N, Leach S, Lee D, Mathewson CA, Olson T, O'Connor K, Pradhu A-L, Smailus DE, Stott JM, Tsai M, Wye NH, Yang GS, Zhuang J, Holt RA, Putnam NH, Vrebalov J, Giovannoni JJ, Grimwood J, Schmutz J, Rokhsar D, Jones SJM, **Marra MA**, Tuskan GA, Bohlmann J, Ellis BE, Ritland K, Douglas CJ, Schein JE. A physical map of the highly *heterozygous Populus* genome: integration with the genome sequence and genetic map and analysis of haplotype variation. ***Plant J.*** 2007 Jun;50(6):1063-1078. PMID: 17488239

111. Mikkelsen TS, Wakefield MJ, Aken B, Amemiya CT, Chang JL, Duke S, Garber M, Gentles AJ, Goodstadt L, Heger A, Jurka J, Kamal M, Mauceli E, Searle SMJ, Sharpe T, Baker ML, Batzer MA, Benos PV, Belov K, Clamp M, Cook A, Cuff J, Das R, Davidow L, Deakin JE, Fazzari MJ, Glass JL, Grabherr M, Greally JM, Gu W, Hore TA, Huttley GA, Kleber M, Jirtle RL, Koina E, Lee JT, Mahony S, **Marra MA**, Miller RD, Nicholls RD, Oda M, Papenfuss AT, Parra ZE, Pollock DD, Ray DA, Schein JE, Speed TP, Thompson K, VandeBerg JL, Wade CM, Walker JA, Waters PD, Webber C, Weidman JR, Xie X, Zody MC, Broad Institute Genome Sequencing Platform and Broad Institute Whole Genome Assembly Team and , Marshall Graves JA, Ponting CP, Breen M, Samollow PB, Lander ES, and Lindblad-Toh K. Genome of the marsupial *Monodelphis domestica* reveals innovation in non-coding sequences. ***Nature.*** 2007 May 10;447(7141):167-177. PMID: 17495919

110. Rhesus Macaque Genome Sequencing and Analysis Consortium (Gibbs RA et al). Evolutionary and biomedical insights from the rhesus macaque genome. ***Science***. 2007 Apr 13;316(5822):222-234. PMID: 17431167

109. Menten B, Buysse K, Zahir F, Hellemans J, Hamilton SJ, Costa T, Fagerstrom C, Anadiotis G, Kingsbury D, McGillivray BC, **Marra MA**, Friedman JM, Speleman F, Mortier G. Osteopoikilosis, short stature and mental retardation as key features of a new microdeletion syndrome on 12q14. ***J Med Genet.*** 2007 Apr;44(4):264-268. PMID: 17220210

108. McGhee JD. Sleumer MC, Bilenky M, Wong K, McKay SJ, Goszczynski B, Tian H, Krich ND, Khattra J, Holt RA, Baillie DL, Kohara Y, **Marra MA,** Jones SJM, Moerman DG, Robertson AG. The ELT-2 GATA-factor and the global regulation of transcription in the *C. elegans* intestine. ***Develop Biol.*** 2007 Feb 15; 302(2): 627-645. PMID: 17113066

107. Quayle SN, Heidi H, Delaney AD, Hirst M, Hwang D, Schein JE, Jones SJM, **Marra MA**, Sadar MD. Novel expressed sequences identified in a model of androgen independent prostate cancer. ***BMC Genomics.*** 2007 Jan 26;8:32. PMID: 17257419

106. Robertson N, Oveisi-Fordorei M, Zuyderduyn S, Varhol R, Fjell C, **Marra MA**, Jones SJM, Siddiqui AS. DiscoverySpace: an interactive data analysis application. ***Genome Biol.*** 2007 Jan 8;8(1):R6. PMID: 17210078

105. Khattra J, Delaney AD, Zhao YJ, Siddiqui A, Hirst M, Asano J, McDonald H, Pandoh P, Dhalla N, Prabhu A, Ma K, Lee S, Ally A, Tam A, Sa D, Rogers S, Charest D, Stott J, Zuyderduyn S, Varhol R, Jones S, Holt R, Hoodless P, **Marra MA**. Large scale production of SAGE libraries from microdissected tissues, flow-sorted cells and cell lines. ***Genome Res.*** 2007 Jan; 17(1) 108-116. PMID: 17135571

104. Chen N, Mah A, Blacque OE, Chu J, Phgora K, Bakhoum MW, Newbury CRH, Khattra J, Chan S, Go A, Efimenko E, Johnsen R, Phirke P, Swoboda P, **Marra M**, Moerman DG, Leroux MR, Baillie DL, Stein LD. Identification of ciliary and ciliopathy genes in *Caenorhabditis elegans* through comparative genomics. ***Genome Biol.*** 2006 Dec 22;7(12):R126. PMID: 17187676

103. Lonergan KM, Chari R, deLeeuw RJ, Shadeo A, Chi B, Tsao M-S, Jones S, **Marra M**, Ling V, Ng R, MacAulay C, Lam S, Lam WL. Identification of Novel Lung Genes in Bronchial Epithelium by Serial Analysis of Gene Expression. ***Am J Respir Cell Mol Biol.*** 2006 Dec;35(6):651-661. PMID: 16809635

102. Sea Urchin Genome Sequencing Consortium (Sodergren E et al) . The Genome of the Sea Urchin *Strongylocentrotus purpuratus*. ***Science.*** 10 Nov 2006; 314(5801):941-952. PMID: 17095691

101. Wang G, Jones SJM, **Marra MA**, Sadar MD. Identification of genes targeted by the androgen and PKA signaling pathways in prostate cancer cells. ***Oncogene.*** 2006 Nov 5;7311-7323. PMID: 16751804

100. McLeod MP, Warren RL, Hsiao WWL, Araki N, Myhre M, Fernandes C, Miyazawa D, Wong W, Lillquist AL, Wang D, Dosanjh M, Hara H, Petrescu A, Morin RD, Yang G, Stott JM, Schein JE. Shin H, Smailus D, Siddiqui AS, **Marra MA**, Jones SJM, Holt R, Brinkman FSL, Miyauchi K, Fukuda M, Davies

JE, Mohn WW, Eltis LD. The complete genome of *Rhodococcus* sp. RHA1: insights into a catabolic powerhouse. ***Proc Natl Acad Sci USA***. 2006 Oct 17;103(42):15582-15587. PMID: 17030794

99. Bainbridge M, Warren R, Hirst M, Romanuik T, Zeng T, Go A, Delaney A, Griffith M, Hickenbotham M, Magrini V, Mardis E, Sadar M, Siddiqui A, **Marra M**, Jones S. Analysis of the prostate cancer cell line LNCaP transcriptome using a sequencing-by-synthesis approach. ***BMC Genomics.*** 2006 Sep 29;7:246. PMID: 17010196

98. Tuskan GA, DiFazio SP, Hessten U, Jansson S, Rombauts S, Putnam N, Sterck L, Bohlmann J, Schein J, Ralph S, Aets A, Bhalerao R, Bhalerao P, Blaudez D, 85 other authors, **Marra M**, Sandberg G, Van de Peer Y, Rokhsar D. The genome of black cottonwood, *Populus trichocarpa* (Torr. & Gray). ***Science.*** 2006 Sep 15;313(5793):1596-1604. PMID: 16973872

97. Friedman JM, Baross A, Delaney AD, Ally A, Arbour L, Asano J, Bailey DK, Barber S, Birch P, Brown-John M, Cao M, Chan S, Charest DL, Farnoud N, Fernandes N, Flibotte S, Go A, Gibson WT, Holt RA, Jones SJM, Kennedy GC, Krzywinski M, Langlois S, Li HI, McGillivray BC, Nayar T, Pugh TJ, Rajcan-Separovic E, Schein JE, Schnerch A, Siddiqui A, Van Allen MI, Wilson G, Yong SL, Eydoux P, **Marra MA**. Oligonucleotide microarray analysis of genomic imbalance in children with mental retardation. ***Am J Hum Genet.*** 2006 Sep;79(3):500-513. PMID: 16909388

96. Bakkeren G, Jiang G, Warren R, Butterfield Y, Shin H, Chiu R, Linning R, Schein J, Lee N, Hu G, Kupfer DM, Tang Y, Roe BA, Jones S, **Marra M**, Kronstad JW. Mating factor linkage and genome evolution in basidiomycetous pathogens of cereals. ***Fungal Genet Biol***. 2006 Sep;43(9):655-666. PMID: 16793293

95. Ralph SG, Yueh H, Friedmann M, Aeschliman D, Zeznik JA, Nelson CC, Butterfield YSN, Kirkpatrick R, Liu J, Jones SJM, **Marra MA**, Douglas CJ, Ritland K, Bohlmann J. Conifer defense against insects: microarray gene expression profiling of Sitka spruce (*Picea sitchensis*) induced by mechanical wounding or feeding by spruce budworms (*Choristoneura occidentalis*) or white pine weevils (*Pissodes strobi*) reveals large-scale changes of the host transcriptome. ***Plant Cell Environ.*** 2006 Aug;29(8): 1545-1570. PMID: 16898017

94. Siddiqui AS, Delaney AD, Schnerch A, Griffith OL, Jones SJM, **Marra MA.** Sequence biases in large scale gene expression profiling data. ***Nucleic Acids Res.*** 2006 Jul 13;34(12):e83. PMID: 16840527

93. Morin RD, Chang E, Petrescu A, Liao N, Griffith M, Chow W, Kirkpatrick R, Butterfield YS, Young AC, Stott J, Barber S, Babakaiff R, Dickson MC, Matsuo C, Wong D, Yang GS, Smailus DE, Wetherby KD, Kwong PN, Grimwood J, Brinkley CP 3rd, Brown-John M, Reddix-Dugue ND, Mayo M, Schmutz J, Beland J, Park M, Gibson S, Olson T, Bouffard GG, Tsai M, Featherstone R, Chand S, Siddiqui AS, Jang M, Lee E, Klein SL, Blakesley RW, Zeeberg BR, Narasimhan, Weinstein JN, Pennacchio CP, Myers RM, Green ED, Wagner L, Gerhard DS, **Marra MA**, Jones SJ, Holt RA. Sequencing and analysis of 10,967 full-length cDNA clones from *Xenopus laevis* and *Xenopus tropicalis* reveals post-tetraploidization transcriptome remodeling. ***Genome Res***. 2006 Jun;16(6):796-803. PMID: 16672307

92. Warren RL, Varabei D, Platt D, Huang X, Messina D, Yang S-P, Kronstad JW, Krzywinski M, Warren WC, Wallis JW, Hillier LW, Chinwalla AT, Schein JE, Siddiqui AS, **Marra MA**, Wilson RK, Jones SJM. Physical map-assisted whole-genome shotgun sequence assemblies. ***Genome Res***. 2006 Jun;16(6):768-775. PMID: 16741162

91. Ralph S, Oddy C, Cooper D, Yueh H, Jancsik S, Kolosova N, Philippe RN, Aeschliman D, White R, Huber D, Ritland CE, Benoit F, Rigby T, Nantel A, Butterfield YSN, Kirkpatrick R, Chun E, Liu J, Palmquist D, Wynhoven B, Stott J, Yang G, Barber S, Holt RA, Siddiqui A, Jones SJM, **Marra MA**, Ellis BE, Douglas CJ, Ritland K, Bohlmann J. Genomics of hybrid poplar *(Populus trichocarpa x deltoids*) interacting with forest tent caterpillars (*Malacosoma disstria*): normalized and full-length cDNA libraries, expressed sequence tags (ESTs), and a cDNA microarray for the study of insect-induced defenses in poplar. ***Mol Ecol***. 2006 Apr; 15(5):1275-1297. PMID: 16626454

90. Wilson GE, Flibotte S, Missirlis PI, **Marra MA**, Jones S, Thornton K, Clark AG, Holt RA. Identification by full coverage array CGH of human DNA copy number increases relative to chimpanzee and gorilla. ***Genome Res***. 2006 Feb;16(2):173-181. PMID: 16365383

89. Siddiqui AS, Khattra J, Delaney AD, Zhao YJ, Astell C, Asano J, Babakaiff R, Barber S, Beland J, Bohacec S, Brown-John M, Chand S, Charters AM, Cullum R, Dhalla N, Featherstone R, Gerhard DS, Hoffman B, Holt R, Hou J, Kuo BY-L, Lee LLC, Lee S, Leung D, Ma K, Matsuo C, Mayo M, McDonald H, Pradhu A, Pandoh P, Riggins GJ, de Algara TR, Rupert JL, Smailus D, Stott J, Tsai M, Varhol R, Vrljicak P, Wong D, Wu MK, Xie Y-Y, Yang G, Zhang I, Hirst M, Jones SJM, Helgason CD, Simpson EM, Hoodless PA, **Marra MA**. A mouse atlas of gene expression: Large-scale digital gene expression profiles from precisely defined developing C57BL/6J mouse tissues and cells. ***Proc Natl Acad Sci USA.*** 2005 Dec 20;102(51):18485-18490. PMID: 16352711

88. Everts-van der Wind A, Larkin DM, Green CA, Elliott JS, Olmstead CA, Chiu R, Schein JE, **Marra MA**, Womack JE, Lewin HA. A high-resolution whole-genome cattle-human comparative map reveals new details of mammalian chromosome evolution. ***Proc Natl Acad Sci USA.*** 2005 Dec 20;102(51):18526-18531. PMID: 16339895

87. Larraya LM, Boyce K, So A, Steen BR, Jones S, **Marra M**, Kronstad J. Serial Analysis of Gene Expression Reveals Conserved Links Between Protein Kinase A, Ribosome Biogenesis and Phosphate Metabolism in Ustilago maydis. ***Eukaryot Cell***. 2005 Dec;4(12):2029-2043. PMID: 16339721

86. Pavy N, Paule C, Parsons L, Crow JA, Morency M-J, Cooke J, Johnson JE, Noumen E, Guillet-Claude C, Butterfield Y, Barber S, Yang G, Liu J, Stott J, Kirkpatrick R, Siddiqui A, Holt R, **Marra M**, Seguin A, Retzel E, Bousquet J, MacKay J. Generation, annotation, analysis and database integration of 16,500 white spruce EST clusters. ***BMC Genomics***. 2005 Oct 19;6:144. PMID: 16236172

85. Smailus DE, Marziali A, Dextras P, **Marra MA**, Holt RA. Simple, robust methods for high-throughput nanoliter-scale DNA sequencing. ***Genome Res.*** 2005 Oct;15:1447-1450. PMID: 16169928

84. Ng SHS, Artieri CG, Bosdet IE, Chiu R, Danzmann RG, Davidson WS, Ferguson MM, Fjell CD, Hoyheim B, Jones SJM, de Jong PJ, Koop BF, Krzywinski MI, Lubieniecki K, **Marra MA,** Mitchell LA, Mathewson C, Osoegawa K, Parisotto SE, Phillips RB, Rise ML, von Schalburg KR, Schein JE, Shin H, Siddiqui A, Thorsen J, Wye N, Yang G, Zhu B. A physical map of the genome of Atlantic salmon, *Salmo salar*. ***Genomics.*** 2005 Oct;86(4):396-404. PMID: 16026963

83. Ivens AC, Peacock C, 50 other authors, **Marra M** et al. The Genome of the Kinetoplastid parasite, *Leishmania major*. ***Science***. 2005 Jul 15;309(5733):436-442. PMID: 16020728

82. Halaschek-Wiener J, Khattra JS, McKay S, Pouzyrev A, Stott JM, Yang GS, Holt RA, Jones SJM, **Marra MA,** Brooks-Wilson AR, Riddle DL. Analysis of Long-lived *C. elegans* daf-2 Mutants using Serial Analysis of Gene Expression. ***Genome Res***. 2005 May;15(5):603-615. PMID: 15837805

81. Blacque OE, Boroevich KA, Inglis PN, Li C, Warner A, Khattra J, Holt RA, Mah AK, McKay SJ, Huang P, Swoboda P, Jones SJM, **Marra MA**, Baillie DL, Moerman DG, Shaham S, Leroux MR. Functional Genomics of the *Cilium*, A Sensory Organelle. ***Curr Biol***. 2005 May 24;15(10):935-941. PMID: 15916950

80. Warren RL, Butterfield YS, Morin RD, Siddiqui AS, **Marra, MA**, Jones SJM. Management and Visualization of Whole Genome Shotgun Assemblies using SAM. ***Biotechiques.*** May 2005;38(5):715-716, 718, 720. PMID: 15945370

79. Hillier LW, Graves TA, 110 other authors, **Marra MA**, Ovcharenko I, Furey TS, Miller W, Eichler EE, Bork P, Suyama M, Torrents D, Waterston RH, Wilson RK. Generation and annotation of the DNA sequences of human chromosomes 2 and 4. ***Nature***. 2005 Apr 7;434(7034):724-731. PMID: 15815621

78. Lian T, Simmer MD, D'Souza CA, Steen BR, Zuyderduyn SD, Jones SJ, **Marra MA,** Kronstad, JW. Iron-regulated transcription and capsule formation in the fungal pathogen *Cryptococcus neoformans*. ***Mol Microbiol*.** 2005;55(5):1452-1472. PMID: 15720553

77. Loftus B, Fung E, Roncaglia P, Rowley D, Amedeo P, Bruno D, Vamethevan J, Miranda M, Anderson I, Fraser JA, Allen J, Bosdet I, Brent MR, Chiu R, Doering TL, Donlin, MJ, D'Souza C. Fox DS, Grinberg V, Fu J, Fukushima M, Haas B, Huang JC, Janbon G, Jones S, Krzywinski MI, Kwon-Chung J, Lengeler KB, Maiti R, **Marra M**, Marra RE, Mathewson C, Mitchell TG, Pertea M, Riggs F, Salzberg SL, Schein J, Shvartsbeyn, Shin H, Specht C, Suh B, Tenny A, Utterback T, Wickes BL, Wye N, Kronstad JW, Lodge JK, Heitman J, Davis RW, Fraser CW, Hyman RW. The Genome of the Basidiomycetous Yeast and Human Pathogen *Cryptococcus neoformans*. ***Science.*** 2005 Feb 25;307(5713):1321-1324**.** PMID: 15653466

76. Yang GS, Stott JM, Smailus D, Barber SA, Balasundaram M, **Marra MA,** Holt RA. High-throughput Sequencing: A Failure Mode Analysis. ***BMC Genomics*.** 2005 Jan 4;6(1):2. PMID: 15631628

75. Hirst M, Astell C, Griffith M, Coughlin SM, Moksa M, Zeng T, Smailus DE, Holt RA, Jones S, **Marra MA,** Petric M, Krajden M, Lawrence D, Mak A, Chow R, Skowronski DM, Tweed A, Goh S, Brunham RC, Robinson J, Bowes V, Sojonky K, Byrne SK, Paetzel M. A novel avian influenza H7N3 strain associated with an Avian Influenza Outbreak in British Columbia. ***Emerg Infect Dis***. 2004 Dec;10(12):2192-2195. PMID: 15663859

74. Warren R, Hsiao WWL, Kudo H, Myhre M, Dosanjh M, Petrescu A, Kobayashi H, Shimizu S, Miyauchi K, Masai E, Yang G, Stott JM, Schein JE, Shin H, Khattra J, Smailus D, Butterfield YS, Siddiqui A, Holt R, **Marra MA**, Jones S, Mohn WW, Brinkman FSL, Fukuda M, Davies J, Eltis LD. Functional Characterization of Catabolic Plasmid from Polychlorinated-Biphenyl-Degrading Rhodococcus sp. RHA1. ***J Bacteriol***. 2004 Nov;186(22)7783-7795. PMID: 15516593

73. The ENCODE Project Consortium (Feingold EA et al). The ENCODE (ENCyclopedia of DNA Elements) Project. ***Science*.** 2004 Oct 22;306(5696):636-640. PMID: 15499007

72. The MGC Project Team (Gerhard DS et al). The Status, Quality and Expansion of the NIH Full-length cDNA project: the Mammalian Gene Collection (MGC). ***Genome Res***. 2004 Oct 14;(10B):2121-2127. PMID: 15489334

71. Baross A, Butterfield Y, Coughlin S, Zeng T, Griffith M, Griffith O, Petrescu A, Smailus D, Khattra J, McDonald H, McKay S, Moksa M, Siddiqui A, Jones S, Holt R, **Marra M**. Systematic Recovery and Analysis of Full-ORF Human cDNA Clones. ***Genome Res***. 2004 Oct 14;(10B): 2083-2092. PMID: 15489330

70. Anglesio MS, Evdokimova V, Melnyk N, Zhang L, Fernandez CV, Grundy PE, Leach S, **Marra MA**, Brooks-Wilson AR, Penninger J, Sorensen PHB. Differential expression of a novel ankyrin containing E3 ubiquitin-protein ligase, Hace1, in sporadic Wilm's tumor versus normal kidney. ***Hum Mol Genet.*** 2004 Sep 15;13(18):2061-2074. PMID: 15254018

69. Krzywinski M, Bosdet I, Smailus D, Chiu R, Mathewson C, Wye N, Barber S, Brown-John M, Chan S, Tsai M, Albertson D, Lam W, Choy C-O, Osoegawa K, Zhao S, de Jong P, Schein J, Jones S, **Marra M**. A Set of BAC Clones Spanning the Human Genome. ***Nucleic Acids Res*.** 2004 Jul 9;32(12):3651-3660. PMID: 15247347

68. Flibotte S, Chiu R, Fjell C, Krzywinski M, Schein JE, Shin H, **Marra MA**. Automated ordering of fingerprinted clones. ***Bioinformatics*.** 2004 May 22;20(8):1264-1271. PMID: 14871860

67. MacAulay C, Lonergan K, Chi B, Zuyderduyn S, Schein J, Tsao M, LeRiche J, Jones S, **Marra M**, Lam S, Lam WL. Serial analysis of gene expression profiles of developmental stages in non-small cell lung carcinoma. ***Chest***. 2004 May;125(5 Suppl):97S**. (Also a Proceedings paper)** PMID: 15136436

66. Henderson L-J, Okamoto I, Lestou VS, Robichaud M, Chhanabhai M, Gascoyne RD, Klasa RJ, Connors JM, **Marra MA**, Horsman DE, Lam WL. Delineation of a minimal region of deletion at 6q16.3 in follicular lymphoma and construction of a bacterial artificial chromosome contig spanning a 6 megabase region of 6q16-q21. ***Gene Chromosome Canc***. 2004 May;40(1):60-65. PMID: 15034870

65. Krzywinski M, Wallis J, Gösele C, Bosdet I, Chiu R, Graves T, Hummel O, Layman D, Mathewson C, Wye N, Zhu B, Albracht D, Asano J, Barber S, Brown-John M, Chan S, Chand S, Cloutier A, Davito J, Fjell C, Gaige T, Ganten D, Girn N, Himmelbauer N, Kreitler T, Leach S, Lee D, Lehrach H, Mayo M, Mead K, Olson T, Pandoh P, Prabhu A-L, Shin H, Tsai M, Walker J, Yang G, Sekhon M, Hillier L, Zimdahl H, Osoegawa K, Zhao S, Siddiqui A, de Jong P, Warren W, Mardis E, McPherson J, Wilson R, Hübner R, Jones S, **Marra M**, Schein J. Integrated and Sequence-Ordered BAC and YAC-based Physical Maps for the Rat Genome. ***Genome Res.*** 2004 Apr;14(4):766-779. PMID: 15060021

64. Baross A, Schertzer M, Zuyderduyn SD, Jones SJM, **Marra MA**, Lansdorp PM. Effect of TERT and ATM on gene expression profiles in human fibroblasts. ***Gene Chromosome Canc.*** 2004 Apr;39(4):298-310. PMID: 14978791

63. Rat Genome Sequencing Project Consortium (Gibbs RA et al). Genome sequence of the brown Norway rat yields insights into mammalian evolution. ***Nature***. 2004 Apr 1;428(6982):493-521.

62. Ishkanian AS, Malloff C, Watson S, deLeeuw R, Chi B, Coe B, Albertson DG, Pinkel D, **Marra M**, Ling V, MacAulay C, Lam WL. A tiling resolution DNA Microarray with complete coverage of the human genome. ***Nat Genet.*** 2004 Mar;36(3):299-303. PMID: 14981516

61. Rise ML, von Schalburg KR, Brown GD, Mawer, MA, Devlin RH, Kuipers N, Busby M, Beetz-Sargent M, Alberto R, Gibbs AR, Hunt P, Shukin R, Zeznik JA, Nelson C, Jones SRM, Smailus DE, Jones SJM, Schein J, **Marra MA,** Butterfield YSN, Stott J, Ng SHS, Davidson WS, Koop BF. Development and Application of a Salmonid EST Database and cDNA Microarray: Data Mining and Interspecific Hybridization Characteristics. ***Genome Res***. 2004 Mar;14:478-490. PMID: 14962987

60. Kingsley DM, Zhu B. Osoegawa K, De Jong PJ, Schein J, Marra M, Peichel C, Amemiya C, Schluter B, Balabhadra S, Friedlander B, Man Cha Y, Dickson M, Grinwood J, Schmutz J, Talbot WS, Myers R. New genomic tools for molecular studies of evolutionary change in threespine sticklebacks. ***Behaviour.*** 2004 Nov-Dec; 141:1331-1344. **(Also a Proceedings paper)**

59. Steen BR, Zuyderduyn S, Toffaletti DL, **Marra M**, Jones SJM, Perfect JR, Kronstad J. *Cryptococcus neoformans* gene expression during experimental cryptococcal meningitis. ***Eukaryot Cell***. 2003 Dec;2(6):1336-1349. PMID: 14665467

58. Stein LD, Bao Z, Blasier D, Blumenthal T, Brent M, Chen N, Chinwalla A, Clarke L, Clee C, Coghlan A, Coulson A, D'Eustachio P, Fulton L, Fulton R, Griffiths-Jones S, Harris T, Hillier L, Kamath R, Kuwabara P, **Marra M**, Mardis E, Miner T, Minx P, Mullikin JC, Plumb R, Rogers J, Schein J, Sohrmann M, Spieth J, Stajich JE, Wei C, Willey D, Wilson R, Durbin R, Waterston R. The Genome Sequence of *Caenorhabditis briggsae*: A Platform for Comparative Genomics. ***PLoS Biol***. 2003 Nov;1(2):E45. PMID: 14624247

57. Boon K, Edwards JB, Siu I-M, Olschner D, Eberhart CG, **Marra MA**, Strausberg RL, Riggins GJ. Comparison of Medulloblastoma and Normal Neural Transcriptomes Identifies a Restricted Set of Activated Genes. ***Oncogene.*** 2003 Oct 23;22(48):7687-7694. PMID: 14576832

56. Hillier LW, Fulton RS, Fulton LA, Graves TA, Pepin KH, Wagner-McPherson C, Layman D, Maas J, Jaeger S, Walker R, Wylie K, Sekhon M, Becker MC, O'Laughlin MD, Schaller ME, Fewell GA, Delehaunty KD, Miner TL, Nash WE, Cordes M, Du H, Sun H, Edwards J, Bradshaw-Cordum H, Ali J, Andrews S, Isak A, Vanbrunt A, Nguyen C, Du F, Lamar B, Courtney L, Kalicki J, Ozersky P, Bielicki L, Scott K, Holmes A, Harkins R, Harris A, Strong CM, Hou S, Tomlinson C, Dauphin-Kohlberg S, Kozlowicz-Reilly A, Leonard S, Rohlfing T, Rock SM, Tin-Wollam AM, Abbott A, Minx P, Maupin R,

Strowmatt C, Latreille P, Miller N, Johnson D, Murray J, Woessner JP, Wendl MC, Yang SP, Schultz BR, Wallis JW, Spieth J, Bieri TA, Nelson JO, Berkowicz N, Wohldmann PE, Cook LL, Hickenbotham MT, Eldred J, Williams D, Bedell JA, Mardis ER, Clifton SW, Chissoe SL, **Marra MA**, Raymond C, Haugen E, Gillett W, Zhou Y, James R, Phelps K, Iadanoto S, Bubb K, Simms E, Levy R, Clendenning J, Kaul R, Kent WJ, Furey TS, Baertsch RA, Brent MR, Keibler E, Flicek P, Bork P, Suyama M, Bailey JA, Portnoy ME, Torrents D, Chinwalla AT, Gish WR, Eddy SR, McPherson JD, Olson MV, Eichler EE, Green ED, Waterston RH, Wilson RK. The DNA sequence of human chromosome 7. ***Nature*.** 2003 Jul 10;424(6945):157-164. PMID: 12853948

55. Fjell CD, Bosdet I, Schein JE, Jones SJM, **Marra MA**. Internet Contig Explorer (iCE) - A tool for visualizing clone fingerprint maps. ***Genome Res*.** 2003 Jun;13(6A):1244-1249. PMID: 12799356

54. Pleasance ED, **Marra MA**, Jones SJM. Assessment of SAGE in transcript identification.***Genome Res***. 2003 Jun;13(6A):1203-1215. PMID: 12743019

53. **Marra MA**, Jones SJ, Astell CR, Holt RA, Brooks-Wilson A, Butterfield YS, Khattra J, Asano JK, Barber SA, Chan SY, Cloutier A, Coughlin SM, Freeman D, Girn N, Griffith OL, Leach SR, Mayo M, McDonald H, Montgomery SB, Pandoh PK, Petrescu AS, Robertson AG, Schein JE, Siddiqui A, Smailus DE, Stott JM, Yang GS, Plummer F, Andonov A, Artsob H, Bastien N, Bernard K, Booth TF, Bowness D, Czub M, Drebot M, Fernando L, Flick R, Garbutt M, Gray M, Grolla A, Jones S, Feldmann H, Meyers A, Kabani A, Li Y, Normand S, Stroher U, Tipples GA, Tyler S, Vogrig R, Ward D, Watson B, Brunham RC, Krajden M, Petric M, Skowronski DM, Upton C, Roper RL. The genome sequence of the SARS-associated coronavirus. ***Science***. 2003 May 30;300(5624):1399-1404. PMID: 12730501

52. Fuhrmann DR, Krzywinski MI, Chiu R, Saeedi P, Schein JE, Bosdet IE, Chinwalla A, Hillier LW, Waterston RH, McPherson JD, Jones SJM, **Marra MA**. Software for automated analysis of DNA fingerprinting gels. ***Genome Res*.** 2003 May;13(5):940-953. PMID: 12727910

51. Gorski SM, Chittaranjan S, Pleasance ED, Freeman JD, Anderson CL, Varhol RJ, Coughlin SM, Jones SJM, **Marra MA**. A SAGE Approach to Discovery of Genes Involved in Autophagic Cell Death. ***Curr Biol*.** 2003 Feb 18;13(4):358-363. PMID: 12593804

50. McKay SJ, Johnsen R, Khattra J, Asano J, Baillie DL, Chan S, Dube N, Fang L, Goszczynski B, Ha E, Halfnight E, Hollebakken R, Huang P, Hung K, Jensen V, Jones SJM, Kai H, Li D, Mah A, **Marra M,** McGhee J, Newbury R, Pouzyrev A, Riddle DL, Sonnhammer E, Tian H, Tu D, Tyson JR, Vatcher G, Warner A, Wong K, Zhao Z, and Moerman DG. Gene Expression Profiling of Cells, Tissues and Developmental Stages of the Nematode *C. elegans*. ***Cold Spring Harb Symp Quant Biol*.** 2003 Jan;68:159-169. **(Also a Proceedings paper)** PMID: 15338614

49. Moore SS, Hansen C, Willimans JL, Fu A, Meng Y, Li C, Zhang Y, Urquhart BSD, **Marra M,** Schein J, Benkel B, de Jong PJ, Osoegawa K, Kirkpatrick BW, Gill CA. A comparative map of bovine chromosome 19 based on a combination of mapping on a bacterial artificial chromosome scaffold map, a whole genome radiation hybrid panel and the human draft sequence. ***Cytogenet Genome Res*.** 2003**;**102:32-38. PMID: 14970675

48. Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD, Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T, Max SI, Wang J, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL, Scheetz TE, Brownstein MJ, Usdin TB, Toshiyuki S, Carninci P, Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH, Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW, Villalon DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J, Helton E, Ketteman M, Madan A, Rodrigues S, Sanchez A, Whiting M, Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW, Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J, Schmutz J, Myers RM, Butterfield YS, Krzywinski MI, Skalska U, Smailus DE, Schnerch A, Schein JE, Jones SJ, **Marra MA**.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences. ***Proc Natl Acad Sci USA.*** 2002 Dec 24;99(26):16899-16903. PMID: 12477932

47. Vatcher G, Smailus D, Krzywinski M, Guin R, Stott J, Tsai M, Chan S, Pandoh P, Yang G, Asano J, Olson T, Prabhu A, Coope R, Marziali A, Schein J, Jones S, and **Marra M**. Resuspension of DNA sequencing reaction products in agarose increases sequence quality on the MegaBACE 1000 automated sequencer. ***Biotechniques.*** 2002 Sep;33(3):532, 534, 538-539. PMID: 12238763

46. Steen BR, Lian T, Zuyderduyn S, MacDonald K, **Marra M**, Jones SJM, Kronstad JW. Temperature-regulated transcription in the pathogenic fungus *Cryptococcus neoformans.* ***Genome Res.*** 2002 Sep;12(9):1386-1400. PMID: 12213776

45. Schein JE, Tangen K, Chiu R, Shin H, Lengeler KB, MacDonald K, Bosdet I, Heitman J, Jones SJM, **Marra M**, Kronstad JW. Physical maps for genome analysis of serotype A and D strains of the fungal pathogen *Cryptococcus neoformans.* ***Genome Res.*** 2002 Sep;12(9):1445-1453. PMID: 12213782

44. Gregory SG, Sekhon M, Schein J, Zhao S, Osoegawa K, Scott CE, Evans RS, Burridge PW, Cox TV, Fox CA, Hutton RD, Mullenger IR, Phillips KJ, Smith J, Stalker J, Threadgold GJ, Birney E, Wylie K, Chinwalla A, Wallis J, Hillier L, Carter J, Gaige T, Jaeger S, Kremitzki C, Layman D, Maas J, McGrane R, Mead K, Walker R, Jones S, Smith M, Asano J, Bosdet I, Chan S, Chittaranjan S, Chiu R, Fjell C, Fuhrmann D, Girn N, Gray C, Guin R, Hsiao L, Krzywinski M, Kutsche R, Lee SS, Mathewson C, McLeavy C, Messervier S, Ness S, Pandoh P, Prabhu AL, Saeedi P, Smailus D, Spence L, Stott J, Taylor S, Terpstra W, Tsai M, Vardy J, Wye N, Yang G, Shatsman S, Ayodeji B, Geer K, Tsegaye G, Shvartsbeyn A, Gebregeorgis E, Krol M, Russell D, Overton L, Malek JA, Holmes M, Heaney M, Shetty J, Feldblyum T, Nierman WC, Catanese JJ, Hubbard T, Waterston RH, Rogers J, de Jong PJ, Fraser CM, **Marra M**, McPherson JD, Bentley DR. A physical map of the mouse genome. ***Nature.*** 2002 Aug 15;418 (6899):743-750. PMID: 12181558

43. Mattman A, Huntsman D, Lockitch G, Langlois S, Buskard N, Ralston D, Butterfield Y, Rodrigues P, Jones S, Porto G, **Marra M**, De Sousa M, Vatcher G. Transferrin receptor 2 (TfR2) and HFE mutational analysis in non-C282Y iron overload: identification of a novel TfR2 mutation. ***Blood.*** 2002 Aug 1; 100(3):1075-1077. PMID: 12130528

42. Butterfield YSN, **Marra MA**, Asano JK, Chan SY, Guin R, Kryzwinski MI, Lee SS, MacDonald KWK, Mathewson CA, Olson TE, Pandoh PK, Prabhu A, Schnerch A, Skalska U, Smailus DE, Stott JM, Tsai MI, Yang GS, Zuyderduyn SD, Schein JE, Jones SJM. An efficient strategy for large-scale high-throughput transposon-mediated sequencing of cDNA clones. ***Nucleic Acids Res.*** 2002 Jun 1;30(11):2460-2468. PMID: 12034834

41. Shevchenko Y, Bouffard GG, Butterfield YSN, Blakesley RW, Hartley JL, Young AC, **Marra MA**, Jones SJM, Touchman JW, Green ED. Systematic sequencing of cDNA clones using the transposon Tn5. ***Nucleic Acids Res.*** 2002 Jun 1;30(11):2469-2477. PMID: 12034835

40. Ness SR, Terpstra W, Krzywinski M, **Marra MA**, Jones SJM. Assembly of fingerprint contigs: parallelized FPC. ***Bioinformatics.*** 2002 Mar;18(3):484-485. PMID: 11934749

39. Gorski S, **Marra M**. Programmed cell death takes flight: Genetic and genomic approaches to gene discovery in *Drosophila*. Review. ***Physiol Genomics.*** 2002;9(2):59-69. PMID: 12006672

38. Cai W-W, Chow C-W, Damani S, Gregory SG, **Marra M,** Bradley A. An SSLP marker-anchored BAC framework map of the mouse genome. Communication. ***Nat Genet.*** 2001 Oct;29(2):133-134. PMID: 11586294

37. Clark MD, Hennig S, Herwig R, Clifton SW, **Marra MA**, Lehrach H, Johnson, SL. An oligonucleotide fingerprint normalised and Expressed Sequence Tag characterised zebrafish cDNA library. ***Genome Res.*** 2001 Sep; 11(9):1594-1602. PMID: 11544204

36. Jones SJM, Riddle D, Pouzyrev AT, Velculescu VE, Hillier L, Eddy SR, Stricklin SL, Baillie DL, Waterston R, **Marra MA**. Changes in gene expression associated with developmental arrest and longevity in *C. elegans*. ***Genome Res.*** 2001 Aug;11(8):1346-1352. PMID: 11483575

35. Gower NJD, Temple GR, Schein JE, **Marra M**, Walker DS, Baylis HA. Dissection of the promoter region of the inositol 1,4,5-trisphosphate receptor gene, itr-1, in *C. elegans*: A molecular basis for cell-specific expression of IP3R isoforms. ***J Mol Biol.*** 2001 Feb 16;306(2):145-157. PMID: 11237590

34. McPherson JD, **Marra M** et al A physical map of the human genome. ***Nature.*** 2001 Feb 15;409(6822):934-941. PMID: 11237014

33. The International Human Genome Sequencing Consortium (Lander ES et al). Initial sequencing and analysis of the human genome. ***Nature.*** 2001 Feb 15;409(6822):860-921. PMID: 11237011

32. Wendl MC, **Marra MA**, Hillier LW, Chinwalla AT, Wilson RK, Waterston RH. Theories and applications for sequencing randomly selected clones. ***Genome Res.*** 2001 Feb;11(2):274-280. PMID: 11157790

31. The Arabidopsis Genome Initiative (Kaul S et al). Analysis of the genome sequence of the flowering plant *Arabidopsis thaliana*. ***Nature.*** 2000 Dec 14;408(6814):796-815. PMID: 11130711

30. The Kazusa DNA Research Institute, the Cold Spring Harbor and Washington University Sequencing Consortium, the European Union Arabidopsis Genome Sequencing Consortium and Institute of Plant Genetics and Crop Plant Research (IPK) (Tabata S et al). Sequence and analysis of chromosome 5 of the plant Arabidopsis thaliana. ***Nature.*** 2000 Dec 14;408(6814):823-826. PMID: 11130714

29. Loging WT, Lal A, Siu IM, Loney TL, Wikstrand CJ, **Marra MA**, Prange C, Bigner DD, Strausberg RL, Riggins GJ. Identifying Potential Tumor Markers and Antigens by Database Mining and Rapid Expression Screening. ***Genome Res.*** 2000 Sep;10(9):1393-1402. PMID: 10984457

28. Emmert-Buck MR, Strausberg RL, Krizman DB, Bonaldo MF, Bonner RF, Bostwick DG, Brown MR, Buetow KH, Chuaqui RF, Cole KA, Duray PH, Englert CR, Gillespie JW, Greenhut S, Grouse L, Hillier LW, Katz KS, Klausner RD, Kuznetzov V, Lash AE, Lennon G, Linehan WM, Liotta LA, **Marra MA**, Munson PJ, Ornstein DK, Prabhu VV, Prange C, Schuler GD, Soares MB, Tolstoshev CM, Vocke CD, Waterston RH. Molecular Profiling of Clinical Tissue Specimens: Feasibility and Applications. ***J Mol Diagn.*** 2000 May;2(2):60-66. (Note: this paper was also published in ***AM J Pathol.*** 2000;156(4):1109-1115. (Review) PMID: 10751334

27. Aamodt E, Shen L, **Marra M**, Schein J, Rose B and McDermott J. Conservation of sequence and function of the *pag-3* genes from *C. elegans* and *C. briggsae*. ***Gene.*** 2000 Feb 8;243(1-2):67-74. PMID: 10675614

26. The Cold Spring Harbor Laboratory, Washington University Genome Sequencing Center, and PE Biosystems Arabidopsis Sequencing Consortium. (McCombie WR et al). The complete sequence of a heterochromatic island from a higher eukaryote. ***Cell.*** 2000 Feb 4;100(3):377-386. PMID: 10676819

25. European Union Arabidopsis Genome, Washington University in St. Louis, and PE Biosystems Arabidopsis Sequencing Consortium (Mayer K et al). Sequence and analysis of chromosome 4 of the plant *Arabidopsis thaliana*. ***Nature.*** 1999;402:769-776. PMID: 10617198

24. Copenhaver GP, Nickel K, Kuromori T, Benito M-I, Kaul S, Lin X, Bevan M, Murphy G, Harris B, Parnell LD, McCombie WR, Martienssen RA, **Marra M,** Preuss D. Genetic definition and sequence analysis of Arabidopsis centromeres. ***Science.*** 1999; 286:2468-2474. PMID: 10617454

23. Lal A, Lash AE, Altschul SF, Velculescu V, Zhang L, McLendon RE, **Marra MA**, Prange C, Morin PJ, Polyak N, Papadopoulos N, Vogelstein B, Kinzler KW, Strausberg RL, Riggins GJ. A Public Database for Gene Expression in Human Cancers. ***Cancer Res.*** 1999;59:5403-5407. PMID: 10554005

22. Ellsworth RE, Ionasescu V, Searby C, Sheffield VC, Braden VV, Kucaba TA, McPherson JD, **Marra MA**, Green ED. The CMT2D Locus: Refined genetic position, construction of a bacterial-based physical map, and evidence of allelic heterogeneity with distal spinal muscular atrophy. ***Genome Res.*** 1999;9:568-574. PMID: 10400924

21. **Marra M**, Kucaba T, Sekhon M, Hillier L, Martienssen R, Chinwalla A, Crockett J, Fedele J, Grover H, Gun C, McCombie WR, McDonald K, McPherson J, Mudd N, Parnell L, Schein J, Seim R, Shelby P, Waterston R, Wilson R. A map for sequence analysis of the *Arabidopsis thaliana* genome. ***Nat Genet.*** 1999;22:265-270. PMID: 10391214

20. Mozo T, Dewar K, Dunn P, Ecker J, Fischer S, Kloska S, Lehrach H, **Marra M**, Martienssen R, Meier-Ewert S, Altmann T. A complete BAC-based physical map of the *Arabidopsis thaliana* genome. ***Nat Genet.*** 1999; 22:271-275. PMID: 10391215

19. Wilson RK, *C. elegans* Genome Consortium. How the worm was won: The *C. elegans* genome sequencing project. ***Trends Genet.*** 1999;15:51-58. PMID: 9851916

18. **Marra M,** Hillier L, Kucaba T, Allen M, Barstead R, Beck C, Blistain A, Bonaldo M, Bowers Y, Bowles L, Cardenas M, Chamberlain A, Chappell J, Clifton S, Favello A, Geisel S, Gibbons M, Harvey N, Hill F, Jackson Y, Kohn S, Lennon G, Mardis E, Martin J, Mila L, McCann R, Morales R, Pape D, Person B, Prange C, Ritter E, Soares M, Schurk R, Shin T, Steptoe M, Swaller T, Theising B, Underwood K, Wylie T, Yount T, Wilson R, Waterston R. An encyclopedia of mouse genes. ***Nat Genet.*** 1999;21:191-194. PMID: 9988271

17. **Marra MA**, Kucaba TA, Hillier LW, Waterston RH. High-throughput plasmid DNA purification for 3 cents per sample. ***Nucleic Acids Res.*** 1999;27(24):e37. PMID: 10572189

16. Thacker C, **Marra MA**, Jones A, Baillie DL, Rose AM. Functional genomics in *Caenorhabditis elegans:* an approach involving comparisons of sequences from related nematodes. ***Genome Res.*** 1999; 9:348-359. PMID: 10207157

15. Streit A, Li W, Robertson B, Schein J, Kamal IH, **Marra M**, Wood WB. Homologs of the *Caenorhabditis elegans* Masculinizing Gene her-1 in *C. briggsae* and the Filarial Parasite *Brugia malayi*. ***Genetics.*** 1999;152:1573-1584. PMID: 10430584

14. Vatcher GP, Barbazuk WB, O'Neil NJ, **Marra MA**, Ha T, Baillie DL. Identification and characterization of a serine hydroxymethyltransferase isoform in *Caenorhabditis briggsae*. ***Gene.*** 1999;230:137-144. PMID: 10216251

13. The Sanger Centre and Genome Sequencing Center. Toward a complete human genome sequence. ***Genome Res.*** 1998 Nov;8(11):1097-1108. PMID: 9847074

12. The *C. elegans* Genome Sequencing Consortium, Washington University Genome Sequencing Center, St. Louis U.S.A., and the Sanger Centre, Hinxton, U.K. Genome sequence of the nematode *Caenorhabditis elegans*: A platform for investigating biology. ***Science.*** 1998;282:2012-2018. PMID: 9851916

11. Manger ID, Hehl A, Parmley S, Sibley LD, **Marra MA**, Hillier L, Waterston RH, Boothroyd JC. Expressed Sequence Tag analysis of the bradyzoite stage of Toxoplasma gondii: Identification of developmentally regulated genes. ***Infect Immun.*** 1998;66:1632-1637.) PMID: 9529091

10. Ajioka J, Boothroyd JC, Brunk BP, Hehl A, Hillier L, Manger ID, Overton GC, **Marra M**, Roos D, Wan KL, Waterston RH, Sibley LD. Gene Discovery by EST sequencing in Toxoplasma gondii reveals sequences restricted to the apicomplexa. ***Genome Res.*** 1998;8:18-28. PMID: 9445484

9. **Marra MA**, Hillier L Waterston RH. Expressed Sequence Tags - ESTablishing bridges between genomes. ***Trends Genet.*** 1998;14:4-7. PMID: 9448457

8. **Marra MA**, Kucaba TK, Dietrich NL, Green ED, Brownstein B, Wilson RK, McDonald KM, Hillier LW, McPherson JD, Waterston RH. High throughput fingerprint analysis of large-insert clones. ***Genome Res.*** 1997;7:1072-1084. PMID: 9371743

7. Chissoe SL, **Marra MA**, Hillier L, Brinkman R, Wilson RK, Waterston RH. Representation of cloned genomic sequences in two sequencing vectors: Correlation of DNA sequence and subclone distribution. ***Nucleic Acids Res*.** 1997;25:2960-2966. PMID: 9224593

6. **Marra MA**, Weinstock LA, Mardis ER. End sequence determination from large insert clones using energy transfer fluorescent primers. ***Genome Res*.** 1996;6:1118-1122. PMID: 8938436

5. Hillier L, Lennon G, Becker M, Bonaldo MF, Chiapelli B, Chissoe S, Dietrich N, DuBuque T, Favello A, Gish W, Hawkins M, Hultman M, Kucaba T, Lacy M, Le M, Le N, Mardis E, Moore B, Morris M, Parsons J, Prange C, Rifkin L, Rohlfing T, Schellenberg K, Soares MB, Tan F, Thierry-Mieg J, Trevaskis E, Underwood K, Wohldman P, Waterston R, Wilson RK, **Marra MA**. Generation and analysis of 280,000 Human Expressed Sequence Tags. ***Genome Res*.** 1996 Sep;(6)9:807-828. PMID: 8889549

4. **Marra MA**, Baillie DL. Recovery of duplications by drug resistance selection in *Caenorhabditis elegans*. ***Genome*.** 1994;37:701-705. PMID: 7958827

3. McKim KS, Matheson C, **Marra MA**, Wakarchuk MF, Baillie DL. The *Caenorhabditis elegans* unc-60 gene encodes proteins homologous to a family of actin-binding proteins. ***Mol Gen Genet.*** 1994;242:346-357. PMID: 8107682

2. Schein JE, **Marra MA**, Benian GM, Fields C, Baillie DL. The use of deficiencies to determine essential gene content in the let-56 - unc-22 region of *Caenorhabditis elegans*. ***Genome.*** 1993;36:1148-1156. PMID: 8112575

1. **Marra MA**, Prasad SS, Baillie DL. Molecular analysis of two genes between let-653 and let-56 in the unc-22(IV) region of *C. elegans.* ***Mol Gen Genet.*** 1993;236:289-298. PMID: 8382340

NON-PEER REVIEWED PUBLICATIONS:

1 Porter VL, O'Neill K, MacLennan S, Corbett RD, Ng M, Culibrk L, Hamadeh Z, Iden M, Schmidt R, Tsaih SW, Chang G, Fan J, Nip KM, Akbari V, Chan SK, Hopkins J, Moore RA, Chuah E, Mungall KL, Mungall AJ, Birol I, Jones SJM, Rader JS, Marra MA. Genomic structures and regulation patterns at HPV integration sites in cervical cancer. bioRxiv. 2023 Nov 5:2023.11.04.564800. doi: 10.1101/2023.11.04.564800. Preprint.

2 Huse JT, Wallace M, Aldape KD, Berger MS, Bettegowda C, Brat DJ, Cahill DP, Cloughesy T, Haas-Kogan DA, **Marra M**, Miller CR, Nelson SJ, Salama SR, Soffietti R, Wen PY, Yip S, Yen K, Costello JF, Chang S. Where are we now? And where are we going? A report from the Accelerate Brain Cancer Cure (ABC^2) Low-grade Glioma Research Workshop. ***Neuro Oncol***. 2014 Jan;16(2):173-178. doi: 10.1093/neuonc/not229.

3 **Marra MA**. Cancer Genomics: Enabling patient rather than disease-driven research. ***Bioscienceworld Magazine***. Feb 2009.

ACADEMIC PRESENTATIONS:

163. Canadian Epigenetic, Environment and Health Research Consortium Network (CEEHRC) Seminar Series. BC. Sep 20, 2024. “Multiomic Analysis of Pediatric AML.”

162. University of British Columbia, Department of Medical Genetics. September Welcome Keynote. Vancouver, BC. Sep 6, 2024.

161. CITAC-CSCI Annual Joint Meeting. Vancouver, BC. Apr 11, 2024. Keynote presentation. "From *C. elegans* genetics to precision cancer genomic medicine, via the Human Genome Project: Reflections on a collaborative scientific journey."

160. CGEn Scientific Advisory Board Meeting. Vancouver, BC. Apr 2, 2024. "Multi-omic Analyses of Treatment Resistance and Cancer Heterogeneity."

159. University of Washington, Department of Genome Sciences. Host: Dr. Elizabeth Buffalo. Apr 10, 2023. "The genomics of treatment resistant cancers".

158. University of British Columbia, Bioinformatics, Integrative Oncology and Genome Sciences Graduate Retreat. Mar 23, 2023. "The genomics of treatment resistant cancers".

157. University of Saskatchewan, Saskatchewan Cancer Agency. Saskatoon, SK. June 19, 2023. "The genomics of treatment resistant cancers."

156. 12th Signalling in Normal and Cancer Cells Conference. Banff, AB. Apr 23 – 27, 2023. Keynote presentation. "The genomics of treatment resistance cancers."

155. University of Alberta, Cancer Research Institute of Alberta, Edmonton, AB. CRINA Connects Seminar Series. Jan 18, 2023. "The genomics of treatment resistant cancers."

154. BC Children's Hospital Research Institute, Vancouver, BC. Nov 21, 2022. "The genomics of treatment resistant cancers."

153. BC Leukemia Network Rapid Fire Talk, Vancouver, BC. Nov 3, 2022. Single cell profiling of primary and relapsed pAML."

152. University of British Columbia. Michael Smith Laboratories Seminar Series. Vancouver, BC. Oct 27, 2022. "The Genomics of Treatment Resistant Cancer."

151. CIHR Institute of Genetics IAB Meeting. Fairmont Hotel Vancouver, BC. May 30, 2022. "Personalized Oncogenomics Program".

150. Realities of Northern Oncology Conference 2022, Prince George, BC. April 28, 2022. "Towards a Canadian national program for genomic profiling of treatment resistant cancers."

149. University of British Columbia-Nanyang Technological University Virtual Symposium on Precision Oncology. Mar 23, 2022. "British Columbia's Personalized Oncogenomics Program" (278 attendees)

148. University of California, Davis. Comprehensive Cancer Center Grand Rounds (Virtual). Apr 27, 2021. "Towards a Canadian national program for comprehensive genomic profiling of treatment resistant cancers."

147. Simon Fraser University. 2021 Molecular Biology and Biochemistry Graduate Colloquium (Virtual). Apr 23, 2021. Keynote presentation. "Towards a Canadian national program for comprehensive genomic profiling of treatment resistant cancers."

146. 1st International Symposium of CCII -Bioinformatics and its application to cancer and other diseases. (Virtual). Kyoto, Japan. Jan 15, 2021. "Towards a Canadian national program for comprehensive genomic profiling of treatment resistant cancers."

145. AGBT Annual General Meeting. Marco Island, FL. Feb 23-26, 2020. Keynote presentation. "Towards a Canadian national program for genomic profiling of treatment resistant cancers."

144. Canadian Anatomic and Molecular Pathology Conference. Whistler, BC. Jan 24-25, 2020. "Cancer Genomics: From Bulk Tissue Cells."

143. The XV11 Genome Sciences Symposium. University of Washington. Seattle, WA. Nov 7-8, 2019. "Genomics from Worm to Human: In Honor of Bob Waterston".

142. 10th Annual ImmunoBC Retreat. Vancouver, BC. June 10, 2019. "BC Cancer's Personalized Oncogenomics (POG) program: Platforms for patient-oriented discovery."

141. PROOF Centre of Excellence's 10th Anniversary Symposium. University of British Columbia Vancouver, BC. Nov 28, 2018. Keynote presentation. "Genomic, Data Analytics and Health: Perspective from POG".

140. BC Cancer Summit. Vancouver, BC. Nov 23-24, 2018. "Genome Sciences Centre: Vision and Impact on Cancer Care".

139. Princess Margaret Cancer Centre's Applied Cancer Genomics and Tumor Immunotherapy: A Clinical Perspective Symposium. University of Toronto. Toronto, ON. Nov 16, 2018. "Personalized Oncogenomics (POG): Taking Whole Genomes to the Cancer Clinic". (Keynote speaker)

138. 25th Anniversary of Michael Smith Nobel Prize Award Symposium. University of British Columbia. Vancouver, BC. Oct 1, 2018. "A perspective on the evolution of technology and science at the Genome Sciences Centre".

137. The Centre de recherche du Centre hospitalier de l'Université de Montréal (CRCHUM) Grand Rounds Seminar. Montreal, QC. June 8, 2018. "From cancer genome landscapes to epigenome dysregulation: perspectives on the evolution of genome science".

136. Genome BC's Annual Genomics Forum 2018. Vancouver, BC. May 24, 2018. "Whole genome analysis to support cancer treatment decision making: The Personalized OncoGenomics (POG) Project."

135. The 7th Annual Norman Bethune Symposium. Vancouver, BC. Apr 10, 2018. Whole genome analysis to support cancer treatment decision making: BC Cancer Personalized Oncogenomics (POG) Project".

134. The Ottawa Hospital Research Institute 2017 Research Day. Keynote lecture. Ottawa, ON. Nov 9, 2017. "Whole genome analysis to inform cancer treatment planning".

133. TFRI 8th Annual Scientific Meeting. Marathon of Hope Lecture. Vancouver, BC. Nov 6, 2017. "Genomic approaches to cancer outcomes".

132. Western Canadian Universities Big Data Health Conference. Banff, AB. Sep 28, 2017. "Whole genome analysis to inform cancer treatment planning".

131. 2nd Annual Fraser Oncology Education Day. Keynote speaker. Surrey, BC. May 27, 2017. "Cancer and The Genome."

130. University of British Columbia, Faculty of Medicine First Annual Graduate Student Research Day. Keynote Lecture. Vancouver, BC. May 26, 2017.

129. BC Tech Summit. Keynote address. Vision of the Industry: How Precision Medicine is Changing Lives Now with Life Changing Stories. Vancouver, BC. Mar 15, 2017.

128. University of British Columbia. Data Analysis and Study Design Workshop Series. Epic Data Group Meeting. Vancouver, BC. Feb 16, 2017. The BC Cancer Agency Personalized Oncogenomics (POG) Project.

127. BC Cancer Agency's Cancer Genomics Education Day. Vancouver, BC. Sep 10, 2016. "Cancer - a disease of the genome".

126. University of Toronto. Princess Margaret Cancer Centre Seminar Series. Toronto, ON. June 9, 2016. "Whole genome analysis to support cancer treatment decision making: the BC Cancer Agency Personalized OncoGenomics (POG) Project".

125. University of British Columbia. Dr. Chew Wei Memorial Prize Lecture. Kelowna, BC. May 27, 2016. “Cancer, It’s Personal”.

124. University of British Columbia. The Vancouver Institute’s Annual UBC Excellence in Research Lecture. Mar 5, 2016. “At the frontier of genetic research: recent advances and future possibilities.”

123. NHGRI Seminar Series (Human Genome Project 25th Anniversary). Bethesda, MD. Apr 28, 2016. “From BAC clones to cancer genomes: the role of the HGP in launching a career in science.” (lecture delivered via video conference)

122. Keystone Symposia Conference: The Cancer Genome. Banff, AB. Feb 7-11, 2016. “The BC Cancer Agency Personalized OncoGenomics (POG) Project.”

121. UBC Radiology Grand Rounds. Vancouver, BC. Jan 13, 2016. “Whole genome analysis to support cancer treatment decision making: the Personalized Oncogenomics (POG) Project.”

120. 2015 Dr. Chew Wei Memorial Prize Lecture. BC Cancer Agency. Vancouver, BC. Dec 7, 2015. “An evolving perspective on cancer gene discovery”.

119. 2015 Canada Gairdner Symposium-Genomics & Cancer. Vancouver, BC. Nov 17, 2015. “Towards Genomic Medicine for Cancer Populations”.

118. HUPO 2015 World Congress. Vancouver, BC. Sep 27, 2015. “Towards Genomic Medicine for Cancer Populations: The BC Cancer Agency Personalized Oncogenomics (POG) Project”.

117. Personalized Medicine Summit. Vancouver, BC. June 7-9, 2015. “The BC Cancer Agency Personalized Onco-Genomics (POG) Project”.

116. 8th Annual Canadian Cancer Immunotherapy Consortium. Vancouver, BC. May 22, 2015. “The BC Cancer Agency Personalized Onco-Genomics (POG) Project”.

115. Memorial University of Newfoundland. St. John’s, NL. May 11, 2015. “The BC Cancer Agency Personalized Onco-Genomics (POG) Project”.

114. Terry Fox Research Institute 6th Annual Scientific Meeting. St. John’s, NL. May 8, 2015. “The BC Cancer Agency Personalized Onco-Genomics (POG) Project”.

113. 2015 Beatrice Hunter Cancer Research Institute/TFRI Cancer Research Workshop. St. John’s, NL. May 6, 2015. “The BC Cancer Agency Personalized Onco-Genomics (POG) Project”.

112. 4th Annual Canadian Human and Statistical Genetics Meeting. Vancouver, BC. Apr 20, 2015. “The BC Cancer Agency Personalized Onco-Genomics (POG) Project”.

111. University of British Columbia Medical Alumni Association’s Tuum Est: Leading Edge Medicine CME Event. Vancouver, BC. Nov 20, 2014. “Sequencing cancer genomes: where to from here?”

110. University of British Columbia. 4th Annual IOP/BTP/GSAT Research Day. Vancouver, BC. Mar 28, 2014. Opening remarks.

109. BC Cancer Agency Radiation Oncology Rounds. Vancouver, BC. Mar 06, 2014. “DNA sequencing for diagnostics and treatment planning.”

108. 2013 Canadian Cancer Research Conference. Toronto, ON. Nov 3-6, 2013. “Large Scale Cancer Genome Analysis Exposes Significant Roles for the Epigenome in Cancer Progression”.

107. Memorial Sloan-Kettering Cancer Center. Clinical Genomics Seminar Series. New York, NY. June 17, 2013. “Genomic Analysis of non-Hodgkin Lymphomas”.

106. Stanford University. 4th Annual Stanford Symposium on Genomics and Personalized Medicine. Stanford, CA. Apr 12, 2013. Keynote speaker. “Next generation cancer sequencing for diagnostics and treatment planning”.

105. University of British Columbia Department of Medicine Research Expo. Vancouver, BC. Oct 30, 2012. “Decoding cancers”.

104. McGill University. Lady Davis Institute for Medical Research, Jewish General Hospital. Distinguished Seminar Series. Montreal, QC. June 05, 2012. “Decoding cancers”.

103. University of British Columbia. Keynote Lecture, Pathology Day. Vancouver, BC. May 25, 2012. “Decoding cancers”.

102. University of British Columbia. The 7th Annual Michael Smith Distinguished Research Lecture. Vancouver, BC. Apr 10, 2012. “Sequencing Cancers”.

101. 15th Biennial Canadian Neuro-Oncology Meeting. Vancouver, BC. Feb 10, 2012. “Current Trends and Future Directions in Cancer Genomics”.

100. University of Northern British Columbia. The Cell & Molecular Biology Interest Group Seminar Series. Prince George, BC. Oct 20, 2011. “Searching for mutations that drive cancers: Early experience in the application of ultra high throughput DNA sequencing”.

99. BC Cancer Agency Radiation Oncology Research Symposium. Vancouver, BC. Sep 23, 2011. “Somatic mutations in cancers”.

98. University of British Columbia. Department of Medical Genetics September Welcome. Vancouver, BC. Sep 09, 2011. “Genomics, genes, and cancers of the immune system”.

97. Keystone Symposia: Changing Landscape of the Cancer Genome, Boston, MA. June 22, 2011. “Do Mutations in Histone Modifying Genes Drive B Cell Lymphomas?”

96. University of British Columbia. The Molecular Epigenetics ‘Waddington Lecture’. Vancouver, BC. June 14, 2011. “Do Mutations in Histone Modifying Genes Drive a Common Human Cancer?” Host: Dr. Carolyn Brown.

95. University of Western Ontario. Dr. Maude L. Menten Lecture Series. London, ON. May 27, 2011. “Do Mutations in Histone Modifying Genes Drive a Common Human Cancer?”

94. University of California San Francisco Helen Diller Family Comprehensive Cancer Center Friday Seminar Series. San Francisco, CA. Apr 08, 2011. “Do Mutations in Histone Modifying Genes Drive a Common Human Cancer?”

93. 15th Annual International Conference on Research in Computational Molecular Biology. Vancouver, BC. Mar 30, 2011. Keynote speaker.

92. University of Calgary. Southern Alberta Cancer Research Institute. Calgary, AB. Jan 14, 2011. “Do Mutations in Histone Modifying Genes Drive a Common Human Cancer?”

91. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 26, 2010. “A Report from the Genome Sciences Centre: Cancer Mutation Discovery”.

90. Genome BC 8th Annual Genomics Forum and Research Exchange. Vancouver, BC. May 28, 2010. “Genome Sequencing”.

89. The Future of Genomic Medicine III Conference. San Diego, CA. Mar 06, 2010. “Individualized Cancer Genomics”.

88. Canadian College of Medical Geneticists 33rd Annual Scientific Meeting, Banff, AB. Nov 14, 2009. Symposium Speaker. “New generation sequencing for genome analysis”.

87. The American Society of Human Genetics 59th Annual Meeting, Honolulu, Hawaii. Oct 22, 2009. Session speaker. “Transcriptome sequencing for mutation detection and gene expression profiling”.

86. University of British Columbia. Centre for High-Throughput Biology Inaugural Symposium, Vancouver, BC. Sep 18, 2009. “Cancer mutation discovery using genome and transcriptome sequencing”.

85. BC Clinical Genomics Network Conference. Vancouver, BC. Apr 20, 2009. “Ultra High-Throughput DNA Sequencing Analysis”.

84. 10th Annual Advances in Genome Biology and Technology Conference. Marco Island, FL. Feb 07, 2009. Plenary Speaker. “Sequencing cancer genomes and transcriptomes: from new technology to cancer treatment".

83. Genome Canada Platform Leaders’ Meeting. Montreal, QC. Jan 07, 2009. “Next generation sequencing technologies”.

82. 7th Annual New Principal Investigators Meeting. Jackson’s Point, ON. Nov 09, 2008. “Scaling up genome and transcriptome sequencing”.

81. International Cancer Genome Consortium Scientific Workshop. Toronto, ON. Oct 28, 2008. “Scaling up cancer genome and transcriptome sequencing”.

80. University of British Columbia. Adventures in Sciences Seminar Series, Vancouver, BC. Oct 16, 2008. “Discovering mutations in cancer cells”.

79. Integrating the Physical and Applied Sciences into Health Research Workshop. Ottawa, ON. Oct 03, 2008. “Changing paradigms in genome analysis”.

78. BC Cancer Agency Breast Tumour Group Meeting, Vancouver, BC. June 20, 2008. “Next-generation DNA sequencing and cancer genomics.”

77. Genome BC Annual Winter Symposium. Vancouver, BC. Jan 22, 2008. “High resolution analysis of follicular lymphoma genomes.”

76. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 29, 2007. “High resolution approaches for analysis of follicular lymphoma genomes.”

75. NCIC’s 60th Anniversary Conference. Toronto, ON. Nov 16, 2007. “High-resolution genome rearrangement discovery in follicular lymphoma.”

74. International Cancer Genomics Consortium Meeting. Toronto, ON. Oct 1, 2007. Speaker, World Tour Session.

73. Canadian Society of Biochemistry, Molecular & Cellular Biology’s 50th Annual Meeting. Montreal, QC. Jul 06, 2007. Merck Frosst Prize Lecture. “High-resolution genome rearrangements discovery in follicular lymphoma”.

72. 16th International Congress of Cytology. Vancouver, BC. May 16, 2007. “High-resolution genome rearrangements discovery in follicular lymphoma”**.**

71. Genome BC Genomics Forum and Research Exchange. Vancouver, BC. Apr 13, 2007. “New sequencing technologies.”

70. The University of Alabama at Birmingham. Birmingham, AL. Mar 30, 2007. “Mapping genome rearrangements in follicular lymphoma”.

69. BC Cancer Agency's Radiation Oncology Academic Rounds. Vancouver, BC. Jan 25, 2007. "Copy Number Variation in the Human Genome: Recent Advances, Candidate Mechanism, and Possible Relevance to Human Disease Research".

68. Cancer Genomics and Emerging Technologies Conference. Cambridge, MA. Oct 02, 2006. "Mapping genome rearrangements in follicular lymphoma".

67. 37th Annual Environmental Mutagen Society Meeting. Vancouver, BC. Sep 18, 2006. Plenary Speaker. "Variation in human genomes and implications for health research".

66. BC Cancer Agency Radiation Oncology Academic Rounds, Vancouver, BC. June 01, 2006. "Tools for Genome Analysis".

65. Canadian Society of Clinical Chemists Annual Conference. Victoria, BC. June 06, 2006. Symposium Speaker. "Variation in human genomes and implications for health research".

64. University of British Columbia. Michael Smith Laboratories Seminar Series. Vancouver, BC. Apr 06, 2006. "A Physical Map of a Follicular Lymphoma Genome". .

63. Advances in Genome Biology and Technology Conference. Marco Island, FL. Feb 2006. "A Physical Map of a Follicular Lymphoma Genome". **(Poster presentation**)

62. Scripps Research Institute. Jupiter, FL. Feb 2006. "A Physical Map of a Follicular Lymphoma Genome". Host: Dr. John Hogenesh.

61. BC Cancer Agency's Lymphoma Group Meeting. Vancouver, BC. Dec 08, 2005. "Towards the Human Cancer Genome Project: A Sequence-Ready Physical Map of a Follicular Lymphoma Genome".

60. 2005 American Society of Hematology Annual Meeting and Exposition. Atlanta, GA. Dec 12, 2005. Abstract presentation: "Towards the Human Cancer Genome Project: A Sequence-Ready Physical Map of a Follicular Lymphoma Genome". **(Poster presentation)**

59. BC Cancer Agency's Monday Noon Seminar Series. Vancouver, BC. Nov 2005. "Towards a human cancer genome project: A sequence-ready map of a follicular lymphoma genome".

58. Genome Quebec, Montreal, PQ. May 2005.

57. University of Wisconsin-Madison. Madison, WI. May 2005. "Of Mice and Humans: Digital Gene Expression Profiling at the British Columbia Cancer Agency Genome Sciences Centre".

56. British Columbia Centre for Disease Control. Vancouver, BC. Apr 2005. "A Strategy for Cloning Genome Rearrangements in Follicular Lymphoma".

55. University of Washington Genome Sciences Department. Seattle, WA. Mar 30, 2005. "A Strategy for Cloning Genome Rearrangements in Follicular Lymphoma".

54. University of British Columbia, Faculty of Medicine. Feb 03, 2005. 2004 NCIC Award for Excellence recipient. "Approaches for Identification and Analysis of Genome Rearrangements in Cancer".

53. National Human Genome Research Institute (NHGRI) Division of Intramural Research, National Institutes of Health. Bethesda, MD. Jan 2005. "Approaches for Identification and Analysis of Genome Rearrangements in Cancer".

52. University of British Columbia. 2004 Genetics Retreat. Vancouver, BC. Oct 21, 2004. Keynote speaker. "An Overview of the GSC".

51. University of British Columbia, Michael Smith Laboratories Official Opening. Vancouver, BC. Sep 2004. Symposium speaker.

50. 47th Canadian Federation of Biological Studies Annual Meeting, First Northern Light Conference. Vancouver, BC. June 18, 2004. Symposium Speaker. "Large-scale gene expression profiling in early mammalian development".

49. National Microbiology Laboratory. Winnipeg, MB. June 2004.

48. University of Northern British Columbia. Prince George, BC. May 2004. "The British Columbia Cancer Agency Genome Sciences Centre". Host: Molecular Biology Interest Group, UNBC.

47. 5th Annual Advances in Genome Biology and Technology Conference. Marco Island, FL. Feb 06, 2004. Plenary Speaker, "Large-scale comparative transcriptome analysis of multiple undifferentiated human embryonic stem cell lines".

46. 5th Annual Advances in Genome Biology and Technology Conference. Marco Island, FL. Feb 05, 2004. Plenary Speaker, "A Functional Genomics Approach to Autophagic Cell Death Gene Discovery".

45. BC Cancer Agency's Medical Oncology Wednesday Seminar Series. Vancouver, BC. Feb 2004. "Genomics and Cancer".

44. BC Cancer Agency, Vancouver Island Centre. Victoria, BC. Jan 2004. "An Update on the Activities at the Genome Sciences Centre".

43. 3rd Annual Western Oncology Winter Conference. Sun Peaks, BC. Feb 2003. Plenary Speaker, "BC experience with the Human Genome Project".

42. University of British Columbia, The Vancouver Institute. Vancouver, BC. Mar 2003. "Genomics Research in BC".

41. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2003. "What Can SNPs Tell Us About Cancer Susceptibility?"

40. Duke University Medical Centre Seminar Series. Durham, NC. Oct 2003. "The Genome Sciences Centre at the BC Cancer Agency".

39. University of British Columbia, Student Biotechnology Network. Vancouver, BC. Sep 2003. "The British Columbia Cancer Agency Genome Sciences Centre: Sequencing the SARS genome".

38. Genome Canada's National Genomics Conference. Montreal, PQ. Oct 2002. "Bioinformatics of Mammalian Gene Expression".

37. Genome Canada's National Genomics Conference. Montreal, PQ. Oct 2002. "Sequencing and Mapping, Arrays, Proteomics and Bioinformatics Technology Platform".

36. BC Cancer Agency's Medical Oncology and Radiation Oncology Rounds. Vancouver, BC. Sept 2002. "Collaborative Opportunities at the BC Cancer Agency at the Genome Sciences Centre".

35. Annual George M. O'Brien Workshop. Vancouver, BC. June 2002. "The British Columbia Cancer Agency Genome Sequence Centre."

34. Simon Fraser University. Burnaby, BC. May 2002. "An Update on Activities at the British Columbia Cancer Agency Genome Sequence Centre".

33. BC Cancer Agency Vancouver Island Cancer Centre Meeting. Vancouver, BC. Apr 2002. "Collaborative Opportunities at the BC Cancer Agency at the Genome Sciences Centre".

32. BC Cancer Agency Fraser Valley Cancer Clinic. Vancouver, BC. Apr 2002. "Collaborative Opportunities at the BC Cancer Agency at the Genome Sciences Centre".

31. Canadian Bioinformatics Workshop. Vancouver, BC. Feb 20, 2002. "The British Columbia Cancer Agency Genome Sequence Centre – Projects and Prospects".

30. BC Centre for Disease Control. Vancouver, BC. Jan 2002. "An Update on Activities at the British Columbia Cancer Agency Genome Sequence Centre".
29. CIHR (Genetics) and Genome Canada's Joint Workshop on Bioinformatics. Aylmer, PQ. Sep 19, 2001. "Bioinformatics in the Context of a Genome Sequence Centre".
28. XVII World Congress of the International Society for Heart Research. Winnipeg, MB. July 6-11, 2001. "Gene Sequencing and Analysis of Sequence Variation in Human Disease".
27. University of Alberta, Department of Biological Sciences. Edmonton, AB. May 2001. "An Update on Activities at the British Columbia Cancer Agency Genome Sequence Centre."
26. Stem Cell Expression Profiling Workshop: The Stem Cell Network. Toronto, ON. May 2001. "SAGE at the BC Cancer Agency Genome Sequence Centre".
25. University of Calgary, Department of Medical Genetics. Calgary, AB. Apr 2001. "DNA Mapping and Sequencing at the British Columbia Cancer Agency Genome Sequence Centre".
24. Genus Capital Management. Vancouver, BC. Mar 2001. "Genomics – A Report".
23. BC Cancer Agency Annual Clinical Cancer Conference. Vancouver, BC. Nov 2000. "An Update on Activities at the Genome Sequence Centre".
22. Cold Spring Harbor Meeting on Mouse Molecular Genetics. Cold Spring Harbor, NY. Aug 30-Sep 3, 2000. "Fingerprinted BAC Clones for Sequencing the Mouse Genome".
21. University of British Columbia's Biotechnology Retreat, UBC. Vancouver, BC. July 11, 2000. "The Genome Sequence Centre – Projects and Prospects".
20. The Fifth Symposium on Cancer Research: Bridging the Straits of Clinical Cancer Research. Cowichan Bay, BC. Oct 1999. "Genomics Today and Tomorrow".
19. Canadian Association of Medical Oncologists Annual Meeting – "Genes and vaccines". Toronto, ON. Apr 1999. The Human Genome Project: A Platform for Gene Identification.
18. Society of Nematologists Meeting. Monterey, CA. July 609, 1999. "Sequence-based Approaches to Exon Identification in *Caenorhabditis elegans*".
17. 12th Annual Cold Spring Harbor Meeting on Genome Sequencing and Biology. Cold Spring Harbor, NY. 1999. "A Database of Fingerprinted Human BACs".
16. Fourth International Strategy Meeting on Human Genome Sequencing. Cold Spring Harbor, NY. 1999. "BAC Fingerprinting to Support the International Human Genome Sequencing Project".
15. Cold Spring Harbor Advanced Genome Sequencing Analysis Course. Cold Spring Harbor, NY. 1999. "Large-Scale High-Throughput Map Construction to Support Genome Sequencing".
14. Full-length cDNA cloning: A Workshop on Problems and Solutions, Banbury Center, Cold Spring Harbor, NY. 1998.
13. National Cancer Institute (USA) Tumor Gene Index Steering Committee Meeting. St. Louis, WA. 1998. "Full-length cDNA Sequencing at Washington University Genome Sequencing Center".
12. Mouse Genome Action Plan Workshop. Bethesda, MD. 1998. "A Summary of the Mouse EST Collection".
11. Arabidopsis Genome Workshop. Cold Spring Harbor, NY. 1997. "Construction of Sequence-Ready Contigs from Fingerprinted BACs".

10. National Cancer Institute (USA) Tumor Gene Index Steering Committee M eeting. 1997. "ESTs and the Tumour Gene Index".

9. BC Cancer Agency. Vancouver, BC. 1997. "Large-scale DNA Sequencing and gene discovery: Comparative Genomics, Expressed Sequence Tags and the Human Genome Project".

8. Nematode Evolution Workshop. Madison, WI. 1997. "Comparing the Genomes of *Caenorhabditis elegans* and *Caenorhabditis briggsae* by Large-Scale DNA Sequencing".

7. Zebrafish Genome Workshop. Boston, MA. 1997. "Sequence Tags for Different Genomes".

6. National Human Genome Research Institute, National Institutes of Health (USA). Bethesda, MD. 1997. "The Washington University EST Sequencing Effort".

5. Molecular Helminthology: An integrated approach. Keynote Symposium on Molecular and Cellular Biology. 1996. "Large-Scale DNA Sequencing and Discovery of *Caenorhabditis elegans* genes".

4. University of British Columbia. Vancouver, BC. 1996. "The Human Genome Project at Washington University Genome Sequencing Center".

3. University of Alberta. Edmonton, AB. 1996. "An Update on the *C. elegans* Genome Sequencing Project".

2. International Quality and Productivity Center Meeting: Gene Function Determination. Washington, D.C. 1996. "Advances in the Identification and Validation of Novel Molecular Targets".

1. HUGO meeting. Ile des Embiez, France. 1995. "Sequencing and Mapping ESTs".

PUBLIC OUTREACH PRESENTATIONS:

64. TFRI Marathon of Hope Cancer Centres Network Panel Discussion at Terry Fox Foundation Donor Reception. Hosted by Mr. John Kearsey. Toronto, ON. May 23, 2024.

63. Presentation on the TFRI Marathon of Hope Cancer Centres Network to Edward Jones. Hosted by Terry Fox Foundation. Mar 28, 2023.

62. Presentation. The Government of Canada's Pan-Canadian Genomics Strategy Consultations – Leaders' Roundtable (Virtual). June 15, 2022. Leaders' table on the genomics landscape.

61. Presentation. Probus Club of North Shore (Virtual). May 10, 2021. "Genomics – The Future of Cancer Care."

60. Presentation. BC Cancer Foundation. Through a New Lens with BC Cancer: POG (Virtual). Apr 8, 2021.

59. Science Plus (Virtual). Nov 24, 2020. "Update on Personalized Oncogenomics (POG) Project.

58. Science Plus-Personalized Genetics for Patient Treatment. Vancouver, BC. May 30, 2017. "The BC Cancer Agency Personalized OncoGenomics (POG) Project".

57. Presentation. Probus Club of North Shore. West Vancouver, BC. Apr 10, 2017. "The BC Cancer Agency Personalized OncoGenomics (POG) Project".

56. Presentation. Rotary Club of White Rock. White Rock, BC. Sep 13, 2016.

55. Presentation. World Presidents' Organization-BC Cancer Agency Meeting. Vancouver, BC. Apr 18, 2016.

54. Presentation. Eric Hamber Secondary School Grade 9 Science Class. Vancouver, BC. Apr 8, 2016.

53. UBC Mini-Med Health Education Series. Kelowna, BC. Oct 27, 2015. "The BC Cancer Agency Personalized Onco-Genomics (POG) Project".

52. 4th Annual INTERFACE Summit. Vancouver, BC. Sep 30, 2015. “Towards Genomic Medicine for Cancer Populations: The BC Cancer Agency Personalized Oncogenomics (POG) Project”.

51. Northern Health Authority Board Meeting. Prince George, BC. Oct 20, 2015. “The BC Cancer Agency Personalized Onco-Genomics (POG) Project”.

50. BC Cancer Foundation Board Meeting. Vancouver, BC. June 3, 2015. “The BC Cancer Agency Personalized Onco-Genomics (POG) Project”.

49. Terry Fox Foundation Run Organizer Workshop. Port Coquitlam, BC. May 30, 2015. “The BC Cancer Agency Personalized Onco-Genomics (POG) Project”.

48. West Vancouver Community Society’s Forum “Cancer Research in BC - The Courage to Say Cure”. West Vancouver, BC. Mar 31, 2015. “The BC Cancer Agency Personalized Onco-Genomics (POG) Project”.

47. PHSA Research Committee Meeting. Vancouver, BC. Feb 25, 2015. “Cancer sequencing for diagnoses and treatment planning: A genomic perspective”.

46. University of British Columbia Board of Governors’ Meeting. Vancouver, BC. Feb 12, 2015 “Cancer sequencing for diagnoses and treatment planning: A genomic perspective”.

45. Michael Smith Foundation for Health Research Board of Directors’ Meeting. Vancouver, BC. Sep 26, 2014. “Canada’s Michael Smith Genome Sciences Centre”.

44 The Leukemia & Lymphoma Society of Canada’s Journey of Hope Event. Vancouver, BC. June 2014. “Genome analysis reveals major tumor suppressors & oncogenes in lymphomas.”

43. BC Cancer Agency’s Lymphoid Education Forum. Vancouver, BC. Apr 4, 2014. “Genome analysis of lymphoma”.

42. Genome BC Board of Directors’ Meeting. June 7, 2013. Vancouver, BC. “Cancer sequencing for diagnoses and treatment planning: A genomic perspective from the BC Cancer Agency”.

41. Illumina 2013 Global Sales Meeting. Whistler, BC. Feb 06, 2013. “Personalized oncogenomics”.

40. Genome BC’s Bringing Genomics Home Event. Prince George, BC. Nov 15, 2012. “Genomics: What is it and why it matters”.

39. BC Cancer Foundation 2011 Inspiration Gala. Vancouver, BC. Oct 2011. “Personalized Medicine Project”.

38. BC Cancer Foundation Annual Donor Recognition Event. Vancouver, BC. Sep 2011.

37. BC Cancer Foundation Inspiration Gala Cocktail Reception. Vancouver, BC. Sep 2011. “Personalized Medicine Project”.

36. The Leukemia & Lymphoma Society of Canada’s Journey of Hope Event. Vancouver, BC. June 2011. “The work –and vision-of the Genome Sciences Centre”.

35. BC Cancer Agency Clinician-Scientist Retreat “Bridging the Bench to the Bedside”. Vancouver, BC. May 06, 2011. Presentation on “The EZH2 Story”.

34. Vancouver Chinatown and Arbutus Lions Club Medal of Merit Award Dinner. Vancouver, BC. May 2011.

33. University of British Columbia. Dr. Donald Riddle Retirement Symposium. Vancouver, BC. Nov 05, 2010. “DNA sequencing for genome analysis”.

32. BC Cancer Foundation Dinner Event. Vancouver, BC. June 2010. Presentation on brain cancer research.

31. The Leukemia & Lymphoma Society of Canada’s Journey of Hope Event. Vancouver, BC. June 2010.

30. Vancouver Chinatown and Arbutus Lions Club Medal of Merit Award Dinner. Vancouver, BC. May 2010.

29. BC Cancer Agency, Lymphoid Cancer Education Forum. Vancouver, BC. Apr 23, 2010. “DNA Mutations in Follicular and Diffuse Large B Cell Lymphomas”.

28. BC Cancer Foundation Dinner Event. Vancouver, BC. Apr 2010. Presentation on lymphoma research.

27. Provincial Health Services Authority Board of Directors Meeting. Langley, BC. Mar 04, 2010. “Genome Analysis for Cancer Mutation Discovery”.

26. Glenwood 2010 Interdisciplinary Seminar Series. Vancouver, BC. Feb 2010. “Cancer Genomics”.

25. BC Cancer Agency, Brain Tumour Symposium, Richmond, BC. Jan 22, 2010. “Cancer Genetics and Brain Tumour”.

24. Vancouver Chinatown and Arbutus Lions Club Meeting. Vancouver, BC. Dec 2009.

23. BC Cancer Foundation Board Meeting. Vancouver, BC. Sep 2009.

22. Vancouver Chinatown and Arbutus Lions Club Medal of Merit Award Dinner. Vancouver, BC. May 2009.

21. BC Cancer Agency’s Bridging the Gulf Between BC Cancer Clinicians and Scientists Retreat. Squamish, BC. Apr 05, 2009. “Cancer genome and transcriptome sequencing”.

20. BC Cancer Foundation Annual Leadership and Legacy Circle Event. Vancouver, BC. Apr 2009.

19. BC Cancer Agency Genome Sciences Centre’s Forum on Genomic Technologies for Cancer Research. “Genomes, Transcriptomes, and Personalized Medicine”. Vancouver, BC. Dec 11, 2008.

18. BC Cancer Agency, Lymphoid Cancer Translational Research Retreat. Vancouver, BC. Oct 31, 2008. “Genomics”.

17. BC Cancer Foundation’s Leadership and Legacy Circle Event. Vancouver, BC. May 2008.

16. Vancouver Chinatown and Arbutus Lions Club Medal of Merit Award Dinner. Vancouver, BC. May 2008.

15. Presentation, “Genomes and Genomics” ~150 Biology high school students, as part of the MORGEN Project Outreach Program. Vancouver, BC. Oct 2007.

14. Genome BC 2007 Board Retreat. Vancouver, BC. July 10, 2007. “Trends in Science and Technology.”

13. Presentation, The Young Presidents' Organization (BC Chapter) “Involved and Engaged, In the Business or Cancer Research” Event. Vancouver, BC. Apr 2007.

12. Vancouver Chinatown and Arbutus Lions Club Medal of Merit Award Dinner. Vancouver, BC. Feb 2007.

11. Simon Fraser University’s Genomics Mini Symposium. Burnaby, BC. Dec 2006. “New opportunities at the Genome Sciences Centre”.

10. Presentation “An Overview of Genomics/Genomics Technology” , ~150 Biology 11 high school students, as part of the MORGEN Project Outreach Program. Vancouver, BC. Nov 2006.

9. Presentation, The Young Presidents' Organization Canadian Council Visit at the BC Cancer Research Centre. Vancouver, BC. May 2006.

8. Probus Club. Surrey, BC. Nov 10, 2004. “Genomics Research in BC”.
7. Simon Fraser University. Burnaby, BC. June 2004. Convocation address.
6. BC Research Institute for Children’s & Women’s Health Mini Med School. “The SARS Coronavirus Genome Sequence”. Vancouver, BC. 2003.
5. 1st Annual BC Cancer Foundation Leadership Circle Reception. Vancouver, BC. 2003. “The Importance of Research”.
4. Genome British Columbia Board Retreat. Vancouver, BC. 2003. “Maintaining the Momentum – Critical Factors for Genome BC Success”.
3. Introduction to Legislative Assembly & Caucus Briefing. Victoria, BC. 2003. “Genomics 101”.
2. BC Biotech and First Forward present: Bioinformatics for Biotech Executives. Vancouver, BC. 2002. “Bioinformatics at the BCCA Genome Sciences Centre”.
1. Presentation to Canadian Federal Minister of Health Alan Rock. Vancouver, BC. 1999. “Genomics: Prospects and Progress”.

MEETING ABSTRACTS AND POSTERS (Marra Trainees in bold or underlined)

1. EHA-SfPM Precision Medicine Meeting. Copenhagen, Denmark. Sep 25-27, 2024. **Krekhno Z**, Wee K, Pleasance E, Titmuss E, Shen YQ, Mungall K, Chuah E, Mungall A, Bonakdar M, Taylor G, Csizmok V, Grisdale CJ, Xu M, Dupuis JH, McConechy MK, Nelson J, Yip S, Sun S, Lim H, Renouf D, Jones SJM, Marra MA, Laskin J. Whole genome and transcriptome-assisted immune profiling of metastatic tumours: a precision medicine approach to immunotherapy trial design. **(Abstract, Presentation)**
2. International Papillomavirus Conference. Edinburgh, UK. Nov 12-15, 2024. **Porter VL**, O’Neill K, Signe MacLennan S, Corbett R, Ng M, Culibrk L, Hamadeh Z, Iden M, Schmidt R, Tsaih SW, Nakisige C, Origa M, Orem J, Chang G, Fan J, Nip KM, Akbari V, Chan SK, Hopkins J, Moore RA. Chuah E, Mungall KL, Mungall AJ, Birol I, Jones SJM, Rader JS, Marra MA Rearrangements of viral and human genomes at human papillomavirus integration events and their allele-specific impacts on cancer genome regulation.
3. 23rd European Conference on Computational Biology. Turku, Finland. Sep 16-20, 2024**.** Dupuis JH, Csizmok V, O’Neill K, Galbraith A, Akbari V, Wee K, Xu M, Grisdale CJ, Krekhno Z, Shen Y, Taylor GA, Bohm AK, Pleasance E, McConechy MK, Nelson JMT, Chuah E, Mungall KL, Moore RA, Mungall AJ, Marra MA, Laskin J, Jones SJM, Enhancing Precision Cancer Treatment Options Using Combined Short- and Long-Read Sequencing Technologies. **(Poster presentation)**
4. The Gordon Research Conference. Manchester, NH. Jun 8-14, 2024. **Yan C,** Pleasance E, Shen Y, McConechy M, Nelson J, Trinh D, Bailey M, Jin D, Laskin J, Marra MA. Single-cell Multiomics for Precision Cancer Medicine (**Poster presentation**)
5. 2024 UBC MBIM Undergraduate Research Symposium. Vancouver, BC. Apr 29, 2024. Jain A, Wee K, Pleasance E, Frey C, Abacan M, McConechy M, Laskin J, Marra M and the POG Team. Immune Checkpoint Inhibitors and Tumor Characteristics in Precision Oncology.
6. BC Cancer Summit. Vancouver, Canada. Nov 16 – Nov 18, 2023. **Takemon Y**, Pleasance ED, Csizmok V, Mungall A, Moore RA, Chua E, Mungall KL, Lewis E, Lim HJ, Renoug DJ, Jones SJM, Laskin J, Marra MA. Using KMT2D deficiency as a COMPASS to identify cancer cell vulnerabilities. (**Poster**).
7. BC Cancer Summit. Vancouver, Canada. Nov 16-18, 2023. **MacLennan, S., Porter, V.**, Marra, M. Characterizing the heterogeneous genomic and epigenomic landscapes of extrachromosomal DNAs (ecDNAs) in cervical cancer (**Poster**).

8. Cancer Research Conference. Halifax, Canada. Nov 12-14, 2023. **MacLennan, S., Porter, V**., Marra, M. Characterizing the heterogeneous genomic and epigenomic landscapes of extrachromosomal DNAs (ecDNAs) in cervical cancer (**Poster**).

9. Canadian Cancer Research Conference. Halifax, Canada. Nov 12-14, 2023. **Ng M**, **Porter V**, Trinh DL, O'Neill K, Corbett R, Iden M, Rader JS, Marra MA. Effect of HPV integration on 3D genome structure and function in cervical cancer. (**Poster**).

10. Canadian Cancer Research Conference (CCRC; in-person event). Nov 12-14, 2023. **Takemon Y**, Pleasance ED, Csizmok V, Mungall AJ, Moore RA[3], Chuah E, Mungall KL, Lewis E, Lim HJ, Renouf DJ, Jones SJM, Laskin J, Marra MA. Using KMT2D deficiency as a COMPASS to identify cancer cell vulnerabilities. **(Poster)**.

11. UBC Medical Genetics Research Day. Vancouver, Canada. Oct 27, 2023. **MacLennan, S., Porter, V**., Marra, M. Characterizing the heterogeneous genomic and epigenomic landscapes of extrachromosomal DNAs (ecDNAs) in cervical cancer (**Poster**).

12. BC Cancer Research Day. Vancouver, Canada. Sep 29, 2023. **MacLennan, S., Porter, V**., Marra, M. Characterizing the heterogeneous genomic and epigenomic landscapes of extrachromosomal DNAs (ecDNAs) in cervical cancer (**Poster**).

13. Cell Symposia: The Conceptual Power of Single Cell Biology (In-person Event). Aug 28-30, 2023. **Yan C**, Janessa Laskin, Marco A. Marra. Precision medicine for advanced cancers at single-cell resolution. **(Poster).**

14. Bioinformatics, interdisciplinary oncology, genome science and technology (BIG) research day (in-person event). Mar 28, 2023. **Takemon Y** and Marra MA. Application of an *in silico* framework to map genetic networks and elucidate biological functions and vulnerabilities of tumour suppressor genes. **(Poster)**.

15. London Calling (London, UK). May 17-19, 2023. **Porter VL**, O'Neill K, Corbett RD, MacLennan S, Iden M, Mutchler R, Tsaih S-W, Nip, Hamadeh Z, Culibrk L, Fan J, Nip KM, Akbari V, Chan SK, Moore R, Mungall KL, Mungall AJ, Birol I, Jones SJM, Rader JS, Marra MA. Identification of novel genomic structures and regulation patterns at HPV integration events in cervical cancer. (**Poster**).

16. Advances in Genome Biology and Technology (AGBT) General Meeting. Hollywood, FL, USA. Feb 5-9, 2023. **Takemon Y,** Gagliardi A, Chan SY, Trinh DL, Topham JT, Huff RD, Hughes CS, Marra MA. Application of an *in silico* framework to map genetic networks and elucidate biological functions of *KMT2D*, a frequently mutated gene across cancer types. **(Poster presentation and rapid fire talk)**

17. UBC Faculty of Medicine Precision Health Symposium, Feb 2023. Erin Pleasance**,** Laura Williamson, Yaoqing Shen, Karen Mungall, Eric Chuah, Richard Moore, Andrew Mungall, Jessica Nelson, Stephen Yip, Kasmintan Schrader, Dean Regier, Sophie Sun, Howard Lim, Daniel J. Renouf, Steven Jones, Janessa Laskin, Marco Marra. Precision Cancer Medicine: The Personalized OncoGenomics Program.

18. UBC Faculty of Medicine Precision Health Symposium, Feb 2023. Laura Williamson, Kieran O'Neill, Erin Pleasance, Richard Corbett, Vahid Akbari, Glenn Chang, Andrew Galbraith, Katherine Dixon, Jeremy Fan, **Signe MacLennan, Vanessa Porter**, Richard Moore, Andrew Mungall, all members of the POG team, Janessa Laskin, Marco Marra, Steven Jones. Oxford Nanopore Long Read Sequencing of Advanced Tumours from the Personalized OncoGenomics and Marathon of Hope Cancer Centres Network Study.

19. BC Cancer Summit. Vancouver, Canada. Nov 24- 26, 2022. **MacLennan, S., Porter, V**., Marra, MA. The genomic structures, diversity, and regulation of extrachromosomal DNAs (ecDNAs) in cervical cancer. **(Oral presentation).**

20. 64th American Society of Hematology Annual Meeting and Exposition. New Orleans, LA. , Dec 10-13, 2022. Haya Shaalan, Nicole Thomas, Merrill Boyle, Barbara Meissner, Marco A. Marra, Christian Steidl, David W. Scott, Laura K Hilton, Ryan D. Morin. Blood (2022) 140 (Supplement 1): 9231–9232. https://doi.org/10.1182/blood-2022-159787

21. 64th American Society of Hematology Annual Meeting and Exposition. New Orleans, LA. Dec 10-13, 2022. Christopher K Rushton, Ryan N Rys, Elizabeth Chavez, Laura K Hilton, Miguel Alcaide, Kostiantyn Dreval, Matthew Cheung, Manuela Cruz, Krysta M. Coyle, Barbara Meissner, Susana Ben-Neriah, Neil R. Michaud, Scott Daigle, Jordan Davidson, Jasper Wong, Annette E. Hay, Michael D. Jain, Lois E. Shepherd, Marco A. Marra, John Kuruvilla, Michael Crump, Koren Kathleen Mann, Sarit Assouline, Christian Steidl, David W. Scott, Nathalie A. Johnson, Ryan D. Morin. Recurrent Copy Number Alterations Contribute to a Unique Genetic Landscape in Relapsed-Refractory DLBCL. Blood (2022) 140 (Supplement 1): 9259–9260. https://doi.org/10.1182/blood-2022-169623

22. 64th American Society of Hematology Annual Meeting and Exposition. New Orleans, LA. Dec 10-13, 2022. Laura K Hilton, Henry S. Ngu, Brett Collinge, Kostiantyn Dreval, Susana Ben-Neriah, Christopher K Rushton, Jasper Wong, Manuela Cruz, Andrew Roth, Merrill Boyle, Barbara Meissner, Graham W. Slack, Pedro Farinha, Jeffrey W. Craig, Alina S. Gerrie, Ciara L. Freeman, Diego Villa, Kerry J. Savage, Laurie H. Sehn, Marco A. Marra, Aly Karsan, Christian Steidl, Ryan D. Morin, David W. Scott. Relapse Timing Is Associated with Distinct Evolutionary Dynamics and Response to Salvage Therapy in DLBCL. Blood (2022) 140 (Supplement 1): 1310–1312. https://doi.org/10.1182/blood-2022-160187

23. 64th American Society of Hematology Annual Meeting and Exposition. New Orleans, LA. Dec10-13, 2022. Kostiantyn Dreval, Laura K Hilton, Krysta M. Coyle, Jasper Wong, Merrill Boyle, Brett Collinge, Manuela Cruz, Barbara Meissner, Christopher K Rushton, Marco A. Marra, David W. Scott, Christian Steidl, Ryan D. Morin. Towards a Unified Genetic Classification System for Diffuse Large B-Cell Lymphoma (DLBCL). Blood (2022) 140 (Supplement 1): 3495–3497. https://doi.org/10.1182/blood-2022-167043.

24. 64th American Society of Hematology Annual Meeting and Exposition. New Orleans, LA. Dec 10-13, 2022. Nicole Thomas, Kostiantyn Dreval, Daniela S. Gerhard, Laura K Hilton, Jeremy S. Abramson, Nancy L. Bartlett, Jeffrey Bethony, Jay Bowen, Anthony Bryan, Corey Casper, Maureen Dyer, Manel Esteller, Carlos Garcia-Prieto, Julie M Gastier-Foster, Alina S. Gerrie, Bruno M. Grande, Timothy C. Greiner, Nicholas B. Griner, Thomas G. Gross, Nancy Lee Harris, John D. Irvin, Elaine S. Jaffe, Fabio Leal, Jean Paul Martin, Marie-Reine Martin, Sam M. Mbulaiteye, Charles G. Mullighan, Andrew J. Mungall, Karen Mungall, Constance Namirembe, Ariela Noy, Martin D Ogwang, Jackson Orem, German Ott, Hilary Petrello, Steven J Reynolds, Steven H. Swerdlow, Alexandra Traverse-Glehen, Wyndham H. Wilson, Marco A. Marra, Louis M. Staudt, David W. Scott, Ryan D. Morin. DNA Methylation-Based Burkitt Lymphoma Epitypes Have Distinct Molecular and Clinical Features. *Blood* (2022) 140 (Supplement 1): 1734–1736. https://doi.org/10.1182/blood-2022-163728.

25. Proceedings of the AACR Special Conference on Pancreatic Cancer. Boston, MA. Sep 13-16, 2022. Andrew Metcalfe, Joanna M. Karasinska, James T. Topham, Steve E. Kalloger, Hassan Ali, Dawn Ashforth, Marco A. Marra, Janessa Laskin, Patricia A. Tang, Rachel Goodwin, Oliver F. Bathe, Daniel J. Renouf, David F. Schaeffer. Targeting SMURF1 with low-dose proteasome inhibitors in pancreatic cancer organoids [abstract]. In: AACR; Cancer Res 2022;82(22 Suppl): Abstract nr B053

26. Proceedings of the AACR Special Conference on Pancreatic Cancer. Boston, MA. Sep 13-16, 2022. Lan V. Tao, James T. Topham, Joanna M. Karasinska, Erica S. Tsang, Andrew Metcalfe, Hassan Ali, Dawn Ashforth, Rachel Goodwin, Patricia A. Tang, Oliver F. Bathe, Janessa Laskin, Marco Marra, Daniel J. Renouf, David F. Schaeffer. Elucidating the role of insulin receptor isoform expression in metastatic pancreatic ductal adenocarcinoma [abstract]. In: AACR; Cancer Res 2022;82(22 Suppl):Abstract nr B066.

27. Annual Research Day - Department of Medical Genetics. Vancouver, Canada. Nov 04, 2022. **MacLennan, S., Porter, V.**, Marra, MA. The genomic structures, diversity, and regulation of extrachromosomal DNAs (ecDNAs) in cervical cancer. **(Oral presentation)**

28. American Society for Human Genetics (ASHG) Meeeting. Los Angeles, USA. Oct 25-29, 2022. **Dixon K**, Shen Y, Hoeschen C, Wong H, Cremin C, Senz J, Lum A, O'Neill K, Ch'ng C, Hong Q, Karasinska J, Topham J, Pleasance ED, Jones M, Zhao E, Young S, Mungall KL, Mungall AJ, Moore R, Ma YP, Fok A, Nelson J, Lee MKC, Yip S, Lim H, Karsan A, Jones SJM, Laskin J, Marra MA, Schaeffer DF, Renouf DJ, Huntsman DG & Schrader KA. Genome and transcriptome landscape of familial pancreatic cancer and implications for altered glucose metabolism in moderate-penetrance cancer susceptibility. **(Oral presentation)**

29. BC Cancer Research Day. Vancouver, Canada. Sep 23, 2022. MacLennan, S., Porter, V., Marra, MA. The genomic structures, diversity, and regulation of extrachromosomal DNAs (ecDNAs) in cervical cancer. **(Oral presentation)**

30. SIOP 2022 International Society of Paediatric Oncology Meeting. Barcelona, Spain. Sep 28-Oct 01 2022. **Lambo S,** Trinh D, Jin D, Wei L, Ries R, Furlan S, Meschinci S, Marra MA. Identifying Mechanisms of Resistance in Pediatric Patients with Acute Myeloid Leukemia using Comprehensive Longitudinal Single Cell Profiling.

31. Gordon Research Conference: Genome Instability, DNA Repair, and Human Diseases. Ventura, CA, USA. July 9-15, 2022. **Takemon Y**, Gagliardi A, Chan SY, Trinh DL, Topham JT, Huff RD, Hughes CS, Marra MA. *In silico* genetic interaction network mapping expands KMT2D's role in maintaining genomic stability. **(Poster presentation)**

32. ICGC ARGO Meeting (Virtual). June 2022. Titmuss E, Corbett RD, Davidson S, Abbasi S, Williamson LM, Pleasance E, Shlien A, Renouf DJ, Jones SMJ, Laskin J, Marra MA. TMBur: A Distributable Tumor Mutation Burden Approach. **(Oral presentation)**

33. ICGC ARGO Meeting (Virtual). June 2022. **Topham JT,** Karasinska JM, Tsang ET, Williamson LM, Jang GH, Metcalfe A, Ali H, Kalloger S, Loree JM, Bathe OF, Tang PA, Goodwin R, Laskin J, Knox J, Gallinger S, Marra MA, Jones S, Schaeffer D, Renouf DJ. Genomic landscape of *KRAS* wildtype pancreatic ductal adenocarcinoma is highly diverse across independent clinical trial cohorts. **(Oral presentation)**

34. Gordon Research Conference - Single-Cell Cancer Biology. Dissecting Evolution and Heterogeneity of Single Cancer Cells. Easton, MA. June 12-17 2022. **Lambo S,** Trinh D, Jin D, Wei L, Ries R, Furlan S, Meschinci S, Marra MA. Identifying Mechanisms of Resistance in Pediatric Patients with Acute Myeloid Leukemia using Comprehensive Longitudinal Single Cell Profiling. **(Oral presentation)**

35. London Calling (Hybird Event). May 18-20, 2022. **Porter VL**, O'Neill K, Corbett R, Culibrk L, Marissa Iden, Rachel Mutchler, Shirng-Wern Tsain, Ka Ming Nip, Vahid Akbari, Simon K. Chan, Karen L. Mungall, Andrew J. Mungall, Inanc Birol, Steven J. M. Jones, Janet S. Rader, Marco A. Marra. Identification of novel genomic structures and regulation patterns at HPV integration events in cervical cancer. **(Oral presentation)**

36. 2022 ASCO Annual Meeting. Chicago, IL. June 3-7, 2022. Regier DA, Weymann D, Chan B, Ho C, Lim HJ, Yip S, Rittberg R, Sun S, Marra MA, Jones SJM, Laskin JJ, Pollard S. Life-cycle health technology assessment for precision oncology.

37. London Calling 2022 (Oxford Nanopore's AGBT-away-from-AGBT) (Hybird Event). May 18-20, 2022. **Akbari V**, O'Neill K, Corbett R, **Porter VL**, Pandoh P, Moore R, Marra MA, Hirst M, Jones SJ. DNA Methylation Analysis In Human Tumor Samples Using Nanpore Sequencing.

38. ICGC-ARGO Research Conference. Virtual. June 2022. Weymann D, Laskin J, Jones ST, Lim HJ, Yip S, Renouf DJ, Schrader KA, Sun S, Marra MA, Regier DA. Downstream patient care and survival impacts of whole-genome and transcriptome analysis for advanced cancers.

39. London Calling (Oxford Nanopore's AGBT-away-from-AGBT) (Hybird Event). May 18-20, 2022. **O'Neill K**, Pleasance E, Dixon K, Akbari V, Fan J, Porter V, Grisdale C, Corbett RD, Taylor G, Shen Y, Mungall KL, Chuah E, Williamson L, Laskin J, Marra MA, Jones S. Nanopore Sequencing for Personalised OncoGenomics. **(Oral presentation)**

40. ICGC-ARGO Research Conference Virtual. June 2022. Laskin J, Pleasance E, Bohm A, Williamson LM, Nelson JMT, Titmuss E, Mungall AJ, Yip S, Regier DA, Weymann D, Schrader K, Sun S, Lim HJ, Renouf DJ, Jones SJM, Marra MA. Assessment of the clinical application of whole genome transcriptome sequencing for people with advanced cancers.

41. AACR Annual Meeting. New Orleans, LA. Apr 8-12, 2022. James Topham, Erica Tsang, Joanna Karasinska, Andrew Metcalfe, Hassan Ali, Steve Kalloger, Veronika Csizmok, Laura Williamson, Emma Titmuss, Hui-Li Wong, Richard Moore, Andrew Mungall, Jonathan Loree, Oliver Bathe, Patricia Tang, Rachel Goodwin, Janessa Laskin, Marco Marra, Steven Jones, David Schaeffer, Daniel Renouf. Analysis of KRAS wildtype pancreatic ductal adenocarcinoma reveals mutation and expression-based similarities to cholangiocarcinoma.

42. 11th Annual BIG Research Day (BIGX). University of British Columbia. Vancouver, BC. Mar 23, 2022. Takemon Y, Gagliardi A, Chan SY, Trinh, DL, Topham JT, Huff RD, Hughes CS, Marra MA. *In Silico* Genetic Interaction Network Expands KMT2D's Role in Maintaining Genomic Stability. **(Rapid-fire talk)**

43. 63rd ASH Annual Meeting and Exposition. Atlanta, GA. Dec 11-14, 2021. Pararajalingam P, Hilton L, Coyle KM, Dreval K, Meissner B, Melnick A, Marra MA2, Scott DW, Morin RD. Complex structural variation associated with enhancer hijacking and loss of tumor suppressors in mantle cell lymphoma.

44. 63rd ASH Annual Meeting and Exposition. Atlanta, GA. Dec 11-14, 2021. Hilton LK, Dreval K, Soudi S, Ben-Neriah S, Cruz M, Collinge B, Coyle K, Grande BM, Duns G, Rushton CK, Boyle M, Meissner B, Farinha P, Slack GW, Mungall AJ, Marra MA, Connors JM, Steidl C, Scott DW, Morin RD. Constrained FL: A Genetically Distinct Subgroup of Follicular Lymphoma with Low Rates of Somatic Hypermutation and a Reduced Propensity for Histologic Transformation.

45. 63rd ASH Annual Meeting and Exposition. Atlanta, GA. Dec 11-14, 2021. Thomas N, Dreval K, Gerhard DS, Hilton LK, Cruz M, Soudi S, Wong J, Abramson JS, Bartlett NL, Bethony J, Bowen J, Bryan AC, Casper C, Dyer M, Gastier-Foster JM, Grande BM, Greiner T, Griner NB, Gross TG, Harris NL, Irvin JD, Jaffe E, Leal F, Martin JP, Martin M-R, Mbulaiteye SM, Mullighan CG, Mungall AJ, Mungall K, Namirembe C, Noy A, Ogwang MD, Orem J, Ott G, Petrello H, Reynolds SJ, Swerdlow SH, Traverse-Glehen A, Wilson WH, Marra MA, Staudt LM, Scott DW, Morin RD. Novel genetic subgroups inform on shared pathobiology within adult and pediatric Burkitt lymphoma.

46. Bioinformatics Open Source Conference (Virtual). July 29-30, 2021. Reisle C, Williamson L, Pleasance E, Bleile D, Davies A, Pellegrini B, Mungall K, Chuah E, Krzywinski M, Pletz RM, Li J, Stevenson R, Wong H, Reisle A, Douglas M, Lewis E, Bonakdar M, Nelson J, Grisdale C, Fisic A, Mitchell T, Renouf D, Yip S, Laskin J, Marra M, Jones S. Robust variant interpretation in precision oncology using a graph knowledge base. **(Oral presentation)**

47. High Throughput Sequencing (HiTSeq), ISMB/ECCB 2021. (Virtual). July 25-27, 2021. Culibrk L, Pleasance ED, Mungall K, Laskin J, Marra MA, Jones SJM. Investigating tumor genome instability with Ploidetec. **(Poster presentation)**

48. 17th Scientific Workshop / 4th ARGO Meeting (Virtual). Beijing, China. May 14-15, 2021. Titmuss E, Pender A, Pleasance E, Brown S, Grisdale CJ, Topham J, Shen Y, Bonakdar M, Taylor GA, Williamson

L, Mungall K, Chuah E, Mungall AJ, Moore RA, Lavoie JM, Yip S, Lim H, Renouf DJ, Sun S, Jones SJM, Holt R, Marra MA, Laskin L. CAPTIV-8: A prospective trial of atezolizumab using a multivariate model incorporating whole genome and transcriptome analysis.

49. American Association for Cancer Research Annual Meeting (Virtual). Apr 10-15, 2021. Williamson L, Rive C, Di Francesco D, Titmuss E, Chun E, Brown S, Milne K, Lee A, Yip S, Dix D, Holt R, Nelson B, Hirst M, Jones S, Rassekh R, Deyell R, Laskin J, Marra M. Response to nivolumab in pediatric chordoma with overexpression of brachyury. **(Poster presentation)**

50. American Association for Cancer Research Annual Meeting (Virtual). Apr 10-15, 2021. Titmuss E, Pender A, Pleasance E, Brown S, Grisdale CJ, Topham J, Shen Y, Bonakdar M, Taylor GA, Williamson L, Mungall K, Chuah E, Mungall AJ, Moore RA, Lavoie JM, Yip S, Lim H, Renouf DJ, Sun S, Jones SJM, Holt R, Marra MA, Laskin L. CAPTIV-8: A prospective trial of atezolizumab using a multivariate model incorporating whole genome and transcriptome analysis. **(Poster presentation)**

51. American Association for Cancer Research Annual Meeting (Virtual). Apr 10-15, 2021. Bohm A, Pleasance E, Titmuss E, Wee K, Taylor G, Bonakdar M, Shen Y, Williamson L, Csizmok V, Jones M, Nelson J, Deol B, Reisle C, Mungall K, Chuah E, Mungall A, Moore R, Sun S, Lim H, Renouf D, Jones S, Marra M, Laskin J. Personalized therapy choice integrating genome and expression data in advanced cancers. **(Oral presentation)**

52. American Association for Cancer Research Annual Meeting (Virtual). Apr 10-15, 2021. Weymann D, Pollard S, Chan B, Titmuss E, Bohm A, Laskin J, Jones SJM, Pleasance E, Nelson J, Fok A, Lim H, Karsan A, Renouf DJ, Schrader KA, Sun S, Yip S, Schaeffer DF, Marra MA, Regier DA. Difference-in-difference analysis of clinical and cost outcomes following genomics-informed advanced cancer treatment . **(Oral presentation)**

53. Virtual Keystone Symposia. Single Cell Biology. Mar 17-19, 2021. LeBlanc VG, Trinh DL, Hughes M, Aslanpour S, Livingstone D, Blough MD, Cairncross JG, Kelly JJ, Marra MA. Single-cell landscapes of primary glioblastoma and matched organoids and cell lines reveal variable retention of inter- and intra-tumour heterogeneity.

54. The Annual AGBT Meeting (Virtual). Mar 1-3, 2021. Haile S, Corbett RD, LeBlanc VG, Wei L, Pleasance S, Bilobram S, Brown K, Trinh E, Smith J, Trinh DL, Bala M, Chuah E, Mungall K, Moore RA, Mungall AJ, Coope RJ, Zhao Y, Jones SJ, Marra MA. A larger scale strand-specific protocol for full-length total RNA sequencing from single cells. **(Poster presentation)**

55. Society of Interventional Oncology 2021 Annual Scientific Meeting (Virtual). Feb 3-6, 2021. Wong SK, Shen Y, Weymann D, Nelson J, Shirvani D, Fisic A, Mungall AJ, Yuan R, Martin M, Ferguson DJ, Cafferty J, Laskin J, Marra MA, Lim HJ, Mar C. British Columbia’s Personalized Oncogenomics Research Program: Predictors of Biopsy Success for Genomic Analysis.

56. 2021 Gastrointestinal Cancers Symposium (Virtual). Jan 15-17, 2021. Tsang ES, Csizmok V, Williamson L, Pleasance ED, Topham JT, Karasinska J, Titmuss E, Schrader KA, Cafferty F, Yip S, Tessier-Cloutier B, Mungall K, Sun S, Lim HJ, Loree JM, Laskin JJ, Marra MA, Jones SJM, Schaeffer DF, Renouf DJ. Beyond BRCA? clinical utility of homologous recombination deficiency in gastrointestinal cancers.

57. 1st International Symposium of CCII - -Bioinformatics and its application to cancer and other diseases (Virtual). Jan 15, 2021. Chun H-J E, Johann PD, Milne K, Zapatka M, Buellesbach A, Ishaque N, Iskar M, Erkek S, Wei L, Tessier-Cloutier B, Lever J, Titmuss E, Topham J, Bowlby R, Chuah E, Mungall KL, Ma Y, Mungall AJ, Moore RA, Taylor MD, Gerhard DS, Jones SJM, Korshunov A, Gessler M, Kerl K, Hasselblatt M, Frühwald MC, Perlman EJ, Nelson BH, Pfister SM, Kool M, Marra MA. Comparative analyses of extra-cranial and cranial rhabdoid tumours reveal subgroups with cytotoxic T cell infiltration**.**

58. 62nd ASH Annual Meeting and Exposition (Virtual). Dec 5-8, 2020. Thomas N, Grande BM, Mungall AJ, Mungall K, Bowen J, Petrello H, Bryan T, Gerhard DS, Marra MA, Staudt LM, Morin RM. Key genetic and molecular aberrations identified in EBV-positive Burkitt lymphoma cell lines.

59. 62nd ASH Annual Meeting and Exposition (Virtual). Dec 5-8, 2020. Wei L, Trinh D, Ries R, Jin D, Corbett R, Smith JL, Furlan S, Meshinchi S, Marra MA. Integrative analysis of single-cell RNA-seq and ATAC-seq data across treatment time points in pediatric AML. ***(Blood. Nov 5, 2020, Vol 136, Suppl 1)***

60. 62nd ASH Annual Meeting and Exposition (Virtual). Dec 5-8, 2020. Rushton CK, Alcaide M, Cheung M, Michaud N, Daigle S, Rys RN, Arthur S, Zymiak M, Davidson J, Bushell K, Yu S, Jain M, Shepherd L, Marra MA, Kuruvilla J, Crump M, Mann K, Assouline S, Connors JM, Steidl C, Johnson N, Scott DW, Morin RD. The copy number landscape of relapsed and refractory diffuse large B-cell lymphoma. ***(Blood. Nov 5, 2020, Vol 136, Suppl 1)***

61. AACR Immunology and Immunotherapy Virtual Conference. Oct 19-20, 2020. Titmuss E, Pender A, Pleasance E, Fan K, Pearson H, Brown S, Grisdale CJ, Topham J, Shen Y, Bonakdar M, Taylor GA, Williamson L, Mungall K, Chuah E, Mungall AJ, Moore RA, Lavoie JM, Yip S, Lim H, Renouf DJ, Sun S, Jones SJM, Holt R, Marra MA, Laskin J. CAPTIV-8: A prospective trial of atezolizumab using a multivariate model incorporating whole genome and transcriptome analysis.

62. 2020 NANETS Multidisciplinary NET Medical Virtual Symposium. Oct 2-3, 2020. Yang KC, Kalloger S, Aird J, Lee M, Rushton C, Spencer S, Mungall K, Mungall A, Colborne S, Morin RD, Loree JM, Marra MA, Renouf DJ, Morin GB, Schaeffer DF, Gorski SM. Proteotranscriptomic classification and characterization of pancreatic neuroendocrine neoplasms.

63. Special Conference on Pancreatic Cancer of American Association for Cancer Research (AACR). Sep 29-30, 2020. Yang KC, Kalloger S, Aird J, Lee M, Rushton C, Spencer S, Mungall K, Mungall A, Colborne S, Morin RD, Loree JM, Marra MA, Renouf DJ, Morin GB, Schaeffer DF, Gorski SM. Proteotranscriptomic classification and characterization of pancreatic neuroendocrine neoplasms. ***(Cancer Res. Nov 2020; 30(22): PR 009)***

64. 2020 BC Cancer Virtual Research Day. Sep 21, 2020. Porter VL, Gagliardi A, Titmuss E. Bowlby R, Zong Z, Namirembe C, Griner N, Petrello H, Bowen J, Chan S, Culibrk L, Darragh T, Stoler MH, Wright T, Gesuwan P, Dyer M, Ma Y, Mungall KL, Jones SJM, Nakisige C, Novik K, Orem J, Origa M, Gastier-Foster JM, Yarchoan R, Casper C, Mills G, Rader JS, Ojesina A, Gerhard DS, Mungall AJ, Marra MA. Analysis of Ugandan cervical carcinomas identifies human papillomavirus clade–specific epigenome and transcriptome landscapes.

65. 28th Conference on Intelligent Systems for Molecular Biology (Virtual). July 13-16, 2020. Grewal JK, Pleasance E, Csizmok V, Williamson L, Bleile D, Wee K, Shen Y, Tessier-Cloutier B, Yip S, Renouf D, Laskin J, Marra M, Jones SJM. Single-sample pathway analysis using Pathway Impact Evaluation (PIE) of machine-learning based cancer classifiers. **(Poster presentation; 2nd Prize in Best Poster category in Translational Medicine)**

66. 17th Annual European-Neuroendocrine-Tumor-Society (ENETS) Conference. Mar 11-13, 2020. Yang KC, Kalloger S, Aird J, Lee M, Colborne S, Loree JM, Marra MA, Morin GB, Renouf DJ, Schaeffer DF, Gorski SM. Pancreatic Neuroendocrine Neoplasms: Dissecting the Molecular Heterogeneity. ***(Neuroendocrinol. 2020 Mar; 110:56 Suppl 1)***

67. USCAP 109th Annual Meeting. Los Angeles, CA. Feb 29-Mar 5, 2020. Naso JR,Topham JT, Lee MCK, Kalloger SE, Karasinska JM, Laskin J, Marra MA, Renouf DJ, Schaeffer DF. Association of Inflammatory Cell Infiltrates with Signatures of Immunogenicity in Metastatic Pancreatic Adenocarcinoma. ***(Lab Invest. 2020 Mar; 100:1664-1665 Suppl 1)***

68. The 20th Annual AGBT Meeting. Marco Island, FL. Feb 23-26, 2020. Zhao YJ, Haile S, Rogic S, Corbett RD, Bilobram S, Smailus D, Pandoh P, Kirk H, McDonald H, Bowlby R, Mungall KL, Chuah E, Coope

R, Mungall AJ, Moore R, Jones S, Stowe R, Marra MA. Automated RNA Extraction and Library Construction Protocols for Strand-Specific RNA Sequencing from Blood Samples. **(Poster presentation)**

69. The 20th Annual AGBT Meeting. Marco Island, FL. Feb 23-26, 2020. Gagliardi A, Porter V, Titmuss E, Zong Z, Bowlby R, Namirembe C, Griner N, Petrello H, Bowen J, Chan S, Darragh TM, Stoler MH, Wright TC, Gesuwan P, Dyer M, Ma Y, Mungall KL, Nakisige C, Novik K, Orem J, Origa M, HTMCP Working Group, Gastier-Foster J-M, Yarchoan R, Casper C, Mills G, Rader JS, Ojesina A, Gerhard DS, Mungall AJ, Marra MA. Analysis of Ugandan cervical carcinomas reveals human papillomavirus clade-specific epigenome and transcriptome landscapes. **(Poster presentation)**

70. The 20th Annual AGBT Meeting. Marco Island, FL. Feb 23-26, 2020. Coope RJN, Pleasance S, Pandoh P, Schlosser C, Corbett R, Zhao YJ, Mungall A, Moore R, Marra MA. Rapid Microdissection of Tissue Sections via Laser Ablation. **(Poster presentation)**

71. The 20th Annual AGBT Meeting. Marco Island, FL. Feb 23-26, 2020. Chuah E, Reisle A, Lim C, Schlosser C, Spothelfer D, Yang J, Reisle C, Davies A, Lewis E, Nelson J, Wang S, Mungall K, Ma Y, Yip S, Marra M, Jones S, Coope R. A platform for annotation and sharing of pathology imaging and integration with personalized genomic data. **(Poster presentation)**

72. 61st ASH Annual Meeting and Exposition. Orlando, FL. Dec 7-10, 2019. Coyle KM, Pararajalingam P, Arthur SE, Thomas N, Alcaide M, Meissner B, Boyle M, Grande BM, Rushton C, Tooman L, Slack GW, Mungall AJ, Gascoyne RD, Steidl C, Connors JM, Villa D, Marra MA, Johnson N, Scott DW, Morin RD. Mutations affecting RNA binding proteins are a novel feature of mantle cell lymphoma.

73. 61st ASH Annual Meeting & Exposition. Orlando, FL. Dec 7-10, 2019. Wei L, Ries R, Plettner P, Mungall K, Mungall A, Meshinchi S, Marra MA. Transcriptome Analysis of Pediatric AML Reveals Non Protein-Coding RNAs Associated with Poor Survival Outcome and Treatment Resistance. **(Poster presentation)**

74. BC Cancer Summit. Vancouver, BC. Nov 21-23, 2019. Tsang ES, Grisdale CJ, Pleasance E, Yip S, Cloutier B, Mungall K, Ng T, Sun S, Lim HJ, Renouf DJ, Laskin J, Marra M, Jones S, Loree JM. Uncovering Clinically Relevant Gene Fusion Events with Integrated Genomic and Transcriptomic Profiling.

75. BC Cancer Summit. Vancouver, BC. Nov 21-23, 2019. Weymann D, Pollard S, Laskin J, Jones SJM, Titmuss E, Pleasance E, Lim H, Karsan A, Renouf DJ, Roscoe R, Ho C, Levasseur N, Schrader KA, Sun S, Yip S, Marra M, Regier DA. An observational study protocol examining the real-world clinical effectiveness of whole genome and transcriptome analysis to guide advanced cancer care. **(Poster presentation)**

76. BC Cancer Summit. Vancouver, BC. Nov 21-23, 2019. Chun H-J E, Johann PD, Milne K, Zapatka M, Buellesbach A, Ishaque N, Iskar M, Erkek S, Wei L, Tessier-Cloutier B, Lever J, Titmuss E, Topham J, Bowlby R, Chuah E, Mungall KL, Ma Y, Mungall AJ, Moore RA, Taylor MD, Gerhard DS, Jones SJM, Korshunov A, Gessler M, Kerl K, Hasselblatt M, Frühwald MC, Perlman EJ, Nelson BH, Pfister SM, Kool M, Marra MA. Identification and analyses of extra-cranial and cranial rhabdoid tumour molecular subgroups reveal tumours with cytotoxic T cell infiltration. **(Poster presentation)**

77. BC Cancer Summit. Vancouver, BC. Nov 21-23, 2019. Takemon Y, Chittaranjan S, Song J, Chan SY, Lee SD, LeBlanc VG, Marra MA. *In-silico* predictions of synthetic lethal interactions in CIC-mutated cancers.

78. The Canadian Cancer Research Conference. Ottawa, ON. Nov 3-5, 2019. Takemon Y, Chittaranjan S, LeBlanc VG, Lee SD, Song J, Chan SY, Marra MA. Application of *in-silico* predictions of synthetic lethal interactions in CIC-mutated cancers.

79. The Canadian Cancer Research Conference. Ottawa, ON. Nov 3-5, 2019. Porter VL*, Gagliardi A*, Mungall AJ, Bowlby R, Titmuss, Zong SZ, Chan S, Mungall K, Novik K, Gerhard DS, Marra MA. *co-first author. Human papillomavirus displays clade-specific epigenome and transcriptome dysregulation in cervical carcinomas.

80. 44th Congress of the European-Society-for-Medical-Oncology (ESMO). Barcelona, Spain. Sep 27-Oct 1, 2019. Pender A, Titmuss E, Pleasance E, Fan K, Pearson H, Bonakdar M, Taylor G, Mungall K, Moore R, Lavoie J-M, Yip S, Lim H, Renouf D, Jones S, Marra M, Laskin J. Predictive markers of checkpoint inhibitor activity in adult metastatic solid tumours. ***(Ann Oncol. 2019 Oct; 30 Suppl 5)***

81. AACR Special Conference on the Advances in Pediatric Cancer Research. Montreal, QC. Sep 17-19, 2019. Garancher A, Suzuki H, Haricharan S, Masihi MB, Rusert JM, Norris PS, Carrette F, Romero MM, Morrissy SA, Skowron P, Cavalli FMG, Farooq H, Ramaswamy V, Morcavallo A, Henderson JJ, Olson JM, Cho YJ, Li XN, Chesler L, Marra MA, Becher OJ, Bradley LM, Ware CF, Taylor MD, Wechsler-Reya RJ. Overcoming immune evasion in pediatric brain tumors. ***(Cancer Res. 2020 Jul; 80(14):22-23 Suppl S)***

82. AACR Special Conference on Pancreatic Cancer - Advances in Science and Clinical Care. Boston, MA. Sep 6-9, 2019. Topham JT, Titmuss E, Pleasance ED, Williamson LM, Karasinska JM, Culibrk L, Lee MKC, Kalloger SE, Mendis S, Moore RA, Mungall AJ, Laskin J, Loree JM, Mager DL, Marra MA, Jones SJ, Schaeffer DF, Renouf DJ. Endogenous retrovirus transcript levels are associated with immunogenic signatures in multiple metastatic cancer types. ***(Cancer Res. 2019 Dec; 79(24) Suppl S).***

83. AACR Special Conference on Pancreatic Cancer - Advances in Science and Clinical Care. Boston, MA. Sep 6-9, 2019. Tsang ES, Topham JT, Karasinska JM, Lee MKC, Mendis S, Culibrk L, Denroche RE, Jang GH, Kalloger SE, Moore RA, Mungall AJ, Laskin J, O'Kane GM, Knox JJ, Gallinger S, Jones SM, Marra MA, Loree JM, Schaeffer DF, Renouf DJ. Early-onset pancreatic ductal adenocarcinomas are characterized by a distinct mutational landscape. ***(Cancer Res. 2019 Dec; 79(24) Suppl S)***

84. 43rd CCMG Annual Scientific Conference. Niagara Falls, ON. June 22-25, 2019. Thibodeau ML, Dixon K, O'Neill K, Krzywinski M, Reisle C, Mungall K, Shen Y, Lim H, Fok A, Sun S, Schaeffer D, Cremin C, Chia S, Young S, Pleasance E, Pleasance S, Pandoh P, Mungall A, Moore R, Karsan A, Laskin J, Marra M, Schrader K, Jones S. Characterization of germline structural variants in moderate-high penetrance hereditary cancer genes in the Personalized OncoGenomics cohort.

85. 15th International Conference on Malignant Lymphoma. Lugano, Switzerland. June 18-22, 2019. Mottok A, Hung SS, Chavez EA, Woolcock B, Telenius A, Chong LC, Meissner B, Nakamura H, Gascoyne RD, Connors JM, Ben Neriah S, Mungall A, Marra MA, Siebert R, Scott DW, Savage KJ, and Steidl C. Integrative genomic analysis identifies key pathogenic concepts in primary mediastinal large B-cell lymphoma.

86. BC Cancer Research Day. Vancouver, BC. June 17, 2019. Luthra I, LeBlanc VG, Shen Y, Culibrk L, Corbett R, Cairncross JG, Marra MA. Genomic and Transcriptomic analysis of a long-term oligodendroglioma survivor with positive response to radiation-free chemotherapy.

87. BC Cancer Research Day. Vancouver, BC. June 17, 2019. Porter V*, Gagliardi A*, Mungall AJ, Titmuss E, Bowlby R, Zong SZ, Namirembe C, Griner N, Allen H, Bowen J, Chan S, Darragh T, Dyer M, Ma Y, Mungall KL, Nakisige C, Novik K, Orem J, Origa M, HTMCP Cervical Working Group, Gastier-Foster J, Yarchoan R, Casper C, Mills G, Rader J, Ojesina A, Gerhard DS, Marra MA. *co-first author. Human papillomavirus displays clade-specific epigenome and transcriptome dysregulation in cervical carcinomas.

88. BC Cancer Research Day. Vancouver, BC. June 17, 2019. Takemon Y, Chittaranjan S, Lee SD, LeBlanc VG, Song J, Chan SY, Marra MA. Application of in-silico predictions of synthetic lethal interactions in CIC-mutated cancers.

89. BC Cancer Research Day. Vancouver, BC. June 17, 2019. Wei L, Ries RE, Trinh D, Meshinchi S, Marra MA. Single cell RNA sequencing of pediatric AML reveals treatment-associated clonal dynamics.

90. ASCO Annual Meeting. Chicago, IL. May 31 - June 4, 2019. Zhao EY, Feng X, Pleasance ED, Ng TL, Grewal J, Mohammad N, Taylor SK, Simmons CE, Srikanthan A, Rassekh SD, Deyell R, Shen Y, Titmuss E, Lim HJ, Renouf DJ, Gelmon KA, Yip S, Jones SJM, Marra MA, Laskin JJ. The Whole Genome Landscape of Adult Metastatic Sarcoma.

91. ASCO Annual Meeting. Chicago, IL. May 31 - June 4, 2019. LeVasseur N, Csizmok V, Bonakdar M, Shen Y, Zibrik L, Zhao EY, Sun S, Gelmon KA, Laskin JJ, Marra MA, Chia SKL. Whole transcriptome sequencing in metastatic cancer – A review of expression outliers in 113 metastatic breast cancer patients.

92. ASCO Annual Meeting. Chicago, IL. May 31 - June 4, 2019. Lavoie J-M, Csizmok V, Wang G, Williamson L, Marra MA, Laskin JJ, Jones SJM, Renouf DJ, Kollmannsberger CK. Whole genome and transcriptome analysis (WGTA) of metastatic adrenocortical carcinoma (mACC).

93. ASCO Annual Meeting. Chicago, IL. May 31 - June 4, 2019. Tsang ES, Grisdale CJ, Pleasance ED, Yip S, Tessier-Cloutier B, Mungall K, Ng TL, Sun S, Lim HJ, Renouf DJ, Laskin JJ, Marra MA, Jones SJM, Loree JM. Uncovering Clinically Relevant Gene Fusion Events with Integrated Genomic and Transcriptomic Profiling.

94. ASCO Annual Meeting. Chicago, IL. May 31 - June 4, 2019. Lee M, Jones MR, Williamson L, Topham JT, Wong H-L, Addison S, Denroche R, Jang GH, Karasinska J, McGhie JP, Gill S, Lim HJ, Yip S, Knox JJ, Gallinger S, Laskin JJ, Marra MA, Jones SJM, Schaeffer DF, Renouf DJ. Comprehensive genomic analysis of metastatic pancreatic ductal adenocarcinoma (mPDAC) reveals a significant proportion of clinical actionable aberrations.

95. ASCO Annual Meeting. Chicago, IL. May 31 - June 4, 2019. Mendis SR, Topham JT, Titmuss E, Williamson L, Pleasance ED, Culibrk L, Karasinska J, Liu SL, Lee M, Aird J, Moore RA, Mungall AJ, Laskin JJ, Jones SJM, Marra MA, Schaeffer DF, Renouf DJ, Loree JM. Comprehensive transcriptome analysis reveals link between epigenetic dysregulation, endogenous retrovirus expression and immunogenicity in metastatic colorectal carcinoma.

96. 15th ICGC -ARGO Scientific Workshop. Glasgow, UK. May 27-29, 2019. Nelson J, Zibrik, L, Carstairs, C, Fok A, Sauve K, Roscoe R, Laskin J, Marra M. Collaborative Publication Process in the Personalized Onco-Genomics Program.

97. 15th ICGC -ARGO Scientific Workshop. Glasgow, UK. May 27-29, 2019. Weymann D, Laskin J, Marra MA, Regier DA. Early-stage economic evaluation of whole-genome and transcriptome analysis to guide advanced cancer care.

98. 15th ICGC -ARGO Scientific Workshop. Glasgow, UK. May 27-29, 2019. Wilson JM, Denroche RE, Dodd A, Hutchinson S, Ramotar S, Chadwick R, Liang S-B, Masoomian M, Lungu I, Bartlett JMS, Notta F, Zhang A, Jang GH, Kryzanowski P, Lam B, Topham J, Lee M, Williamson L, r M, Jones M, Marra M, Nelson J, Taylor G, Metcalfe A, Warren C, Karasinska J, Wang Y, Schaeffer D, Tang P, Fischer SE, Goodwin R, Spratlin J, Bathe O, Biagi J, Zogopolous G, Tehfe M, Renouf D, O'Kane GM, Knox JJ, Gallinger S. Enhanced Pancreatic Cancer Profiling for Individualized Care (EPPIC): An ICGC-ARGO Project.

99. Keystone Symposia: 3D Genome. Banff, AB. Mar 17-21, 2019. Porter VL, Topham JT, Trinh DL, Gagliardi A, Jin D, Huff RD, Mungall AJ, Lorzadeh A, Moksa M, Hirst M, Marra MA. Global enhancer dysregulation in histone methyl-transferase KMT2D mutant cells. **(Poster presentation)**

100. B.I.G. Research Day, University of British Columbia. Vancouver, BC. Mar 14, 2019. LeBlanc VG, Trinh D, Hughes M, Luthra I, Livingstone D, Blough MD, Cairncross JG, Kelly JJ, Marra MA. Exploring

cellular subpopulations in glioblastoma and matched patient-derived organoids using single-cell RNA-seq. **(Poster presentation)**

101. The 19th Annual AGBT Meeting. Marco Island, FL. Feb 27-Mar 3, 2019. Zhao YJ, Pandoh P, Kirk H, Smailus D, Corbett RD, MacLeod T, McDonald H, Haile S, Bilobram S, Coope R, Mungall AJ, Moore R, Jones S, Marra MA. Automated Bead-based Total Nucleic Acid Extraction Including Micro RNAs (miRNAs) from Mammalian Tissue. **(Poster presentation)**

102. The 19th Annual AGBT Meeting. Marco Island, FL. Feb 27-Mar 3, 2019. Coope R, Schlosser C, Pleasance S, Corbett R, Ma Y, Zhao YJ, Mungall A, Moore R, Tessier-Cloutier B, Yip S, Marra MA. Large Scale Tumour Enrichment by Laser Microdissection. **(Poster presentation)**

103. The 19th Annual AGBT Meeting. Marco Island, FL. Feb 27-Mar 3, 2019. Chuah E, Reisle C, Zadeh A, Bozoky Z, Martin N, Davies J, Pelligrini B, Lewis E, Wang S, Nelson J, Mungall K, Marra M, Jones S. A platform for generation and sharing of clinical genomic data. **(Poster presentation)**

104. The 2019 Gastrointestinal Cancers Symposium, San Francisco, CA. Jan 17-19, 2019. Lee M, Jones MR, Williamson L, Topham JT, Addison S, Wong H-I, Denroche R, Jang GH, Karasinska J, McGhie JP, Gill S, Lim HJ, Yip S, Knox JJ, Gallinger S, Laskin JJ, Marra MA, Jones SJM, Sschaeffer DF, Renouf DJ. Comprehensive genomic analysis of metastatic pancreatic ductal adenocarcinoma (mPDAC) reveals a significant proportion of clinical actionable aberrations.

105. Keystone Single-Cell Biology. Breckenridge, CO. Jan 12-17, 2019. LeBlanc VG, Trinh D, Hughes M, Luthra I, Livingstone D, Blough MD, Cairncross JG, Kelly JJ, Marra MA. Exploring cellular subpopulations in glioblastoma and matched organoids using single-cell RNA-seq. **(Poster presentation)**

106. 60th ASH Annual Meeting & Exposition. San Diego, CA. Dec 1-4, 2018. Ennishi D, Jiang A, Boyle M, Collinge B, Grande BM, Ben-Neriah S, Slack GW, Farinha P, Mottok A, Meissner B, Saberi S, Bashashati A, Villa D, Savage KJ, Sehn LH, Kridel R, Marra MA, Shah SP, Steidl C, Connors JM, Gascoyne RD, Morin RD, Scott DW. The double-hit gene expression signature defines a clinically and biologically distinct subgroup within GCB-DLBCL.

107. Cell Symposia: TCGA Legacy: Multi-Omic Studies in Cancer Symposium. Washington, DC. Sep 27-29, 2018. Lavoie J-M, Mitchell T, Lee S-E, Deol B, Jones S, Marra M, Laskin J, Renouf DJ. Patient Selection for a Developmental Therapeutics Program Using Multi-Omics.

108. 18th International Symposium on Pediatric Neuro-Oncology. Denver, CO. June 30-July 3, 2018. Johann P, Chun E, Erkek S, Iskar M, Perlman E, Hasselblatt M, Pfister SM, Marra M, Kool M. Whole genome and epigenome characterization links ATRT-MYC to a subgroup of renal rhabdoid tumors. ***(Neuro-Oncol. 2018 Jun;20:29 Suppl 2)***

109. Inaugural AACR International Meeting Advances in Malignant Lymphoma: Maximizing the Basic-Translational Interface for Clinical Application. Boston, MA. June 22-26, 2018. Ennishi D, Takata K, Beguelin W, Duns G, Mottok A, Farinha P, Bashashati A, Saberi S, Meissner B, Boyle M, Ben-Neriah S, Kridel R, Savage KJ, Sehn LH, Morin RD, Marra MA, Shah SP, Connors JM, Gascoyne RD, Scott DW, Melnick AM, Steidl C. MHC class II expression is associated with a distinct mutational profile and immune cell landscape in the microenvironment in Germinal Center B-Cell-like Diffuse Large B-Cell Lymphoma.

110. BC Cancer Research Day. Vancouver, BC. June 11, 2018. Culibrk L, Grewal J, Pleasence ED, Jones MR, Mungall KL, Laskin L, Marra MA, Jones SJM. TC-seqR: A statistical framework for estimation of tumour purity and ploidy from whole genome sequencing data.

111. American Society of Clinical Oncology Annual Meeting. Chicago, IL. June 1-5, 2018. Zhao EY, Pleasance ED, Jones MR, Shen Y, Reisle CR, Mungall AJ, Moore R, Zhao YJ, Renouf DJ, Laskin JJ, Marra MA, Jones SJM. Evolution of Genomic Instability in Metastatic Cancer.

112. American Society of Clinical Oncology Annual Meeting. Chicago, IL. June 1-5, 2018. Thibodeau ML, Zhao EY, Bonakdar M, Taylor G, Reisle C, Mungall AJ, Williamson L, Nelson BH, Ergin EK, Ng T, Renouf DJ, Lim HJ, Marra MA, Laskin J, Jones SJM, Schrader KA. Genomic profiling and mutational signatures associated with the germline deletion polymorphism APOBEC3A_B in diverse cancer types.

113. Genome BC's Annual Genomics Forum 2018. Vancouver, BC. May 24, 2018. Culibrk L, Grewal J, Pleasence ED, Jones MR, Mungall KL, Laskin J, Marra MA, Jones SJM. TC-seqR: A statistical framework for estimation of tumour purity and ploidy from whole-genome sequencing data.

114. 107th Annual Meeting of the United States and Canadian Academy of Pathology. Vancouver, BC. Mar 17-23, 2018. Tessier-Cloutier B, Grewal J, Jones M, Pleasance E, Zhong EZ, Mungall K, Lee TH, Cai E, Sheffiled B, Lee CH, Hoang L, Skinnider B, Smith T, Schaeffer D, Lee AF, Ng T, Ionescu D. Nielsen T, Dunham C, Jones S, Laskin J, Marra M, Yip S. Genomic Integrative Pathology: A Large Scale Tumour Next Generation Sequencing Initiative. ***(Mod Pathol. 2018 Mar;31:708)***

115. 18th Biennial Canadian Neuro-Oncology Meeting. Banff, AB. May 10 - 12, 2018. LeBlanc VG, Trinh D, Hughes M, Luthra I, Livingstone D, Blough MD, Cairncross JG, Kelly JJ, Marra MA. Exploring cellular subpopulations in glioblastoma and matched organoids using single-cell RNA-seq.

116. 15th Annual European Neuroendocrine Tumor Society Conference. Barcelona, Spain. March 7-9, 2018. Yang KC, Wong H, Shen1 Y, Colborne S, Kalloger S, Karasinska J, Laskin J, Morin GB, Marra MA, Schaeffer DF, Renouf DJ, Gorski SM. Molecular Characterization of Primary and Metastatic Pancreatic Neuroendocrine Tumors.

117. The 18th Annual AGBT Meeting. Orlando, FL. Feb 12-15, 2018. Moore RA, Shen Y, Pleasance E, Jones M, Mungall KL, Thiessen N, Ma Y, Mungall AJ, Zhao YJ, Yip S, Lim H, Renouf D, Roscoe R, Jones SJM, Laskin J, Marra MA. Utilization of Whole Genome Analysis Approaches for Personalized Therapy Decision Making in Patients with Advanced Malignancies. **(Poster presentation)**

118. The 18th Annual AGBT Meeting. Orlando, FL. Feb 12-15, 2018. Mungall AJ, Bleile D, Mungall1 KL, Chong L, Jones M, Ma Y, Moore RA, Connors J, Jones SJM, Laskin JJ, Steidl C, Scott DW, Marra MA. Recurrent raftlin gene fusions in cancer. **(Platform presentation)**

119. The 18th Annual AGBT Meeting. Orlando, FL. Feb 12-15, 2018. Zhao YJ, Pandoh P, McDonald H, Corbett RD, Alcaide M, Kirk H, Haile S, Trinh E, Bilobram S, Jones M, Miller D, Coope R, Mungall AJ, Ma Y, Moore R, Roscoe R, Jones S, Holt R, Karsan A, Morin R, Marra MA. A rapid, high throughput protocol for characterization of circulating tumour DNA isolated from plasma and whole blood. **(Poster presentation)**

120. The 18th Annual AGBT Meeting. Orlando, FL. Feb 12-15, 2018. Jones M, Shen Y, Pleasance E, Zhao E, Mungall K, Mungall A, Moore R, Ma Y, Jones S, Laskin J, Marra MA. Whole genome and transcriptome analysis in a metastatic cancer clinical setting. **(Poster presentation)**

121. The 18th Annual AGBT Meeting. Orlando, FL. Feb 12-15, 2018. Coope RJN, Schlosser C, Corbett R, Pleasance S, Ma Y, Zhao YJ, Mungall A, Moore R, Tessier-Cloutier B , Marra MA. Automated Tissue Mapping and Microdissection for Large Scale Tumour Enrichment. **(Poster presentation)**

122. The 18th Annual AGBT Meeting. Orlando, FL. Feb 12-15, 2018. Shen Y, Jones MR, Pleasance E, Mungall K, Thiessen N, Ma Y, Moore RA, Mungall AJ, Zhao YJ, Yip S, Lee AF, Laskin J, Rassekh R, Deyell R, Marra MA, Jones SJM. Bioinformatic Integration of Whole Genome Sequencing and RNA Sequencing for Personalized Therapy Decision Making in Pediatric Cancer. **(Poster presentation)**

123. Society for Laboratory Automation and Screening Conference. San Diego, CA. Feb 3-7, 2018. Haile S, Pleasance S, Zhan H, Laks E, LeBlanc V, Trinh D, Chittaranjan S, Hansen C, Aparicio S, Marra M, Coope R. Nano-Well Based Single Cell Whole Genome and Whole Transcriptome Sequencing.

124. 59th American Society of Hematology Annual Meeting. Atlanta, GA. Dec 9-12, 2017. Wei L, Trinh D, Meshinchi S, Marra MA. Single cell transcriptome analysis reveals changing levels and distributions of stemness across disease states in pediatric AML. **(Poster presentation)**

125. 59th American Society of Hematology Annual Meeting. Atlanta, GA. Dec 9-12, 2017. Collinge B, Chong L, Ben-Neriah S, Slack GW, Ennishi D, Mottok A, Farinha P, Boyle M, Meissner B, Gerrie A, Villa D, Savage KJ, Sehn LH, Morin RD, Mungall A, Gascoyne RD, Marra MA, Connors JM, Steidl C, Scott DW. Mutations in exon 2 of *MYC* and the N11S polymorphism disrupt the relationship between *MYC* mRNA and MYC IHC results in diffuse large B-cell lymphoma.

126. 59th American Society of Hematology Annual Meeting. Atlanta, GA. Dec 9-12, 2017. Grande, BM, Gerhard DS, Griner NB, Casper C, Namirembe C, Omoding A, Orem J, Mbulaiteye SM, Mullighan CG, Sandlund JT, Alexander T, Choi JK, Abramson JS, Gross TG, Noy A, Bethony J, Greiner TC, Jaffe ES, Harris NL, Gastier Foster JM, Bowen J, Allen H, Schmitz R, Wilson W, Martin JP, Martin MR, Irvin JD, Dyer M, Gesuwan P, He Y, Davidsen TM, Novik K, Mungall AJ, Ma Y, Marra MA, Morin RD, Staudt LM. Burkitt Lymphoma Genome Sequencing Project (BLGSP): Integrative Genomic and Transcriptomic Characterization of Burkitt Lymphoma.

127. 9th American Society of Hematology Annual Meeting. Atlanta, GA. Dec 9-12, 2017. Jiang A, Grande BM, Arthur SE, Alcaide M, Ennishi D, Jessa S, Pararajalingam P, Meissner B, Boyle M, Chong L, Lai D, Davidson J, Bushell KR, Shah S, Mungall A, Gascoyne RD, Marra M, Steidl C, Connors J, Scott D, Morin D. Identification of recurrent non-coding driver mutations in non-Hodgkin lymphomas through integrative genomic analysis of 777 patients.

128. 59th American Society of Hematology Annual Meeting. Atlanta, GA. Dec 9-12, 2017. Ries RE, Smith JL, Triche Jr. T, Farrar J, Alonzo T, Ma Y, Wei L, Guidry-Auvil J, Smith M, Gerhard D, Bolouri H, Meshinchi S. Cancer Testis Antigens as Immuno-therapeutic Targets in Pediatric AML.

129. 59th American Society of Hematology Annual Meeting. Atlanta, GA. Dec 9-12, 2017. Chong L, Ben-Neriah S, Slack GW, Ennishi D, Mottok A, Collinge B, Farin ha P, Boyle M, Meissner B, Kridel R, Gerrie A, Villa D, Savage KJ, Sehn LH, Morin RD, Gascoyne RD, Marra MA, Connors JM, Mungall A, Steidl C, Scott DW. High-resolution architecture and partner genes of *MYC* rearrangements in lymphoma with DLBCL morphology.

130. 59th American Society of Hematology Annual Meeting. Atlanta, GA. Dec 9-12, 2017. Arthur SA, Mottok A, Alcaide M, Rushton C, Grande B, Ennishi D, Davidson J, Bushell KR, Gascoyne RD, Marra M, Connors J, Morin G, Scott D, Steidl C, Morin RD. Functional Investigation of the Gene *NFKBIZ* and the Impact of 3'UTR Mutations in Diffuse Large B-Cell Lymphoma.

131. 59th American Society of Hematology Annual Meeting. Atlanta, GA. Dec 9-12, 2017. Ennishi D, Mottok A, Farinha P, Chan FC, Bashashati A, Saberi S, Meissner B, Boyle M, Ben-Neriah S, Kridel R, Savage KJ, Sehn LH, Morin RD, Marra MA, Shah SP, Connors JM, Gascoyne RD, Scott DW, Steidl C. Genetic Characterization and Clinical Impact of Loss of MHC Class I and II Expression in *de novo* Diffuse Large B-cell Lymphoma.

132. 4th Canadian Conference on Epigenetics. Whistler, BC. Nov 26-29, 2017. Pellacani D, Bilenky M, Kannan N, Heravi-Moussavi2 A, Knapp DJHF, Gakkhar S, Moksa M, Carles A, Moore R, Mungall A, Marra MA, Jones SJM, Aparicio S, Hirst M, Eaves CJ. Identification of frequently mutated regulatory regions in human breast cancer.

133. 22nd Annual Scientific Meeting and Education Day of the Society for Neuro-Oncology. San Francisco, CA. Nov 15-19, 2017. Wong D, Lounsbury K, LeBlanc V, Chittaranjan S, Marra M, Yip S. Exploring the functional relationship between Capicua (CIC) and Ataxin-1-like (ATXN1L) in glioma. ***(Neuro-Oncology. 2017 Nov;19:52 (Supp 6).***

134. AACR-NCI-EORTC International Conference on Molecular Targets and Cancer Therapeutics. Boston, MA. Nov 5-9, 2017. Shen Y, Jones MR, Pleasance E, Bonakdar M, Ch'ing C, Reisle C, Williamson L, Majounie E, Taylor G, Chan S, Song Y, Pierce B, Zhang W, Zadeh A, Zhao E, Bleile D, Mungall K, Thiessen N, Chuah E, Wong T, Corbett R, Ma Y, Moore RA, Mungall AJ, Zhao YJ, Yip S, Lee AF, Rassekh R, Deyell R, Lim H, Renouf D, Roscoe R, Jones SJM, Laskin J, Marra MA. Clinical application of whole genome and transcriptome sequencing in cancer care.

135. 4th Canadian Cancer Research Conference. Vancouver, BC. Nov 5 - 7, 2017. Chun H-JE, Johann PD, Bilenky M, Lim E, Heravi-Moussavi A, Cheng Dean, Cheng Y, Wong T, Chuah E, Thiessen N, Ma Y, Gerhard DS, Mungall AJ, Moore RA, Jones SJM, Perlman EJ, Hirst M, Huang A, Kool M, Marra MA. Extra-cranial malignant rhabdoid tumours exhibit molecular similarities to the MYC-subgroup of cranial AT/RTs. **(Poster presentation)**

136. 4th Canadian Cancer Research Conference. Vancouver, BC. Nov 5 - 7, 2017. Wei L, Lim E, Trinh D, Meshinchi S, Marra M. Single cell transcriptome analyses of paediatric AML reveals disparate gene expression patterns across disease states. **(Poster presentation)**

137. 4th Canadian Cancer Research Conference. Vancouver, BC. Nov 5 - 7, 2017. Titmuss E, Lim H, Ng T, Milne K, Nelson B, Marra M. Angiotensin Receptor Blocker as a Potential Immunotherapy in Colorectal Cancer. **(Poster presentation)**

138. 4th Canadian Cancer Research Conference. Vancouver, BC. Nov 5 - 7, 2017. Topham JT, Trinh D, Gagliardi A, Huff RD, Mungall AJ, Schein J, Marra MA. Comprehensive and Integrative Analysis of the KMT2D Regulome. **(Poster presentation)**

139. 4th Canadian Cancer Research Conference. Vancouver, BC. Nov 5 - 7, 2017. LeBlanc VG, Trinh D, Hughes M, Kelly J, Marra MA. Exploring cellular subpopulations in primary GBM and GBM-derived organoid models.

140. 4th Canadian Cancer Research Conference. Vancouver, BC. Nov 5 - 7, 2017. Pearson H, Pleasance E, Scott B, Titmuss E, Jones M, Zong S, Sipahimalani P, Ma Y, Holt R, Jones S, Yip S, Lim H, Renouf D, Marra M, Laskin J. Genomic biomarkers of response to checkpoint inhibitor immunotherapy in the Personalized OncoGenomics cohort.

141. 4th Canadian Cancer Research Conference. Vancouver, BC. Nov 5 - 7, 2017. Shen Y, Lai YY, Bose P, Lever J, Grisdale C, Grinshtein N, Zhao E, Ma Y, Mungall AJ, Moore RA, Senger DL, Robbins SM, Luchman HA, Weiss S, Chan JA, Blough MD, Cairncross G, Kaplan D, Marra MA, Jones SJM. Comprehensive genomic profiling of matched glioblastoma tumours, cell-lines, and xenografts.

142. 4th Canadian Cancer Research Conference. Vancouver, BC. Nov 5 - 7, 2017. Lever J, Grinshtein N, Shen Y, Lai YY[1], Bose P, Grisdale C, Zhao E, Ma Y, Mungall AJ, Moore RA, Senger DL, Robbins SM, Luchman HA, Weiss S, Chan JA, Blough MD, Cairncross G, Kaplan D, Marra MA, Jones SJM. Identifying drug resistance markers in glioblastoma cell-lines.

143. 4th Canadian Cancer Research Conference. Vancouver, BC. Nov 5 - 7, 2017. Wong D, Lounsbury K, LeBlanc V, Chittaranjan S, Marra M, Yip S. Exploring the Functional Relationship between Capicua (CIC) and Ataxin-1-like (ATXN1L) in Oligodendroglioma.

144. 4th Canadian Cancer Research Conference. Vancouver, BC. Nov 5 - 7, 2017. Grewal J, Gakkhar S, Ma Y, Zhao YJ, Mungall A, Moore R, Lim H, Renouf D, Gelmon K, Yip S, Laskin J, Marra M, Jones SJM. Using machine learning to identify the site of origin of metastatic tumours.

145. 4th Canadian Cancer Research Conference. Vancouver, BC. Nov 5 - 7, 2017. Wang YK, Bashashati A, Anglesio M, Cochrane D, Grewal D, Ha G, McPherson A, Horlings H, Senz J, Prentice L, Karnezis A, Lai D, Aniba M, Zhang A, Shumansky K, Siu C, Wan A, McConechy M, Li-Chang H, Tone A, Provencher D, Provencher M, Fleury H, Okamoto A, Yanagida S, Yanaihara N, Saito M, Mungall A,

Moore R, Marra M, Gilks B, Mes-Masson A-M, McAlpine J, Aparicio S, Huntsman D, Shah S. Genomic consequences of aberrant DNA repair mechanisms stratify ovarian cancer histotypes.

146. 4th Canadian Cancer Research Conference. Vancouver, BC. Nov 5 - 7, 2017. Weymann D, Laskin J, Roscoe R, Schrader KA, Chia S, Yip S, Cheung WY, Gelmon KA, Karsan A, Renouf DJ, Marra M, Regier DA. The costs of translating whole-genome analysis into clinical practice in oncology.

147. 42nd European Society for Medical Oncology Congress. Madrid, Spain. Sep 8-12, 2017. Lim HJ, Schrader KA, Young S, Nelson J, Fok A, Pleasance E, Jones M, Shen YQ, Armstrong L, Virani A, Rassekh SR, Deyell R, Yip S, Roscoe R, Karsan A, Marra M, Laskin JJ. Management of germline findings revealed throughout the course of tumor-normal whole genome sequencing in oncology.

148. International Human Epigenome Consortium (IHEC) Annual Meeting & Science Days 2017. Berlin, Germany. Oct 12-14, 2017. Heravi-Moussavi A, Bilenky M, Gakkhar S, Carles A, Brooks D, Parker J, Brown CJ, Karimuddin AA, Phang PT, Raval M, Filipenko D, Ma Y, Moore R, Mungall A, Marra1 MA, Jones SJM, Karsan A, Hirst M. miR-92b expression is a marker of the CpG island methylator phenotype in colorectal cancer.

149. Pancreatic Diseases. Gordon Research Conference. Waterville Valley, NH. June 18-23, 2017. Yang K, Wong H-l, Shen Y, Colborne S, Hughes C, Kalloger S, Loree J, Kennecke H, Schaeffer D5, Lim H, Mungall A, Feng X, Davies J, Schrader K, Zhou C, Karsan A, Laskin J, Morin G, Marra M, Renouf D, Gorski S. Molecular characterization of metastatic pancreatic neuroendocrine tumours.

150. 53rd Annual Meeting of the American Society of Clinical Oncology. Chicago, IL. June 2-6, 2017. Lim HJ, Schrader KA, Young S, Nelson J, Fok A, Pleasance E, Jones M, Shen YQ, Armstrong J, Virani A, Rassekh SR, Deyell R, Yip S, Roscoe R, Karsan A, Marra MA, Laskin JJ. Management of germline findings revealed throughout the course of tumor-normal whole genome sequencing in oncology. ***(Journal of Clinical Oncology. 2017 May 20;35 (Supp 15).***

151. 53rd Annual Meeting of the American Society of Clinical Oncology. Chicago, IL. June 2-6, 2017. Tsang ES, Shen YQ, Chooback N, Ho C, Jones M, Renouf DJ, Him HJ, Sun S, Yip S, Pleasance E, Ma Y, Zhao YJ, Mungall AN, Moore R, Jones S, Marra M, Laskin JJ. Clinical outcomes after whole genome sequencing in patients with metastatic non-small cell lung cancer. ***(Journal of Clinical Oncology. 2017 May 20;35 (Supp 15).***

152. 53rd Annual Meeting of the American Society of Clinical Oncology. Chicago, IL. June 2-6, 2017. Chooback N, Ho C, Shen Y, Tsang ED, Zhao YJ, Mungall AJ, Moore R, Lim HJ, Renouf DJ, Gelmon KA, Yip S, Jones S, Laskin J, Marra M. Whole genome and transcriptome sequencing of lung cancer: Options for personalized cancer treatment. ***(Journal of Clinical Oncology. 2017 May 20;35 (Supp 15).***

153. AACR Annual Meeting 2017. Washington, DC. Apr 1-5, 2017. Ennishi D, Bashashati A, Saberi S, Mottok A, Meissner B, Boyle M, Ben-Neriah S, Kridel R, Savage KJ, Sehn LH, Connors JM, Morin RD, Marra MA, Shah SP, Steidl C, Scott DW, Gascoyne RD. Integrative genetic analysis identifies therapeutic relevance of cell of origin-specific genetic alterations in diffuse large B-cell lymphoma.

154. 58th American Society of Hematology Annual Meeting and Exposition. San Diego, CA. Dec 3-6, 2016. Gerhard DS, Grande B, Griner N, Corey C, Gerdts SE, Omoding A, Orem J, Mbulaiteye SM, Ogwang MD, Reynolds SJ, Bhatia K, Ayers L, Choi JK, Mullighan CG, Sandlund JT, Alexander TB, Abramson JS, Gross TG, Noy A, Bethony J, Leal F, Greiner TC, Jaffe ES, Harris NL, Gastier-Foster JM, Bowen J, Hanf B, Schmitz R, Martin J-P, Martin M-R, Irvin JD, Miller E, Gesuwan P, Hermida LC, Davidsen TM, Mungall AJ, Ma Y, Marra MA, Morin RD, Staudt LM. Burkitt Lymphoma Genome Sequencing Project (BLGSP): Introduction. **(Poster presentation)**

155. 58th American Society of Hematology Annual Meeting and Exposition. San Diego, CA. Dec 3-6, 2016. Triche TJ, Jr., Farrar JE, Bolouri H, Ries RE, Lim EL, Alonzo TA, Ma Y, Moore R, Mungall A, Marra MA, Guidry Auvil JM, Davidsen TM, Gesuwan P, Hermida LC, Kolb EA, Gamis AS, Smith MA,

Piccolo S, Gernard DS, Meshinchi S. Divergent epigenomes in pediatric and adult acute myeloid leukemia implicate cell of origin and transcriptional silencing of immune responses as sources of clinically relevant heterogeneity: A Report from the Children's Oncology Group and NCI/COG Therapeutically Applicable Research to Generate Effective Treatments (TARGET) Initiative. **(Oral presentation)**

156. 58th American Society of Hematology Annual Meeting and Exposition. San Diego, CA. Dec 3-6, 2016. Chan FC, Kridel R, Mottok A, Boyle M, Farinha P, Tan K, Meissner B, Bashashati A, McPherson A, Roth A, Shumansky3 K, Yap D, Ben-Neriah S, Rosner J, Smith MA, Nielsen C, Telenius A, Ennishi D, Mungall AJ, Moore R, Morin RD, Johnson NA, Sehn LH, Connors JM, Scott DW, Steidl C, Marra MA, Gascoyne RD, Shah SP. Divergent Modes of Tumor Evolution Underlie Histological Transformation and Early Progression of Follicular Lymphoma. **(Oral presentation)**

157. 58th American Society of Hematology Annual Meeting and Exposition. San Diego, CA. Dec 3-6, 2016. Tarlock K, Kaeding AJ, Alonzo TA, Loken MR, Ries RE, Pardo L, Gerbing R, Farrar JE, Guidry Auvil JM, Gerhard DS, Smith MA, Davidsen TM, Gesuwan P, Hermida LC, Marra MA, Mungall AJ, Mungall K, Ma Y, Zong S, Long W, Gamis AS, Kolb EA, Meshinchi S. Discovery and Validation of Cell-Surface Protein Mesothelin (MSLN) As a Novel Therapeutic Target in AML: Results from the COG/NCI Target AML Initiative. **(Poster presentation)**

158. 58th American Society of Hematology Annual Meeting and Exposition. San Diego, CA. Dec 3-6, 2016. Alexander TB, Gu Z, Choi JK, Loh ML, Horan J, Buldini B, Basso G, Elitzur S, Zwaan CM, de Haas V, Yeoh AEJ, Reinhardt D, Tomizawa D, Lammens T, De Moerloose B, Zhou Li, Hori H, Moorman AV, Moore AS, Hrusak O, Meshinchi S, Orgel E, Devidas M, Hunger SP, Guidry Auvil JM, Smith MA, Davidsen TM, Hermida LC, Gesuwan P, Marra MA, Ma Y, Mungall AJ, Moore R, Gerhard DS, Cao X, Shi L, Pounds S, Inaba H, Mullighan C. Genomic Landscape of Pediatric Mixed Phenotype Acute Leukemia. **(Oral presentation)**

159. 58th American Society of Hematology Annual Meeting and Exposition. San Diego, CA. Dec 3-6, 2016. Mottok A, Chong L, Ben-Neriah S, Woolcock B, Zhao YJ, Marra MA, Scott DW, Gascoyne RD, Mungall AJ, Steidl C. Characterization of Genomic Rearrangements Involving CIITA and SOCS1 Using Targeted Capture Sequencing of Archival Tissue Specimens. **(Poster presentation)**

160. 58th American Society of Hematology Annual Meeting and Exposition. San Diego, CA. Dec 3-6, 2016. Farrar JE, Bolouri H, Ries RE, Triche TJ, Jr., Lim EL, Alonzo TA, Ma Y, Moore R, Mungall AJ, Marra MA, Guidry Auvil J, Davidsen TM, Gesuwan P, Hermida LC, Kolb EA, Gamis AS, Smith MA, Gerhard DS, Meshinchi S. Marked Differences in the Genomic Landscape of Pediatric Compared to Adult Acute Myeloid Leukemia: A Report from the Children's Oncology Group and NCI/COG Therapeutically Applicable Research to Generate Effective Treatments (TARGET) Initiative. **(Oral presentation)**

161. 58th American Society of Hematology Annual Meeting and Exposition. San Diego, CA. Dec 3-6, 2016. Kridel R, Chan FC, Mottok A, Boyle M, Farinha P, Tan K, Meissner B, Bashashati A, Ben-Neriah S, Gine E, Ennishi D, Mungall AJ, Morin RD, Johnson NA, Sehn LH, Tousseyn T, Dogan A, Connors JM, Scott DW, Steidl C, Marra MA, Gascoyne RD, Shah SP. Targeted Sequencing Reveals Novel Gene Mutations Associated with Transformation and Early Progression in Follicular Lymphoma. **(Poster presentation)**

162. 58th American Society of Hematology Annual Meeting and Exposition. San Diego, CA. Dec 3-6, 2016. Ennishi D, Bashashati A, Saberi S, Mottok A, Meissner B, Boyle M, Ben-Neriah S, Kridel R, Dominguez-Sola D, Savage KJ, Sehn LH, Connors JM, Morin RD, Marra MA, Shah SP, Steidl C, Scott DW, Gascoyne RD. Frequent Genetic Alterations of PI3K-AKT Pathway and Their Clinical Significance in Germinal Center B-Cell-like Diffuse Large B-Cell Lymphoma. **(Oral presentation)**

163. 58th American Society of Hematology Annual Meeting and Exposition. San Diego, CA. Dec 3-6, 2016. Ries RE, Bolouri H, Farrar JE, Lim EL, Triche TJ, Jr., Tarlock K, Guidry Auvil J, Hirsch BA, Raimondi

SC, Ma Y, Marra MA, Aplenc R, Guest EM, Kolb EA, Gamis AS, Smith MA, Gerhard DS, Meshinchi S. Alteration of Chromatin Modifiers and Misregulation of Transcription Factors Define the Genomic Profile of Infant AML. **(Oral presentation)**

164. 2016 CSCI-CITAC Annual Scientific Meeting. Toronto, ON. Nov 212-23, 2016. Zhao EY, Shen Y, Pleasance E, Kasaian K, Jones M, Ch'ng C, Reisle C, Eirew P, Mungall KL, Thiessen N, Ma Y, Fok A, Mungall AJ, Zhao YJ, Moore RA, Villa D, Shenkier T, Lohrisch C, Chia S, Yip S, Gelmon K, Lim H, Sun S, Schrader KA, Young S, Karsan A, Roscoe R, Laskin J, Marra MA, Jones SJM. Guiding Platinum-based Chemotherapy in Breast Cancer with a Somatic Mutation Signature of Homologous Recombination Deficiency.

165. 6th Annual TFRI BC Node Research Day. Vancouver, BC. Nov 23, 2016. LeBlanc VG, Firme M, Chan SY, Song J, Lee A, Yip S, Chittaranjan S, Marra MA. Investigating the role of CIC mutations in malignancy.

166. 6th Annual TFRI BC Node Research Day. Vancouver, BC. Nov 23, 2016. Wong D, LeBlanc V, Chittaranjan S, Chan S, Song J, Lee MH, Marra M, Yip S. Functional Investigations of CIC and ATXN1L in Oligodendroglioma.

167. 6th Annual TFRI BC Node Research Day. Vancouver, BC. Nov 23, 2016. Chun H-JE, Heravi-Moussavi A, Carles A, Wong T, Chuah E, Gerhard DS, Mungall AJ, Moore RA, Ma Y, Jones SJM, Perlman EJ, Hirst M, Marra MA. Extra-Cranial Malignant Rhabdoid Tumors Exhibit Heterogeneous DNA Methylation and Histone 3 Lysine 27 Trimethylation Profiles.

168. 6th Annual TFRI BC Node Research Day. Vancouver, BC. Nov 23, 2016. MacLeod T, Brooks D, Pandoh P, Haile S, Corbett RD, Smailus D, Tsao P, McDonald H, Kirk H, Bala M, Miller D, Mungall AJ, Coope R, Ma Y, Moore R, Zhao Y, Holt R, Jones S, and Marra MA. An Automated miRNA Library Construction Protocol Capturing a Greater Diversity of miRNA Species.

169. 6th Annual TFRI BC Node Research Day. Vancouver, BC. Nov 23, 2016. Weymann D, Laskin J, Roscoe R, Schrader KA, Chia S, Yip S, Cheung WY, Gelmon KA, Karsan A, Renouf DJ, Marra M, Regier DA. Cost and cost-trajectory of whole-genome analysis to guide treatment of patients with advanced cancers.

170. 6th Annual TFRI BC Node Research Day. Vancouver, BC. Nov 23, 2016. Grewal J, Gakkhar S, Ma Y, Zhao Y, Mungall A, Moore R, Lim H, Renouf D, Gelmon K, Yip S, Laskin J, Marra M, Jones SJM. Using machine learning to identify site of origin of metastatic tumours.

171. 6th Annual TFRI BC Node Research Day. Vancouver, BC. Nov 23, 2016. Lai YYY, Shen Y, Grinshtein N, Lever J, Zhao E, Ma Y, Mungall A, Moore R, Senger D, Robbins S, Luchman H, Weiss S, Chan J, Blough M, Cairncross G, Kaplan D, Marra M, Jones S. Identification of Therapeutic Targets in Glioblastoma Multiforme.

172. 2016 Till & McCulloch Meetings. Whistler, BC. Oct 24-26, 2016. Pellacani D, Bilenky M, Kannan N, Heravi-Moussvi A, Knapp D, Gakkhar S, Moksa M, Carles A, Moore R, Mungall A, Marra M, Jones S, Aparicio S, Hirst M, Eaves C. Human mammary cell transcription factor networks predicted from analyses of differences in enhancer states.

173. ASHG 2016 Annual Meeting. Vancouver, BC. Oct 18-22, 2016. Weymann D, Laskin L, Roscoe R, Marra M, Schrader K, Chia S, Yip S, Cheung W, Gelmon K, Karsan A, Renouf D, Regier DA. The cost and cost-trajectory of whole-genome analysis to guide treatment of patients with advanced cancers.

174. ASHG 2016 Annual Meeting. Vancouver, BC. Oct 18-22, 2016. Shen YQ, He A, Zhang W, Thiessen N, Ma Y, Mungall AJ, Moore RA, Gibson W, Marra MA, Jones SJM. Identification of causal genes for rare genetic disorders using whole genome and whole exome sequencing.

175. ASHG 2016 Annual Meeting. Vancouver, BC. Oct 18-22, 2016. Zhao EY, Shen YQ, Pleasance E, Kasaian K, Jones M, Ch'ng C, Reisle C, Eirew P, Mungall KL, Thiessen N, Ma Y, Fok A, Mungall AJ,

Zhao YJ, Moore RA, Villa D, Shenkier T, Lohrisch C, Chia S, Yip S, Gelmon K, Lim H, Sun S, Schrader KA, Young S, Karsan A[5], Roscoe R, Laskin J, Marra MA, Jones SJM. Guiding Platinum-based Chemotherapy with a Somatic Mutation Signature of BRCA1/2 Impairment.

176. ASHG 2016 Annual Meeting. Vancouver, BC. Oct 18-22, 2016. LeBlanc VG, Firme M, Chan SY, Song J, Lee A, Yip S, Chittaranjan S, Marra MA. Investigating the role of *CIC* mutations in malignancy.

177. 48th Congress of the International Society of Paediatric Oncology (SIOP). Dublin, Ireland. Oct 19–22, 2016. Ooms AHAG, Gadd S, Gerhard DS, Smith MA, Gaidry Auvil JM, Meerzaman D, Ma M, Marra MA, Huff V, Dome JS, Chi YY, Geller JI, Mullighan CG, Wheeler DA, Hampton OA, Van den Heuvel-Eibrink MM, De Krijger RR, Ross N, Gastier-Foster JM, Perlman EJ. Prognostic Impact of TP53 Mutation Status in Wilms Tumors with Diffuse Anaplasia. ***(Pediatr Blood & Cancer. 2016 Nov;63 Suppl S34-S35)***

178. 48th Congress of the International Society of Paediatric Oncology (SIOP). Dublin, Ireland. Oct 19–22, 2016. Gu Z, Liu Y, Roberts K, Shao Y, Harvey R, Chen IM, Valentine M, Pei D, Marra M, Larsen E, Spinelli O, Minden M, Fielding A, Bhatia R, Stock W, Konopleva M, Willman C, Loh M, Hunger S, Mullighan C. Recurrent MEF2D Fusions Define A New Subtype of Acute Lymphoblastic Leukemia Associated with Older Age at Diagnosis and Poor Outcome. ***(Pediatr Blood & Cancer. 2016 Nov;63 Suppl S14-S15)***

179. Epigenomics in Development and Disease - CEEHRC Annual Meeting. Vancouver, BC. Sep 18-21, 2016. Pellacani D, Bilenky M, Kannan N, Heravi-Moussvi A, Knapp D, Gakkhar S, Moksa M, Carles A, Moore R, Mungall A, Marra MA, Jones SJM, Aparicio S, Hirst M, Eaves C. Derivation of transcription factor networks from analyses of active enhancer states in different subsets of normal human mammary cells.

180. Cold Spring Harbor Laboratory Meeting on Epigenetics & Chromatin. New York, NY. Sep 13-17, 2016. Chun H-JE, Heravi-Moussavi A, Carles A, Wong T, Chuah E, Gerhard DS, Mungall AJ, Moore RA, Ma Y, Jones SJM, Perlman EJ, Hirst M, Marra MA. Extra-cranial malignant rhabdoid tumors exhibit heterogeneous DNA methylation and histone 3 lysine 27 trimethylation profiles. **(Poster presentation)**

181. IHEC Science Days and Annual Meeting. Brussels, Belgium. Sep 7-9, 2016. Eaves CJ, Pellacani D, Bilenky M, Kannan N, Heravi-Moussavi A, Knapp DJHF, Gakkhar S, Moksa M, Carles A, Moore R, Mungall A, Marra MA, Jones SJM, Aparicio S, Hirst M. Molecular determinants of functionally distinct normal human mammary cell types.

182. 16th IUBMB Conference. Vancouver, BC. July 17-21, 2016. Jones SJM on behalf of BC Cancer Agency's Personalized OncoGenomics Project. Cancer Genomics and Personalized Medicine **(Platform presentation)**

183. ISMB 2016. Orlando, FL. July 8-12, 2016. Topham J, Gagliardi A, Marra M. Genomic analysis of primary tumors identifies association between KMT2D mutation status and genome instability. **(Poster presentation)**

184. 2016 ASH Meeting on Lymphoma Biology. Colorado Springs, CO. June 18-21, 2016. Kridel R, Chan FC, Mottok A, Boyle M, Farinha P, Tan K, Meissner B, Bashashati A, McPherson A, Roth A, Shumansky K, Yap D, Ben-Neriah S, Rosner J, Smith MA, Gine E, Telenius A, Ennishi D, Mungall A, Moore R, Morin RD, Johnson NA, Sehn LH, Tousseyn T, Dogan A, Connors JM, Scott DW, Marra MA, Gascoyne RD, Shah SP. Clonal Dynamics Shaping Histological Transformation and Progression in Follicular Lymphoma Clinical Histories.

185. 2016 ASH Meeting on Lymphoma Biology. Colorado Springs, CO. June 18-21, 2016. Mottok A, Chong LC, Ben-Neriah S, Woolcock BW, Zhao YJ, Marra MA, Scott DW, Gascoyne RD, Mungall AJ, Steidl C. Characterization of genomic rearrangements involving *CIITA* and *SOCS1* using targeted capture sequencing of archival tissue specimens.

186. 17th International Symposium on Pediatric Neuro-Oncology. Liverpool, England. June 12-15, 2016. Garzia L, Morrissy AS, Marra M, Taylor M. Divergent Clonal Selection Dominates Medulloblastoma at Recurrence. ***(Neuro-Oncol. 2016 Jun;18:119 (Supp 3))***

187. 17th International Symposium on Pediatric Neuro-Oncology. Liverpool, England. Kijima N, Garzia L, Morrissy A, Donovan L, Wu XC, Luu B, Ramaswamy V, Peacock J, Lopez-Holgado B, Wang X, Cavalli F, Roider A, Shih D, Skowron P, Lee J, Michealraj A, Malkin D, Fults D, Marra M. Taylor M. June 12-15, 2016. Functional roles of CCL2 in medulloblastoma leptomeningeal metastasis. ***(Neuro-Oncol. 2016 Jun;18:98 (Supp 3)).***

188. ASCO Annual Meeting. Chicago, IL. June 3-7, 2016. Wong H-L, Jones M, Eirew P, Karasinska J, Schrader KA, Lim HJ, Shen YQ, Jones S, Yip S, Laskin JL, Schaeffer DF, Marra M, Renouf DJ. Comprehensive genomic analysis in metastatic pancreatic ductal adenocarcinoma (PDAC). ***(ASCO Annual Meeting Proceedings. 2016; 34 (4_suppl): 285)***

189. TFRI 7th Annual Scientific Meeting. Vancouver, BC. May 12-14, 2016. Chun H-JE, Moussavi A, Carles A, Wong T, Chuah E, Schein JE, Gerhard DS, Mungall AJ, Moore RA, Ma Y, Jones SJM, Perlman EJ, Hirst M, Marra MA. Extra-cranial malignant rhabdoid tumours exhibit heterogeneous DNA methylation and gene expression profiles.

190. TFRI 7th Annual Scientific Meeting. Vancouver, BC. May 12-14, 2016. Topham J, Gagliardi A, Huff RD, Trinh DL, Mungall AJ, Schein J, Marra MA. *KMT2D* loss of function is associated with increased mutational load and down regulation of genes involved in DNA damage response pathways.

191. AACR 107th Annual Meeting. New Orleans, LA. Apr 16-20, 2016. Gadd A, Walz A, Ooms A, Huff V, Gerhard D, Smith M, Guidry Auvil J, Meerzaman D, Ma Y, Marra M, Dome J, Mullighan C, Wheeler D, Hampton O, Gastier-Foster J, Ross N, Perlman E. The Genetic Landscape of Wilms tumor. ***(Cancer Res. 2016 Jul;76:80 (Suppl 18))***

192. AACR 107th Annual Meeting. New Orleans, LA. Apr 16-20, 2016. Wong H-L, Karasinska J, Jones M, Eirew P, Schrader K, Lim H, Shen YQ, Jones S, Yip S, Laskin J, Marra M, Schaeffer DF, Renouf D. Gene expression analysis demonstrates prognostic subtypes in metastatic pancreatic ductal adenocarcinoma (PDAC).

193. AACR 107th Annual Meeting. New Orleans, LA. Apr 16-20, 2016. Laskin J, Shen YQ, Renouf D, Jones M, Lim H, Fok A, Ho C, Deol B, Gelmon K, Chia S, Moore R, Mungall A, Yip S, Jones S, Marra M. Restrictions on access to systemic therapy limit the application of whole genome sequencing in clinical care.

194. AACR 107th Annual Meeting. New Orleans, LA. Apr 16-20, 2016. Schrader KA, Chu'ng C, Zhao E, Wong H, Shen Y, Jones M, Thomson T, Lim H, Young S, Cremin C, Holt R, Eirew P, Karasinska J, Schein J, Zhao YJ, Mungall A, Moore R, Ma Y, Fok A, Roscoe R, Yip S, Mitchell G, Karsan A, Jones S, Schaeffer D, Laskin J, Marra M, Renouf D. Genomic analysis of pancreatic ductal adenocarcinoma in a patient with MUTYH-associated Polyposis.

195. B.I.G. Research Day, University of British Columbia. Vancouver, BC. Mar 11, 2016. Goya R, Meyer IM, Aparicio SA, Marra MA. Profiling Alternative Splicing in Triple Negative Breast Cancer Subgroups.

196. B.I.G. Research Day, University of British Columbia. Vancouver, BC. Mar 11, 2016. LeBlanc VG, Firme M, Song J, Lum A, Chan SY, Chittaranjan S, Yip S, Marra MA. Oncogenic CIC mutations in oligodendrogliomas deregulate mitogen-activated protein kinase signaling.

197. B.I.G. Research Day, University of British Columbia. Vancouver, BC. Mar 11, 2016. Topham J, Gagliardi A, Trinh DL, Huff RD, Mungall AJ, Schein J, Marra MA. *KMT2D* loss of function is associated with increased mutational load and down regulation of genes involved in DNA damage response pathways.

198. B.I.G. Research Day, University of British Columbia. Vancouver, BC. Mar 11, 2016. Couse MH, Dias C, Shen Y, Zahir FR, Townsend K, Marra MA, Jones SJ, Friedman JM. Non-coding variation in patients with Aicardi Syndrome. **(Poster presentation)**

199. The 16th Annual AGBT Meeting. Orlando, FL. Feb 10-13, 2016. Chong CC, Mottok A, Twa DDW, Ben-Neriah S, Chan FC, Kirk H, McDonald H, Pandoh P, Zhao YJ, Coope R, Ma Y, Moore R, Shah SP, Scott DW, Gascoyne RD, Marra MA, Steidl C, Mungall AJ. Detection of genomic rearrangements in archival lymphoma tissues using targeted capture sequencing.

200. The 16th Annual AGBT Meeting. Orlando, FL. Feb 10-13, 2016. Moore RA, Shen Y[1], Kasaian K, Leelakumari S, Pleasance E, Eirew P, Jones M, Corbett R, Mungall KL, Thiessen N, Ma Y, Fok A, Schein J, Tsang P, Mungall AJ, Zhao YJ, Yip S, Gelmon K, Lim H, Renouf D, Tinker A, Sun S, Roscoe R, Jones SJM, Laskin J, Marra MA. Whole Genome and Transcriptome sequencing for Personalized Cancer Therapy: Lessons learned from first 300 cases.

201. The 16th Annual AGBT Meeting. Orlando, FL. Feb 10-13, 2016. Ma Y, Craig DW, Nasser S, Corbett R, Chan S, Long W, Murray L, Legendre C, Tembe W, Enriquez D, Adkins J, Kim N, Wong S, Baker A, e Pond S, Mungall AJ, Moore R, Pleasance E, Jones S, McDaniel T, Marra M, Carpten JD, Liang WS. Benchmarking a cancer genome sequencing pipeline using a new reference standard.

202. The 16th Annual AGBT Meeting. Orlando, FL. Feb 10-13, 2016. Coope R, Smailus D, Tsao P, Haile S, Pandoh P, McDonald H, MacLeod T, Kirk H, Zhao YJ, Mungall AJ, Hirst M, Marra M. One Method to Rule Them All: Harmonized Robotic Library Construction for Seven Sample Types.

203. The 16th Annual AGBT Meeting. Orlando, FL. Feb 10-13, 2016. Zhao YJ, Merhu S, Tsao P, Corbett R, MacLeod T, Pandoh P, McDonald H, Kirk H, Smailus D, Bala M, Miller D, Ma Y, Coope R, Mungall A, Moore R, Hirst M, Holt RA, Jones SJM, Marra MA. An Automated and Streamlined Strand-specific RNA-Seq Pipeline Allows High Throughput Processing of Low Input Samples.

204. The 16th Annual AGBT Meeting. Orlando, FL. Feb 10-13, 2016. Zhao EY, Shen Y, Pleasance E, Kasaian K, Leelakumari S, Jones M, Bose P, Ch'ng C, Reisle C, Eirew P, Corbett R, Mungall KL, Thiessen N, Ma Y, Fok A, Schein J, Mungall AJ, Zhao YJ, Moore RA, Wilson S, Villa D, Shenkier T, Lohrisch C, Chia S, Yip S, Gelmon K, Lim H, Renouf D, Sun S, Schrader KA, Roscoe R, Laskin J, Marra MA, Jones SJM. BRCA-Related Genomic Signature Predicts Clinical Improvement with Cisplatin.

205. Gastrointestinal Cancers Symposium. San Francisco, CA. Jan 21-23, 2016. Wong HL, Jones M, Eirew P, Karasinska J, Schrader KA, Lim HJ, Shen YQ, Jones S, Yip S, Laskin JJ, Marra M, Schaeffer DF, Renouf DJ. Comprehensive genomic analysis in metastatic pancreatic ductal adenocarcinoma (PDAC). ***(J. Clin. Oncol.2016 Feb;34(4):285 (Suppl S))***

206. Annual Canadian MD/PhD & CIP Trainee Conference. Toronto, ON. Nov 23-25, 2015. Zhao EY, Shen Y, Pleasance E, Kasaian K, Leelakumari S, Jones M, Bose P, Ch'ng C, Reisle C, Eirew P, Corbett R, Mungall KL, Thiessen N, Ma Y, Fok A, Schein J, Mungall AJ, Zhao YJ, Moore RA, Wilson S, Villa D, Shenkier T, Lohrisch C, Chia S, Yip S, Gelmon K, Lim H, Renouf D, Sun S, Schrader KA, Roscoe R, Laskin J, Marra MA, Jones SJM. A BRCA-Related Genomic Signature Associated With Clinical Improvement On Cisplatin.

207. 5th Annual TFRI BC Node Research Day. Vancouver, BC. Nov 16, 2015. Haile S, McDonald H, Pandoh P, Corbett R, Kirk H, Tsao P, Smailus D, Bilobram S, MacLeod T, Jones M, Bala M, Hirst M, Miller D, Moore R, Mungall A, Schein J, Steidl C, Ma Y, Coope R, Zhao YJ, Holt R, Jones S, Marra MA. A Streamlined, High Throughput and Automated Suite of Protocols for Extraction and Total RNA/gDNA Sequencing of Formalin-Fixed Paraffin-Embedded Clinical Specimens.

208. Cell Symposia: Human Genomics. Singapore. Nov 8-10, 2015. Lim EL, Trinh DL, Ries R, Ma Y, Hughes M, Gerhard DS, Alonzo TA, Arceci RJ, Meshinchi S, Marra MA. Comprehensive sequence

analysis of relapse and refractory pediatric acute myeloid leukemia identifies miRNA and mRNA transcripts associated with treatment resistance. **(Poster presentation)**

209. Cell Symposia: Human Genomics. Singapore. Nov 8-10, 2015. Chun HJ, Lim EL, Heravi-Moussavi A, Saberi S, Mungall KL, Bilenky M, Jones SJM, Perlman EJ, Hirst M, Marra MA. Genome-wide profiles of extra-cranial malignant rhabdoid tumours reveal molecularly distinct subgroups with dysregulated developmental pathways. **(Poster presentation)**

210. AACR Precision Medicine Series: Integrating Clinical Genomics and Cancer Therapy. Salt Lake, UT. June 13-16, 2015. Bose P, Pleasance E, Jones M, Shen YQ, Ch'ng C, Reisle C, Schein JE, Mungall A, Moore R, Ma Y, Sheffield BS, Thomson T, Rasmussen S, Lee C, Yip S, Marra MA, Laskin J, Ho C, Jones SJM. Integrated genome analysis of a recurrent ghost cell odontogenic carcinoma. ***(Clin Cancer Res. 2016 Jan 1;22 Suppl 1)***

211. Personalized Medicine Summit. Vancouver, BC. June 7-9, 2015. Zhao E, Shen Y, Pleasance E, Kasaian K, Leelakumari S, Jones M, Bose P, Eirew P, Corbett R, Mungall KL, Thiessen N, Ma Y, Fok A, Schein J, Mungall AJ, Zhao YJ, Moore RA, Wilson S, Villa D, Shenkier T, Lohrisch C, Chia S, Yip S, Gelmon K, Lim H, Renouf D, Sun S, Schrader I, Roscoe R, Laskin J, Marra MA, Jones SJM. Searching for Targetable Mutation Signatures in a Mixed Cancer Cohort.

212. Personalized Medicine Summit. Vancouver, BC. June 7-9, 2015. Deyell R, Rassekh SR, Shen Y, Lee A, Dunham C, Yip S, Virani A, Armstrong L, Laskin J, Marra M. Pediatric personalized oncogenomics (PedsPOG) – initial outcomes.

213. BC Cancer Agency Research Day. Vancouver, BC. June 11, 2015. Pon J, Wong J, Saberi S, Moksa M, Hirst M, Marra M. Transcriptional regulation by MEF2B affects mediators of cell proliferation, migration and epithelial to mesenchymal transition.

214. Clinician Investigator Program Annual Research Fellows Day, University of British Columbia. Vancouver, BC. June 5, 2015. Zhao E, Shen Y, Pleasance E, Kasaian K, Leelakumari S, Jones M, Bose P, Eirew P, Corbett R, Mungall KL, Thiessen N, Ma Y, Fok A, Schein J, Mungall AJ, Zhao YJ, Moore RA, Wilson S, Villa D, Shenkier T, Lohrisch C, Chia S, Yip S, Gelmon K, Lim H, Renouf D, Sun S, Schrader I, Roscoe R, Laskin J, Marra MA, Jones SJM. Searching for Targetable Mutation Signatures in a Mixed Cancer Cohort.

215. Annual Meeting of the American Society of Clinical Oncology. Chicago, IL. May-June 2015. Koyoma T, Jones S, Utro F, Ma Y, Rhrissorrakrai K, Shen YQ, Carmeli J, Jones M, Waks Z, Pleasance E, Norel R, Moore R, Bilal E, Mungall AJ, Beaty K, Schein J, Michelini VV, Marra M, Royyuru A, Laskin J. Implementation of Watson genomic analytics processing to improve the efficiency of interpreting whole genome sequencing data on patients with advanced cancers. ***(J Clin Oncol. 2015 May 20; 33 (15) Suppl S)***

216. The American Society of Pediatric Hematology/Oncology's 28th Annual Meeting. Phoenix, AZ. May 6-9, 2015. Rassekh S, Deyell R, Shen YQ, Lee A, Dunham C, Virani A, Armstrong L**,** Morin R, Yip S, Pleasance E, Jones M**,** Schein J, Mungall A, Zhao YJ, Moore R, Ma Y, Jones S, Laskin J, Marra, M. Pediatric personalized oncogenomics (PedsPOG) - initial outcomes. ***(Pediatr Blood & Cancer. 2015 Jun; 62:25 Suppl 2)***

217. ARCC Conference 2015. Montreal, QC. May 24-25, 2015. Costa S, Connors JM, Cromwell I, Gascoyne R, Marra MA, Meissner B, Mungall AJ, Regier DA, Steidl C, Teckle P, van der Hoek K, Peacock S. Micro-Costing of Next Generation Sequencing (NGS) Using a Time-Motion Approach.

218. ISPOR 20th Annual International Meeting. Philadelphia, PA. May 16-20, 2015. Costa S, Connors JM, Cromwell I, Gascoyne R, Marra MA, Meissner B, Mungall AJ, Regier DA, Steidl C, Teckle P, van der Hoek K, Peacock S. Micro-Costing of High-Throughput Genomic Assays Using a Time-Motion Approach.

219. 104th Annual Meeting of the United States and Canadian Academy of Pathology. Boston, MA. Mar 21-27, 2015. Yip S, Sheffield B, Jones M, Pleasance E, Schaeffer D, Ng T, Li-Chang H, Lim H, Renouf D, Shen YQ, Jones S, Laskin J, Marra M. Next Generation Pathology: The Integration of Next Generation Sequencing With Glass-Based Histomorphology and Immunohistochemistry. ***(Mod Pathol. 2015 Feb; 28:465A Suppl 2)***

220. 104th Annual Meeting of the United States and Canadian Academy of Pathology. Boston, MA. Mar 21-27, 2015. Alassiri A, Ali R, Lum A, Goytain A, Shen YQ, Sorensen P, Strahlendorf C, Laskin J, Marra M, Nielsen T, Yip S, Lee C-H, Ng T. ETV6-NTRK3 is expressed in a subset of ALK-negative inflammatory myofibroblastic tumors: Case series of 20 patients demonstrated by comprehensive genomic profiling. ***(Mod Pathol. 2015 Feb; 28: 13A Suppl 2)***

221. B.I.G. Research Day 2015. Vancouver, BC. Mar 20, 2015. Topham J, Lim EL, Ma Y, Schuback HL, Mungall A, Moore R, Zhao YJ, Pleasance E, Gerhard DS, Meshinchi S, Arceci RJ, Marra MA. Integrative genomic and transcriptomic analysis of pediatric acute myeloid leukemia. **(Poster presentation)**

222. 56th ASH Annual Meeting and Exposition. San Francisco, CA. Dec 6-9, 2014. Totten S, Gaucher D, Morin RD, Assouline S, Connors JM, Marra MA, Scott D, Gascoyne RD, Pelletier J, Mann KK, Johnson NA. *FAS* Mutations Accelerate Lymphoma Growth and Induce Therapeutic Resistance.

223. 56th ASH Annual Meeting and Exposition. San Francisco, CA. Dec 6-9, 2014. Holm F, Hellqvist E, Mason C, Barrett C, Ali S, Chun E, Marra M, Runza V, Frazer K, Sadarangani A, Jamieson C. Malignant Reprogramming of Progenitors into Leukemia Stem Cells is Enhanced by Upregulation of CD44 transcript variant 3 in Malignant Microenvironments.

224. 56th ASH Annual Meeting and Exposition. San Francisco, CA. Dec 6-9, 2014. Ennishi D, Hoffer C, Shulha H, Mottok A, Farinha P, Chan FC, Meissner B, Boyle M, Ben-Neriah S, Morin R, Marra M, Savage K, Sehn L, Connors JM, Steidl C, Scott DW, Gascoyne RD. Clinical Significance of Genetic Aberrations in Diffuse Large B Cell Lymphoma.

225. Beyond the Genome: Cancer genomics. Boston, MA. Oct 8-10, 2014. Kasaian K, Shen Y, Leelakumari S, Pleasance E, Jones M, Li YY, Mungall KL, Schein J, Mungall AJ, Zhao YJ, Moore RA, Ma Y, Yip S, Gelmon K, Lim H, Renouf D, Laskin L, Marra MA, Jones SJM. Bioinformatic Analyses Approaches for Personalized Oncogenomics.

226. European Society for Medical Oncology 2014 Congress. Madrid, Spain. Sep 26-30, 2014. Laskin J, Moore R, Shen Y, Lim H, Gelmon K, Renouf D, Yip S, Huntsman D, Ng T, Mungall A, Fok A, Ho C, Chia S, Pleasance E, Kasaian K, Eirew P, Ma Y, Aparicio S, Jones S, Marra M. Demonstration of temporal heterogeneity identified by genome sequencing and the potential effect on treatment decisions for advanced cancer patients. **(Oral presentation)**

227. European Society for Medical Oncology 2014 Congress. Madrid, Spain. Sep 26-30, 2014. Lim H, Virani A, Fox A, Karsan A, Renouf D, Gelmon K, Yip S, Chia S, Sun S, Tinker A, Lee SJ, Rassekh R, Deyell R, Roscoe R, Jones S, Pleasance E, Marra M, Laskin J. Practical guidance for ethical and policy issues that arise from the clinical application of whole genome sequencing in cancer patients.

228. 10th Biennial Ovarian Cancer Research Symposium. Seattle, WA. Sep 2014. Ramos P, Karnezis AN, Craig DW, Sekulic A, Russell ML, Hendricks WP, Corneveaux JJ, Barrett MT, Shumansky K, Yang Y, Shah SP, Prentice LM, **Marra MA**, Kiefer J, Zismann VL, McEachron TA, Salhia B, Prat J, D'Angelo E, Clarke BA, Pressey JG, Farley JH, Anthony SP, Roden RB, Cunliffe HE, Huntsman DG, Trent JM.

Small cell carcinoma of the ovary, hypercalcemic type displays frequent inactivating germline and somatic mutations in SMARCA4. ***(Clic Cancer Res. 2015 Aug 15; 21 Suppl 16)***

229. 10th Biennial Ovarian Cancer Research Symposium. Seattle, WA. Sep 2014. Anglesio MS, Bashashati A, Wang YK, Ha G, Senz J, Yang W, Kalloger SE, Prentice LM, Yanagida S, Salamanca C, Soukhatcheva G, Karnezis AN, Chang N, Mes-Mason AM, Okamomo A, **Marra MA**, Gilks B, Shah SP, Huntsman DG. The somatic mutational landscape of endometriosis associated ovarian cancers and precursor lesions. ***(Clic Cancer Res. 2015 Aug 15; 21 Suppl 16)***

230. 20th International Conference on Brain Tumor Research and Therapy. Lake Tahoe, CA. Jul 20-22, 2014. Kaplan D, Grinshtein N, Rioseco C, Luchman A, Datti A, Aman A, Uehling D, Prakesch M, Wrana J, Cairncross G Shen YQ, Jones S, Marra M, Senger D, Robbins S, Al-Awar R, Moran M, Weiss W. Combined drug screening and phosphoproteomics identifies candidate brain tumor therapeutics and novel targets in primary human brain tumor-initiating cells. ***(J Neurooncol. 2014 Jul; 16(3)***

231. 16th International Symposium on Pediatric Neuro-Oncology. Singapore. Jun 28-Jul 2, 2014. Remke M, Ramaswamy V, Wang X, Jorgensen F, Morrissy AS, Marra MA, Packer R, Bouffet E, Pfister S, Jabado N, Taylor. Integrated genomics reveals relative spatial homogeneity of pediatric brain tumors. ***(J Neurooncol. 2014 Jul. Vol 16, Suppl 1:145)***

232. Genome BC Genomics Forum. Vancouver, BC. May 9, 2014. MacLeod T, Docking R, Swanson L, Corbett R, Smailus D, Pandoh P, Merhu S, Kirk H, McDonald H, Jones M, Parker J, Lee J, Kirkpatrick R, Roos A, Mungall AJ, Moore RA, Coope R, Zhao YJ, Langlois S, Karsan A, Marra MA. Circulating cell free DNA sequencing: Non-invasive detection of trisomies.

233. Genome BC Genomics Forum. Vancouver, BC. May 9, 2014. McDonald H, Jones M, Pandoh P, Tsao P, Smailus D, Corbett R, Merhu S, Kirk H, MacLeod T, Cruz K, Miller D, Schein J, Mungall AJ, Moore RA, Ma Y, Coope R, Zhao YJ, Jones SJM, Marra MA. A New High Throughput Pipeline for DNA Extraction and Illumina Library Construction from Archival FFPE samples.

234. AACR Annual Meeting. San Diego, CA. Apr 5-9, 2014. Laskin J, Shen Y, Lim H, Gelmon K, Renouf D, Yip S, Huntsman D, Tinker A, Ho C, Li Y, Kasaian K, Eirew P, Leelakumari S, Ma Y, Aparicio S, Jones S, Marra M. Whole genome sequencing is superior to cancer panels to aid in decision-making in patients with advanced malignancies. **(Poster presentation**)

235. AACR Annual Meeting. San Diego, CA. Apr 5-9, 2014. Kasaian K, Shen Y, Leelakumari S, Eirew P, Li YY, Corbett R, Mungall KL, Schein J, Mungall AJ, Zhao YJ, Moore RA, Yip S, Gelmon K, Lim H, Renouf D, Roscoe R, Ma Y, Marra MA, Laskin J, Jones SJM. Bioinformatics Analysis Approaches for Personalized Oncogenomics.

236. Keystone Symposia: Tumor Metabolism (X6). Whistler, BC. Mar 16-21, 2014. Chittaranjan S, Chan S, Yang C, Yang KC, Moradian A, Firme M, Chen V, Go NC, Blough M, Song J, Chan JA, Cairncross JG, Gorski SM, Morin G, Yip S, Marra MA. CIC interacts with ACLY and regulates cell proliferation in coordination with IDH1.

237. The 15th Annual AGBT Meeting. Feb 12-15, 2014. Marco Island, FL. Gascard P, Bilenky M, Sigaroudinia M, Zhao J, Tam A, Kamoh B, Cheung D, Li I, Li L, Moussavi A, Carles A, Nagarajan RP, Hong C, Echipare L, O'Geen H, Hangauer M, Cheng JB, Neel D, McManus M, Moore R, Wang T, Farnham P, Jones SJM, Marra MA, Tlsty TD, Costello JP, Hirst M. Persistent and transient epigenomic states in mammary gland development. **(Oral presentation)**

238. The 15th Annual AGBT Meeting. Feb 12-15, 2014. Marco Island, FL. Mungall AJ, Bowlby R, Mungall KL, Nip KM, Chu J, Chu A, Robertson AG, Brooks D, Sipahimalani P, Chiu R, Qian JQ, Thiessen N, He A, Tam A, Birol I, Ma Y, Moore RA, Schein JE, Jones SJM, Marra MA and TCGA Research Network. Detection of pathogen messenger RNA and microRNA transcripts in human cancer transcriptomes. **(Oral presentation)**

239. The 15th Annual AGBT Meeting. Feb 12-15, 2014. Marco Island, FL. Coope R, Tsao P, Merhu S, Corbett R, Pleasance S, Cruz K, Moore RA, Zhao YJ, Mungall AJ, Marra M. Flexible automation of Poly-A capture RNASeq sample prep and validation analysis**. (Poster presentation)**

240. The 15th Annual AGBT Meeting. Feb 12-15, 2014. Marco Island, FL. Docking R, Bosdet I, Chan S, Swanson L, Yang L, Mungall A, Zeng T, Coope R, Munro S, Jadersten M, Sung S, Chang L, Duns G, Parker J, Birol I, Moore R, Jones S, Hogge D, Marra M, and Karsan A. RNA-Seq and Gene-panel Assays for Risk Stratification in Acute Myeloid Leukemia. **(Poster presentation)**

241. 2014 Gastrointestinal Cancers Symposium. San Francisco, CA. Jan 16-18, 2014. Renouf DJ, Laskin JJ, Lim HJ, Yip S, Schaeffer D, Huntsman D, Morin R, Li Y, Shen Y, Zhao YJ, Kasaian K, Leelakumari S, Corbett R, Eirew P, Mungall K, Mungall A, Schein J, Roscoe R, Jones S, Marra M. Detailed genomic analysis in patients with pancreatic ductal adenocarcinoma (PDAC).

242. 55th Annual Meeting of the American Society of Hematology. New Orleans, LA. Dec 7-10, 2013. Recart ACC, Sadarangani A, Chun E, Mason CN, Jiang F, Barrett CL, Wall R, Goff DJ, Geron J, shih A, Leu HS, Ma WX, Minden MD, Fraser KA, Marra MA, Crews LA, Jamieson CHM. Inhibition of Inflammation Driven Leukemia Stem Cell Self-Renewal with a Selective JAK2 Antagonist. ***(Blood. 2013 Nov 15; 122(21):1481)***

243. 55th Annual Meeting of the American Society of Hematology. New Orleans, LA. Dec 7-10, 2013. Berg T, Thoene S, Yap D, Wee T, Schoeler N, Rosten P, Lim E, Bilenky M, Mungall AJ, Oellerich T, Umlandt P, Salmi A, Chang H, Yue L, Lai D, Cheng G, Serve H, Morin RD, Hirst M, Marra MA, Morin GB, Gascoyne RD, Aparicio SA, Humphries RK. Characterization of the Effects of Mutated EZH2 on Expression and Epigenome in a Mouse Lymphoma Model. ***(Blood. 2013 Nov 15; 122(21):346)***

244. 55th Annual Meeting of the American Society of Hematology. New Orleans, LA. Dec 7-10, 2013. Ennishi D, Chan FC, Scott DW, Hother C, Meissner B, Boyle M, Morin RD, Sehn LH, Marra MA, Connors JM, Steidl C, Gascoyne RD. Genetic Alterations in Immune Cell Crosstalk Genes in Diffuse Large B-Cell Lymphoma Predict Survival. ***(Blood. 2013 Nov 15; 122(21):500)***

245. 55th Annual Meeting of the American Society of Hematology. New Orleans, LA. Dec 7-10, 2013. Sloma I, Mitjavila-Garcia M, Feraud O, Oudrhiri N, Tosca L, El Marsafy L, Gobbo E, Divers D, Proust A, Griscelli F, Tachdjian G, Marra M, Eaves CJ, Bennaceur-Griscelli A, Turhan AG. Whole genome sequencing of chronic myeloid leukemia (CML)-derived induced pluripotent stem cells (iPSC) reveals faithful genocopying of highly mutated primary leukemic cells. ***(Blood. 2013 Nov 15; 122(21):514)***

246. 55th Annual Meeting of the American Society of Hematology. New Orleans, LA. Dec 7-10, 2013. Gunawardana J, Chan FC, Telenius A, Woolcock B, Kridel R, Tan KL, Ben-Neriah S, Lim R, Rogic S, Boyle M, Guiter C, Haioun C, Leroy K, Rimsza LM, Gaulard P, Savage KJ, Connors JM, Marra MA, Shah SP, Gascoyne RD, Steidl C. Protein tyrosine phosphatase type-1 (*PTPN1*) is frequently mutated in Primary Mediastinal B cell lymphoma and Hodgkin Lymphoma. ***(Blood. 2013 Nov 15; 122(21):242)***

247. 18th Annual Meeting of the Society of Neuro Oncology. San Francisco, CA. Nov 21-24, 2013. Johnson B, Mazor T, Hong CB, Barnes M, Yamamoto S, Ueda H, Tatsuno K, Aihara K, Jalbert L, Nelson S, Bollen A, Hirst M, Marra M, Mukasa A, Saito N, Aburatani H, Berger M, Chang SS, Taylor B, Costello J. Therapy-induced evolution of low-grade glioma genomes during malignant progression. ***(J Neurooncol. 2013 Nov. Vol 15 Suppl 3: 143)***

248. 2013 Canadian Cancer Research Conference. Toronto, ON. Nov 3-6, 2013. Lim EL, Trinh DL, Scott DW, Chu A, Morin RD, Mungall AJ, Boyle M, Johnson NA, Connors JM, Gascoyne RD, Marra MA. Deep Sequencing of the DLBCL miRnome Reveals Novel and Prognostic miRNA. **(Poster presentation)**

249. 2013 Canadian Cancer Research Conference. Toronto, ON. Nov 3-6, 2013. Pon J, Chittaranjan S, Wong J, Firme M, Tamura-Wells J, O’Brien K, Chan S, Trinh D, Mendez-Lago M, Morin R, Connors JM,

Gascoyne RD, Marra M. Regulatory Networks Impacted by *MEF2B* Mutations Recurrent in Non Hodgkin's Lymphoma. **(Poster presentation)**

250. 2013 Canadian Cancer Research Conference. Toronto, ON. Nov 3-6, 2013. Huff RD, Mendez-Lago M, Morin RD, Scott DW, Connors JM, Gascoyne RD, Marra MA. MLL2 interactions in follicular and diffuse large B-cell lymphoma. **(Poster presentation)**

251. 2013 Canadian Cancer Research Conference. Toronto, ON. Nov 3-6, 2013. Firme M, Chittaranjan S, Chan S, Yang C, Pon J, Trinh D, Butterfield Y, Blough M, Chan J, Cairncross G, Yip S, Marra M. Nuclear localization of the transcriptional repressor Capicua is regulated by intracellular calcium through an interaction with Calmodulin. **(Poster presentation)**

252. 2013 Canadian Cancer Research Conference. Toronto, ON. Nov 3-6, 2013. Trinh D, Lim E, Scott D, Chu A, Morin R, Mungall A, Boyle M, Johnson N, Connors J, Gascoyne R, Marra M. Investigating the Consequences of miR-21 and miR-148a Dysregulation in Diffuse Large B-cell Lymphoma. **(Poster presentation)**

253. 2013 Canadian Cancer Research Conference. Toronto, ON. Nov 3-6, 2013. Chittaranjan S, Chan S, Yang C, Moradian A, Yang K, Firme M, Chen V, Butterfield Y, Blough M, Chan J, Gorski S, Cairncross G, Morin G, Yip S, Marra M. Cytoplasmic Capicua is tethered to mitochondria and regulates cell proliferation and survival in coordination with Isocitrate Dehydrogenase1. **(Poster presentation)**

254. 3rd Annual TFRI-BC Node Research Day. Vancouver, BC. Oct 31, 2013. Yu S, Zong Z, Fornika D, Nielsen J, Connors J, Nelson B, Gascoyne R, Marra M, Johnson N, Morin RD. Mutational analysis in the non-Hodgkin lymphomas and development of minimally invasive biomarkers for monitoring disease progression.

255. Clinician Investigator Trainee Association of Canada Annual Meeting. Ottawa, ON. Sep 17-18, 2013. Pon J, Chittaranjan S, Wong J, Chan S, Trinh D, Tamura-Wells J, Firme M, O'Brien K, Mendez-Lago M, Morin R, Connors JM, Gascoyne RD, Marra M. Regulatory Networks Impacted by MEF2B Mutations Recurrent in Non Hodgkin Lymphoma. **(Poster presentation)**

256. Annual Meeting of the American Society of Clinical Oncology. Chicago, IL. May 31-June 4, 2013. Laskin JJ, Lim HJ, Gelmon KA, Ho C, Renouf DJ, Yip S, Huntsman D, Tinker A, Pleasance E, Li Y, Shen YQ, Kasaian K, Corbett R, Mungall K, Mungall A, Zhao YJ, Schein J, Roscoe R, Jones S, Marra M. Practical application of whole genome and transcriptome tumour analysis to guide chemotherapy decision-making for patients with advanced cancers. ***(J Clin Oncol. 2013 May 30; 31(15) Suppl S)***

257. AACR Precision Medicine Series. Synthetic Lethal Approaches to Cancer Vulnerabilities. Bellevue, WA. May 19-20, 2013. Huff R, Mendez-Lago M, Morin RD, Scott DW, Connors JM, Gascoyne RD, Marra MA. MLL2 interactions in follicular and diffuse large B-cell lymphoma. **(Poster presentation)**

258. 2nd Annual Pediatric Neuro-Oncology Basic and Translational Research Conference. Fort Lauderdale, FL. May 16-17, 2013. Morrissy AS, Mayoh C, Lo A, Thiessen N, Tse K, Moore R, Mungall A, Wu XC, Van Meter TE, Cho YJ, Collins VP, MacDonald TJ, Li XN, Fernandez-Lopez A, Malkin D, Marra MA, Taylor MD. Uncovering clonal evolution patterns in medulloblastoma metastases using whole genome sequencing. ***(J Neurooncol. 2013 Apr. Vol 15 Suppl 1:34-35)***

259. 2nd Annual Pediatric Neuro-Oncology Basic and Translational Research Conference. Fort Lauderdale, FL. May 16-17, 2013. Cavalli MG, Morrissy AS, Li Y, Chu A, Remke M, Thiessen N, Mungall AJ, Bader GD, Malkin D, Marra MA, Taylor MD. Identification of the microRNAs contributing to the regulation and molecular specificities of the medulloblastoma subgroups. ***(J Neurooncol. 2013 Apr. Vol 15 Suppl 1:20-21)***

260. TFRI 4th Annual Scientific Meeting. Ottawa, ON. May 9-11, 2013. Trinh DL, Scott DW, Morin RD, Mendez-Lago M, An J, Jones SJM, Mungall AJ, Zhao YJ, Schein J, Steidl C, Connors JM, Gascoyne

RD, Marra MA. Analysis of *FOXO1* Mutations in Diffuse Large B-Cell Lymphoma. **(Poster presentation)**

261. TFRI 4th Annual Scientific Meeting. Ottawa, ON. May 9-11, 2013. Huff RD, Mendez-Lago M, Morin RD, Scott DW, Connors JM, Gascoyne RD, Marra MA. MLL2 Interactions in Follicular and Diffuse Large B-Cell Lymphoma. **(Poster presentation)**

262. TFRI 4th Annual Scientific Meeting. Ottawa, ON. May 9-11, 2013. Lim E, Trinh D, Scott D, Chu A, Morin R, Mungall A, Boyle M, Johnson N, Connors J, Gascoyne R, Marra M. Deep Sequencing of the DLBCL miRnome Reveals Novel Prognostic miRNA. **(Poster presentation)**

263. TFRI 4th Annual Scientific Meeting. Ottawa, ON. May 9-11, 2013. Pon J, Chittaranjan S, Firme M, Tamura-Wells J, O’Brien K, Chan S, Trinh D, Mendez-Lago M, Morin R, Connors J, Gascoyne R, Marra M. Regulatory Networks Impacted by *MEF2B* Mutations. **(Poster presentation)**

264. The Fifth Annual Canadian National Proteomic Network Symposium. Vancouver, BC. April 20-24, 2013. Morin GB, Chen VC, Moradian A, Cheng GSW, McLean M, Chittaranjan S, Yap DB, Aparicio S, Marra MA, Huntsman DG. Detection and quantitation of mutated and alternatively processed oncogenic driver proteins in cancers. **(Oral presentation)**

265. 104th Annual Meeting of the American Association for Cancer Research. Washington, DC. Apr 6-10, 2013. Wood AC, Pugh TJ, Morozova O, Molenaar JJ, Koster J, Pineros V, Bosse K, Perin J, Diskin S, Diamond M, Versteeg R, Marra M, Meyerson M, Maris JM. Rare DNA variants are enriched at the BARD1 locus and likely influence neuroblastoma susceptibility. ***(Cancer Res. 2013 Apr 15;73(8) Suppl 1: 3804)***

266. 104th Annual Meeting of the American Association for Cancer Research. Washington, DC. Apr 6-10, 2013. Laskin JJ, Gelmon K, Lim H, Renouf D, Yip S, Huntsman D, Tinker A, Ho C, Pleasance E, Li Y, Shen YQ, Kasaian K, Corbett R, Mungall K, Zhao YJ, Mungall A, Schein J, Roscoe R, Jones S, Marra M. Genome analysis informs chemotherapy decision-making in patients with advanced malignancies. ***(Cancer Res. 2013 Apr 15; 73(8) Suppl 1)***

267. Joint Conference of Human Genome Meeting 2013 and 21st International Congress of Genetics. Singapore. Apr 13-18, 2013. Zahir F, Shen Y, Adam S, F. FORGE Canada Consortium, Marra M, Jones S, Friedman F. Whole Exome Sequencing For Siblings With Severe Intellectual Disability.

268. The 14th Annual AGBT Meeting. Marco Island, FL. Feb 20-23, 2013. Mungall AJ, Bowlby R, Chu A, Chun H-J, Robertson AG, Lim E, Mungall KL, Chiu R, Hamilton K, Chu J, Nip KM, Qian JQ, Sipahimalani P, Stoll D, Thiessen N, He A, Schein JE, Varhol R, Tam A, Zhao YJ, Moore RA, Birol I, Jones SJM, Marra MA, and TCGA Research Network. High-grade serous ovarian adenocarcinoma transcriptome sequencing. **(Oral presentation)**

269. The 14th Annual AGBT Meeting. Marco Island, FL. Feb 20-23, 2013. Zhao YJ, Mwenifumbo J, McDonald H, Corbett R, Kasaian K, Lim R, Slobodan J, Thorne T, Moksa M, Pandoh P, Kirk H, Haile Merhu S, Cruz K, Scott D, Neriah SB, Chun Chan F, Coope R, Moore RA, Mungall AJ, Gascoyne R, Steidl C, Jones SJM, Marra MA. High Throughput Genome Sequencing Protocol Development for Archival Formalin-Fixed Paraffin-Embedded (FFPE) Samples. **(Poster presentation)**

270. The 14th Annual AGBT Meeting. Marco Island, FL. Feb 20-23, 2013. Hirst M, Bilenky M, Tam A, Kamoh B, Cho S, Cheung D, Li I, Carles A, Cheng J, Moore R, Jones SJM, Tlsty T, Aparicio S, Farnham P, Eaves C, Connors J, Wang A, Huntsman D, Karsan A, Wang T, Marra MA, Costello J. Reference Human Epigenomes. **(Poster presentation)**

271. The 14th Annual AGBT Meeting. Marco Island, FL. Feb 20-23, 2013. Lam LT, Slobodan J, Pleasance SJ, Moore R, Docking R, Karsan A, Marra MA, Coope RNJ. Accurate Determination of Sample Molarity for Successful NGS Cluster Generation. **(Poster presentation)**

272. 2013 Gastrointestinal Cancers Symposium. San Francisco, CA. Jan 24-26, 2013. Peixoto R, Li Y, Pleasance E, Yip S, Zhao YJ, Schein J, Shen Y, Lim HJ, Renouf DJ, Gelmon KA, Huntsman D, Jones S, Marra M, Laskin JJ. A case of the utilization of genomic information in the management of metastatic colorectal cancer.

273. Keystone Conference: Noncoding RNAs in Cancer and Development. Vancouver, BC. Jan 20-25, 2013. Lim EL, Morin RD, Chu A, Gascoyne RD, Marra MA. An Integrative Analysis of miRNA:mRNA Interactions Acting in Cancers. **(Poster presentation)**

274. The Eleventh Asia Pacific Bioinformatics Conference. Vancouver, BC. Jan 21-23, 2013. Shen Y, Zhan SH, Varhol R, Khodabakhshi AH, Fejes AP, He A, Thiessen N, FORGE Canada Consortium, Mungall A, Birol I, Marra MA, Jones SJM. Finding of Rare Disease Genes in Canada.

275. 54th ASH Annual Meeting and Exposition. Atlanta, GA. Dec 8-11, 2012. Leu HS, Goff DJ, Low-Marchelli J, Court Recart A, Smith KM, Ma W, Sadarangani A, Shih AY, Wei J, Zhai D, Gotlib J, Minden M, Martinelli G, Marra M, Frazer KA, Pellecchia M, Reed JC, Jamieson CHM. Sabutoclax, a Novel Pan BCL2 Family Inhibitor, Sensitizes Dormant Blast Crisis Chronic Myeloid Leukemia Stem Cells to Dasatinib.

276. 54th ASH Annual Meeting and Exposition. Atlanta, GA. Dec 8-11, 2012. Court Recart A, Goff D, Sadarangani A, Mason C, Shih A, Wall R, Leu H, Ma W, Marra M, Barrett C, Frazer K, Jamieson C. Combined JAK/STAT5A and BCR-ABL Inhibition Impairs Blast Crisis Chronic Myeloid Leukemia Stem Cell Self-Renewal.

277. 54th ASH Annual Meeting and Exposition. Atlanta, GA. Dec 8-11, 2012. Chun Chan F, Ben-Neriah S, Lim R, Hu S, Rogic S, Johnson N, Morin R, Ha G, Ding J, Scott DW, Sehn L, Connors JM, Marra MA, Gascoyne RD, Shah S, Steidl C. Large-Scale High Resolution Integration of Copy Number and Gene Expression in DLBCL Reveals Focal and Frequent Deletions in Chromatin Modifying Genes with Outcome Correlation**.**

278. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 29-Dec 1, 2012. Chun H-J, Pleasance ED, Varhol R, Corbett R, Guin R, Schein JE, Mungall AJ, Zhao YJ, Moore RA, Perlman EJ, Gerhard DS, Marra MA. Whole genome sequencing of rhabdoid tumours of the kidney. **(Poster presentation)**

279. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 29-Dec 1, 2012. Swanson L, Mungall KL, Robertson G, Chiu R, Fentiman A, Jackman SD, Lee S, Moore RA, Nip KM, Parker J, Qian J, Raymond A, Yorukoglu D, Zhao YJ, Sahinalp SC, Hoodless PA, Jones SJM, Marra MA, Karsan A, Birol I. Detecting and characterizing fusions and tandem duplications in assembled mouse transcriptomes using Barnacle. **(Poster presentation)**

280. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 29-Dec 1, 2012. Goya R, Meyer IM, Marra MA. A Centralized Framework for Analyzing and Comparing Alternative Splicing Profiles.

281. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 29-Dec 1, 2012. Li Y, Pleasance E, Shen Y, Kasaian K, Corbett R, Mungall K, Zhao YJ, Mungall A, Yip S, Lim H, Laskin J, Jones S, Marra M. Utilization of Genomic Information for Personalized Therapy in Patients with Incurable Malignancies.

282. Genome Canada’s Genomics: The Power and the Promise Conference. Ottawa, ON. Nov 27-28, 2012. Kasaian K, He A, Thiessen N, Mungall KL, Qian J, Varhol R, Zhao YJ, Birol I, Moore R, Mungall AJ, Hirst M, Marra MA, Walker BAM, Wiseman SM, Jones SJM. Profiling Thyroid Cancers on the Molecular Level. **(Poster presentation)**

283. Cold Spring Harbor Laboratory Meeting on Mechanisms and Models of Cancer. NY, USA. Aug 14-18, 2012. Chittaranjan S, Yang C, Moradian A, Chan A, Firme M, Morozova O, Chen G, Butterfield Y,

Blough M, Chan J, Cairncross G, Morin G, Yip S, Marra MA. Characterizing the role of Capicua in oligodendroglioma.

284. 22nd Biennial European Cancer Research Congress. Barcelona, Spain. July 7-10, 2012. Mendez-Lago M, Morin RD, Mungall AJ, Goya R, Trinh DL, Corbett R, Rogic S, Gascoyne RD, Connors JM, Marra MA. Genomic Analysis of Non-Hodgkin Lymphomas Reveals Mutations in Chromatin Remodelling Genes. (***Eur J Cancer. 2012 Jul 31;48:S135)***

285. ISBER 2012 Annual Meeting. Vancouver, BC. May 2012. Schein J, Carter C, Guin R, Bala M, Carlsen R, Dhalla N, Hirst C, Lee D, Miller D, Shafiei A, Tam A, Wye N, Zhao YJ, Roscoe R, Mungall A, Birol I, Jones S, Marra M. Sample Receipt and Management at the Genome Sciences Centre.

286. Gordon Research Seminar and Conference: Autophagy in Stress, Development & Disease. Ventura, CA. Mar 11-16, 2012. Lebovitz C, Morin R, Marra M, Gorski S. Investigation of human autophagy genes as targets of somatic mutation in cancer. **(Poster presentation)**

287. AAAS Annual Meeting. Autophagy: An Emerging Therapeutic Target in Human Disease. Vancouver, BC. Feb 16-20, 2012. Lebovitz C, Morin R, Marra M, Gorski S. Investigation of human autophagy genes as targets of somatic mutation in cancer. **(Poster presentation)**

288. Keystone Advances in Islet Biology Symposium. Monterey, CA. Mar 2012. Tennant BR, Robertson AG, Beach M, Li L, Zhang X, Whiting CJ, Kim A, Zhang SH, Gottardo R, Marra MA, Jones SJM, Hoodless PA, Hoffman BG. Identification and analysis of pancreatic islet enhancers.

289. 13th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. Feb 2012. Mendez-Lago M, Morin RD, Mungall AJ, Mungall KL, Bolger-Munro M, Goya R, Khodabakhshi AH, Johnson NA, Chiu R, Jackman S, Krzywinski M, Scott D, Trinh DL, Griffith M, Corbett R, Smailus D, Moksa M, Brooks-Wilson A, Meissner B, Woolcock B, Boyle M, McDonald H, Tam A, Zhao YJ, Delaney A, Zeng T, Tse K, Birol I, Holt R, Schein J, Horsman DE, Moore R, Hirst M, Jones SJM, Connors JM, Gascoyne RD, Marra MA. Integrative Genomic Analysis of Diffuse Large B-cell Lymphoma**. (Poster presentation)**

290. 13th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. Feb 2012. Mwenifumbo JC, Griffith M, Zhao YJ, Owen D, Gill S, Marra M. Exploring Mutational Evolution of Metastatic Colorectal Cancer. **(Poster presentation)**

291. 13th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. Feb 2012. Mendez-Lago M, Morin RD, Mungall AJ, Gascoyne RD, Marra MA. *MLL2* Mutations in Follicular Lymphoma and Diffuse Large B-Cell Lymphoma.

292. 13th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. Feb 2012. Hirst M, Gascard P, Delaney A, Zhao YJ, Sigaroudinia M, Cheng J, Bilenky M, Tam A, Kamoh B, Cheung D, Li I, Varhol R, Nagarajan R, Hong C, Echipare L, O'Geen H, Hangauer M, Neel D, Haussler D, Weiss A, McManus M, Moore R, Wang T, Aparicio S, Shah S, Farnham P, Jones SJM, Tlsty T, Marra MA, Costello J. Epigenetic Contributions to Cell Identity in Human Breast.

293. 13th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. Feb 2012. Goya R, Griffith M, Shah SP, Aparicio SA, Meyer IM, Marra MA. Alternative Splicing in Triple Negative Breast Cancers Suggests Differences in Precursor Differentiation State.

294. 13th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. Feb 2012. Zhao YJ, Schein JE, Zeng T, Moore RA, Li I, Chuah E, Varhol R, Stoll D, Moksa M, Smailus DE, Slobodan J, Dhalla N, Tam A, Prabhu A, Ally A, Asano J, Tam B, Sze W, Kamoh B, Kirk H, Trinh E, Cruz K, Thorne T, Mah D, Deng M, Azrahimi N, Cho S, Chahal S, McDonald H, Pandoh P, Ma K, Lee D, Mayo M, Carlsen R, Candace C, Hirst C, Pleasance ED, Chu A, Chun HJE, Thiessen N, Mungall K, Wong T, Guin R, Butterfield Y, Sipahimalani P, Stazyk G, Coope R, Robertson G, Birol I, Hirst M, Mungall AJ,

Jones SJM, Marra MA and the BCCA GSC team. TCGA Pipelines for RNA-Seq and miRNA-Seq at the Genome Sciences Centre, British Columbia Cancer Agency.

295. 13th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. Feb 2012. Mungall AJ, Chu A, Robertson G, Ally A, Ben-Neriah S, Boyle M, Carter C, Carlsen R, Chiu R, Choe G, Chun HJE, Corbett R, Dhalla N, Johnson NA, Lee D, Li I, Mayo M, McDonald H, Meissner B, Morin RD, Mendez-Lago M, Moksa M, Mungall KL, Munro S, Pandoh P, Scott DW, Slobodan J, Smailus D, Rimsza L, Tam A, Trinh DL, Woolcock B, Wu S, Wye N, Zhao YJ, Bala M, Birol I, Butterfield Y, Coope R, Hirst M, Holt R, Jones SJM, Moore R, Schein J, Varhol R, Horsman DE, Connors JM, Gascoyne RD, Marra MA. MicroRNA expression profiling of diffuse large B-cell lymphoma samples.

296. 13th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. Feb 2012. Coope R, Slobodan J, Lam LT, Drewbrook C, Ouellette C, Chun HJE, Fong J, Goodacre E, Henderson S, Corbett R, Chu A, Moksa M, Smailus D, Wye N, Hirst M, Marra MA. Post Size Selection Automation for Large Scale Library Construction.

297. 13th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. Feb 2012. Kasaian K, Thiessen N, Mungall KL, Fejes AP, Zhao YJ, Birol I, Marra MA, Walker BAM, Nabi IR, Wiseman SM, Jones SJM. Whole Transcriptome Analysis of Anaplastic Thyroid Carcinomas.

298. 13th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. Feb 2012. Moore R, Bosdet I, Docking R, Butterfield Y, Chan S, Young S, Kirkpatrick R, Hirst M, Mungall A, Zhao YJ, Birol I, Holt R, Karsan A. Implementation of a Clinically-Compliant Diagnostic High Throughput Sequencing Pipeline.

299. Pediatric Cancer Translational Genomics Conference. Scottsdale, AZ. Feb 2012. Morozova O, Attiyeh EF, Asgharzadeh S, Birol I, Corbett RD, Mungall KL, Zhao YJ, Moore RA, Thiessen N, Chiu R, Jackman SD, Qian J, Krzywinski M, Hirst M, Diskin SJ, Mosse YP, Cole KA, Diamond M, Sposto R, Pugh TJ, Smith MA, Guidry Auvil JM, Gerhard DS, Meyerson M, Hogarty M, Jones SJM, Seeger RC, Khan J, Maris JM, Marra MA. RNA sequencing of primary neuroblastoma tumors reveals aberrations in the BRCA1/BARD1 pathway.

300. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Dec 2011. Mungall AJ, Chu A, Chun HJE, Bolger-Munro M, Mungall K, Robertson G, Bala M, Butterfield Y, Chiu R, Chuah E, Coope R, Deng A, Dhalla N, Guin R, Hirst C, Lee D, Li I, Ma K, McDonald H, Mayo M, Moksa M, Munro S, Pleasance ED, Prabhu A, Qian J, She R, Slobodan J, Smailus DE, Stoll D, Tam A, Thiessen N, Varhol R, Wang T, Wong T, Zeng T, Birol I, Hirst M, Moore RA, Schein JE, Stazyk G, Zhao YJ, Jones SJM, Marra MA and the TCGA Research Network. Expression Analyses and Mutation Discovery from Acute Myeloid Leukemia Messenger/Micro-RNA Transcriptomes.

301. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Dec 2011. Gascard P, Delaney A, Zhao YJ, Sigaroudinia M, Cheng J, Nielsen C, Tam A, Kamoh B, Cheung D, Li I, Varhol R, Nagarajan R, Hong C, Echipare L, O'Geen H, Hangauer M, Neel D, Haussler D, Weiss A, McManus M, Moore R, Wang T, Farnham P, Jones SJM, Tlsty T, Marra MA, Costello J, Hirst M. Epigenetic Contributions to Cell Identity in Human Breast.

302. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Dec 2011. Mendez-Lago M, Morin RD, Mungall AJ, Trinh DL, Be-Neriah S, Goya R, Gascoyne RD and Marra MA. MLL2 mutations in follicular and diffuse large B-cell lymphomas.

303. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Dec 2011. Trinh DL, Mendez-Lago M, Morin RD, Scott DW, Mungall AJ, Chittaranjan S, Zhao YJ, McDonald H, Gascoyne RD, Marra MA. Recurrent Mutations Affecting the *FOXO1* Gene in Non-Hodgkin Lymphomas.

304. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Dec 2011. Goya R, Griffith M, Shah SP, Aparicio SA, Meyer IM, Marra MA. Alternative Expression Profiling Of Triple Negative Breast Cancers.

305. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Dec 2011. Lim EL, Bilenky M, Morin RD, Berg T, Marra MA. Elucidating the Mechanisms by which EZH2 Contributes to Lymphomagenesis.

306. 53rd Annual Meeting and Exposition of the American Society of Hematology. San Diego, CA. Dec 2011. Roberts KG, Morin RD, Zhang J, Hirst M, Harvey RC, Kasap C, Edmonson MN, Chen I-M, Shah NP, Devidas M, Reaman G, Smith M, Pui C-H, Downing JR, Gerhard DS, Willman CL, Loh M, Hunger SP, Marra M, Mullighan CG and the Children's Oncology Group. Novel Chromosomal Rearrangements and Sequence Mutations in High-risk Ph-like Acute Lymphoblastic Leukemia. ***(Blood. 2011 Nov 18;118(21):32)***

307. 53rd Annual Meeting and Exposition of the American Society of Hematology. San Diego, CA. Dec 2011. Berg T, Yap D, Thoene S, Wee T, Schoeler N, Umlandt P, Chang H, Yue L, Lai D, Cheng G, Morin RD, Hirst M, Marra MA Morin GB, Gascoyne RD, Aparicio SA, Humphries RK. Mutated EZH2 Collaborates with Myc in Inducing Lymphoma in a Mouse Model. ***(Blood. 2011 Nov 18;118(21):104).***

308. Canadian Cancer Research Conference. Toronto, ON. Nov 2011. Lim E, Bilenky M, Yap D, Berg T, Humphries K, Aparicio S, Marra M. Investigating the Mechanisms by which EZH2-Y641 Mutation Contributes to Lymphomagenesis**. (Poster presentation)**

309. Canadian Cancer Research Conference. Toronto, ON. Nov 2011. Mendez-Lago M, Morin RD, Mungall AJ, Trinh DL, Be-Neriah S, Goya R, Gascoyne RD and Marra MA. MLL2 mutations in follicular and diffuse large B-cell lymphomas.

310. Canadian Cancer Research Conference. Toronto, ON. Nov 2011. Trinh DL, Mendez-Lago M, Morin RD, Scott DW, Mungall AJ, Chittaranjan S, Zhao YJ, McDonald H, Gascoyne RD, Marra MA. Recurrent Mutations Affecting the *FOXO1* Gene in Non-Hodgkin Lymphomas.

311. Medical Genetics Research Day, University of British Columbia. Vancouver, BC. Nov 2011. Pon J, Chittaranjan S, Tamura-Wells J, Firme M, Mendez-Lago M, Trinh D, Morin R, Goya R, Chan S, Marra M. Functional characterization of MEF2B mutations recurrent in non-hodgkin lymphoma.

312. Medical Genetics Research Day, University of British Columbia. Vancouver, BC. Nov 2011. Huff RD, Morin RD, Mendez-Lago ML, Johnson NA, Scott DW, Rogic SR, Ben-Neriah S, Meissner B, Mungall AJ, Goya R, Chan S, Woolcock B, Boyle M, Connors JM[2], Gascoyne RD[2], Marra MA. Investigating the role of GNA13 in Diffuse Large B-cell lymphoma.

313. The Cancer Genome Atlas 1st Annual Scientific Symposium. National Harbor, MD. Nov 2011. Mungall AJ, Chu A, Chun HJE, Bolger-Munro M, Pleasance ED, Robertson G, Bala M, Butterfield Y, Chiu R, Chuah E, Coope R, Deng A, Dhalla N, Guin R, Hirst C, Lee D, Li I, Ma K, McDonald H, Mayo M, Moksa M, Mungall K, Munro S, Prabhu A, Qian J, She R, Slobodan J, Smailus DE, Stoll D, Tam A, Thiessen N, Varhol R, Wang T, Wong T, Zeng T, Birol I, Moore RA, Schein JE, Stazyk G, Zhao YJ, Hirst M, Jones SJM, Marra MA and the TCGA Research Network. Expression analyses and mutation discovery from acute myeloid leukemia messenger/microRNA transcriptomes.

314. The Cancer Genome Atlas 1st Annual Scientific Symposium. National Harbor, MD. Nov 2011. Chu A, Robertson G, Wu S, Chun E, Mungall A, Schein J, Varhol R, Tam A, Zhao YJ, Moore R, Hirst M, Jones SJM, Birol I, Marra MA. Comparison of expression correlation networks between miRNA and mRNA.

315. The Cancer Genome Atlas 1st Annual Scientific Symposium. National Harbor, MD. Nov 2011. Chu A, Corbett R, Robertson G, Chun E, Birol I, Jones S, Marra MA. BLISS (Batch anaLysIS Suite) : A Tool for Contrasting and *De Novo* Grouping of Expression Data.

316. The Cancer Genome Atlas 1st Annual Scientific Symposium. National Harbor, MD. Nov 2011. Chun HJE, Thiessen N, Mungall K, Chu A, Robertson G, Chua E, Varhol R, Zhao YJ, Schein JE, Moore RA, Stoll D, Mungall AJ, Birol I, Jones JSM, Marra MA. Analyses of RNA-sequencing data from stomach adenocarcinoma.

317. The Cancer Genome Atlas 1st Annual Scientific Symposium. National Harbor, MD. Nov 2011. Butterfield Y, Corbett R, Thiessen N, Birol I. RNASeq-Align: RNA sequencing junction alignment and repositioning tool.

318. CSHL/Wellcome Trust Conference on Genome Informatics. Cold Spring Harbor, New York, Nov 2011. Jones S, Fejes A, Khodabakshi A-H, Kasaian K, Mungall K, Morin R, Goya R, Qian J, Nip KM, Chui R, Li S, Raymond A, Jackman S, Birol I, Marra M. Identifying oncogenically relevant mutation events in human cancers.

319. ASHG/ICHG 2011 Meeting. Montreal, QC. Oct 2011. Schrader K, Heravi-Moussavi A, Waters P, Senz J, Whelan J, Ha G, Eydoux P, Nielsen T, Gallagher B, Oloumi A, Boyd N, Fernandez BA, Young TL, Jones SJM, Hirst M, Shah SP, Marra MA, Green J, Huntsman DG. A next-generation sequencing approach to diagnosis of a family's skeletal abnormalities and retinitis pigmentosa.

320. 51st Canadian Association of Neuropathologists Annual Meeting. Sep 2011. Vancouver, BC. Yip S, Butterfield Y, Morozova O, Blough M, Chan J, Maslova A, Chittaranjan S, Corbett R, Cairncross JG, Marra M. Next generation sequencing of oligodendroglioma.

321. ISEH 2011 Annual Meeting. Vancouver, BC. Aug 2011. Berg T, Yap D, Wee T, Schoeler N, Thoene S, Umlandt P, Chang H, Yue L, Cheng G, Morin RD, Hirst M, Marra MA, Morin GB, Gascoyne RD, Aparicio SA and Humphries RK. A transgenic mouse model demonstrating the oncogenic role of mutations in the polycomb-group gene EZH2 in lymphomagenesis. ***(Exp Hematol. 2011 Aug;39(8) Suppl 1:S33)***

322. ISEH 2011 Annual Meeting. Vancouver, BC. Aug 2011. Heuser M, Yung E, Yun H, Berg T, Argiropoulos B, Kuchenbauer F, Hamwi I, Palmgvist L, Lai CK, Leung M, Bilenky M, Thiessen N, Robertson G, Hirst M, Wilson NK, Gottgens B, Marra M, Ganser A, Humphries R. The Potent OncogenesMN1 and MEIS1 Co-Localize at a Large Proportion of their Chromatin Target Sites Suggestive of a Higher Order Leukemogenic Regulatory Complex. ***(Exp Hematol. 2011 Aug;39(8) Suppl 1:S66-S67)***

323. 19th Annual International Conference on Intelligent Systems for Molecular Biology and 10th European Conference on Computational Biology, Vienna, Austria. Jul 2011. Krzywinski M, I Birol, S Jones, M Marra. Hive Panels – Understanding Network Structure with Rational Visualization.

324. 19th Annual International Conference on Intelligent Systems for Molecular Biology and 10th European Conference on Computational Biology, Vienna, Austria. July 2011. B irol I, Robertson G, Chu A, Westervelt P, Wilson RK, Ley TJ, Marra MA, Jones SJM. Establishing correlation networks between gene and miRNA expression.

325. 11th International Conference on Malignant Lymphoma. Lugano, Switzerland. June 2011. Steidl C, Shah SP, Woolcock BW, Rui L, Kawahara M, Farinha P, Telenius A, Ben Neriah S, Connors JM, Siebert R, Savage KJ, Jaffe ES, Staudt LM, Steidl U, Marra MA, Gascoyne RD. Discovery of CIITA Gene Fusions in B Cell Lymphomas by Next Generation Sequencing. ***(Ann Oncol. 2011 Jun;22 Suppl 4:148)***

326. 11th International Conference on Malignant Lymphoma. Lugano, Switzerland. June 2011. Gascoyne RD, Morin R, Mendez-Lago M, Mungall A, Johnson N, Scott D, Moore R, Connors J, Hirst M, Goya R, Rimsza L, Jones S, Horsman D, Mungall K, Marra MA. Next Generation Sequencing Reveals Genes Involved in Histone Modification are Frequently Mutated in Non-Hodgkin Lymphoma. ***(Ann Oncol. 2011 Jun;22 Suppl 4:101)***

327. 11th International Conference on Malignant Lymphoma. Lugano, Switzerland. June 2011. Schuetz J, Johnson N, Morin R, Marra M, Connors J, Brooks-Wilson A, Gascoyne R. BCL2 Mutations in Diffuse Large B-Cell Lymphoma. ***(Ann Oncol. 2011 Jun;22 Suppl 4:207)***

328. 87th Annual Meeting of the American Association of Neuropathologists. Seattle, WA. June 2011. Yip S, Butterfield Y, Morozova O, Blough M, Chan J, Maslova A, Chittaranjan S, Cairncross JG, Marra MA. Next Generation Sequencing of Oligodendroglioma - A Work in Progress. (***J Neuropathol Exp Neurol.*** 2011 Jun;70(6):505)

329. Garrod Symposium 2011. Calgary, AB. June 2011. KA Schrader, PJ Waters, A Heravi-Moussavi, M Marra, J Green, D Huntsman. A typical mucolipidosis III, diagnosed via whole-exome sequencing with biochemical confirmation. **(Platform presentation)**

330. Western Regional Islet Study Group 2011. Lake Arrowhead, CA. Apr 2011. Hoffman BG, Robertson G, Zhang X, Tennant B, Li L, Beach M, Whiting C, Marra MA, Gottardo R, Jones SJM, Hoodless PA. Identification of pancreatic islet specific enhancers.

331. 102nd American Association of Cancer Research Annual Meeting. Orlando, FL. Apr 2011. Morozova O, Birol I, Corbett R, Mungall K, Attiyeh EF, Asgharzadeh S, Zhao YJ, Moore RA, Hirst M, Jones S, Hogarty MD, Diskin S, Mosse YP, Diamond M, Sposto R, Ji L, Gerhard DS, Smith MA, Khan J, Seeger RC, Marra MA, Maris JM. Whole genome and transcriptome sequencing defines the spectrum of somatic changes in high-risk neuroblastoma.

332. 15th Annual International Conference on Research in Computational Molecular Biology. Vancouver, BC. Mar 2011. Butterfield B, Morozova O, Maslova A, Blough M, Chittaranjan S, Chan J, Thiessen N, Varhol N, Zhao YJ, Hirst M, Corbett R, Yip S, Cairncross G, Marra M. Integrative genomic and transcriptome analysis of oligodendroglioma using next generation sequencing technology.

333. 15th Annual International Conference on Research in Computational Molecular Biology. Vancouver, BC. Mar 2011. Swanson L, Birol I, Sahinalp SC, Robertson G, Mungall K, Chiu R, Jackman S, Qian J, Lee S, Yorukoglu D, She R, Zhao YJ, Moore R, Marra M, Jones SJM, Karsan A, Hoodless H. Detecting Chimeric Transcripts in RNA-seq Data.

334. 12th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. Feb 2011. Morin RD, Mendez-Lago M, Mungall AJ, Goya R1, Johnson NA, Severson TM, Mungall KL, Chiu R, Field M, Jackman S, Krzywinski M, Scott D, Trinh DL, Griffith M, Corbett R, Chan S, Zhao E, Smailus D, Moksa M, Rimsza L, Brooks-Wilson A, Meissner B, Woolcock B, Boyle M, McDonald H Tam A, Zhao YJ, Delaney A, Zeng T, Tse K, Butterfield Y, Birol I, Holt R, Schein J, Horsman DE, Moore R, Jones SJM, Connors JM, Hirst M, Gascoyne RD, Marra MA. Genome, Exome and Transcriptome sequencing reveals genes involved in histone modification and B-cell-receptor signalling are frequently mutated in non-Hodgkin lymphoma.

335. 12th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. Feb 2011. Morrissy AS, Marra MA. Prognostic Value of Antisense-Correlated Splicing Events to Glioblastoma Multiforme.

336. 12th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. Feb 2011. Goya R, Griffith M, Shah SP, Aparicio SA, Meyer IM, Marra MA. Exploring Alternative Splicing with RNA-Seq in Triple Negative Breast Cancers.

337. 12th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. Feb 2011. Mungall AJ, Chu A, Chun HJE, Pleasance ED, Robertson G, Butterfield Y, Chiu R, Chuah E, Coope R, Dhalla N, Guin R, Hirst C, Lee D, Li I, Ma K Mayo M, Moksa M, Mungall K, Munro S, Prabhu A, Qian J, She R, Slobodan J, Smailus DE, Stoll D, Tam A, Thiessen N, Varhol R, Wong T, Zeng T, Birol I, Moore RA, Schein JE, Stazyk G, Zhao YJ, Hirst M, Jones SJM, Marra MA and the TCGA Research

Network. Analyses of Approximately Two Hundred Acute Myeloid Leukemia Tumour Messenger and MicroRNA transcriptomes.

338. 12th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. Feb 2011. Hirst M, Zhao YJ[1], Nielsen C, Tam A, Kamoh B, Ally A, Delaney A, Cheung D, Varhol R, Sigaroudinia M, Gascard P[2], Tlsty T, Choi Y[2], McManus M, Nagarajan R, Hong C, Echipare L, O'Geen H, Farnham P, Richards H, Wang T, Haussler D, Weiss A, Moore R, Jones SJM, Costello J, Marra MA. Reference Human Epigenomes.

339. 12th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. Feb 2011. Coope R, Slobodan J, Smailus D, Jackman S, Hirst M, Marra M. Automated Size Selection and the Role of Separation Media in Insert Size Bias.

340. 12th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. Feb 2011. Jones SJM, Birol I, Morozova O, Mungall K, Li S, Corbett R, Krzywinski M, Swanson L, Chiu R, Jackman SD, She R, Qian JQ, Attiyeh EF, Asgharzadeh A[4], Bilenky M, Kasaian K, Yorukoglu D, Thiessen N, Butterfield Y, Kamoh B, Ally A, Tam A, Hirst M, Zhao YJ, Robertson G, Varhol R, Moore R, Hogarty MD, Diskin S, Mosse YP, Diamond M, Sposto R, Ji L, Gerhard DS, Smith MA, Khan J, Seeger RC, Maris JM, Marra MA, the NCI TARGET Initiative. Integrative analysis of genome and transcriptome sequencing data from 10 neuroblastoma patients identifies nine transcript rearrangements.

341. 12th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. Feb 2011. Butterfield YS, Morozova O, Maslova A, Blough MD[2], Chittaranjan S, Chan J, Thiessen N, Varhol R, Zhao YJ[1], Corbett R, Hirst M, Cairncross JG, Yip S, Marra MA. Integrative genomic and transcriptome analysis of oligodendroglioma using next generation sequencing technology.

342. 12th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. Feb 2011. Fejes AP, An J, Li Y, Leach S, Zhao YJ, Varhol R, Qian J, Jackman S, Chiu R, Mungall K, Robertson G, She W, Hirst M, Birol I, Marra MA, Brooks-Wilson A, Jones SJM. Comparative Analysis of 4 Matched Normal Ductal Carcinoma in Situ Breast Cancer Cell-lines with 1600 NGS sequenced Libraries.

343. American Society of Hematology Annual Meeting. Orlando, FL, Dec 2010. Mungall AJ, Chu A, Chiu R, Corbett R, Field MA, Jackman SD, Mungall KL, Wong K, Boyle M, Carlsen R, Chan SY, Coope RJN, Hirst CA, Hirst M, Johnson N, Krzywinski M, Lee D, Lin JBX, Moore R, Severson T, Simpson JT, Steidl C, Zeng T, Zhao YJ, Birol I, Holt RA, Jones SJ, Gascoyne RD, Horsman DE, Connors JM, Schein JE, Marra MA. Base-Pair Resolution of Somatic and Germline-Derived Genome Rearrangement Breakpoints in Follicular Lymphoma.

344. American Society of Hematology Annual Meeting. Orlando, FL, Dec 2010. Mendez-Lago M, Morin RD, Mungall AJ, Chan S, Chittaranjan S, Severson TM, Goya R, Mungall K, Johnson NA, Boyle M, Woolcock B, Zeng T, McDonald H, An J, Yakovenko O, Tam A, Zhao YJ, Hirst M, Moore R, Schein JE, Jones SJ, Horsman DE, Gascoyne RD, Connors JM, Marra MA. Mutations in MLL2 and MEF2B Genes in Follicular Lymphoma and Diffuse Large B-Cell Lymphoma.

345. American Society of Hematology Annual Meeting. Orlando, FL, Dec 2010. Morin RD, Mendez-Lago M, Mungall AJ, Johnson NA, Goya R, Severson TM, Mungall K, An J, Yakovenko O, Jackman S, Krzywinski M, Griffith M, Chan S, Tam A, Smailus D, McDonald H, Moksa M, Woolcock B, Boyle M, Zeng T, Zhao YJ, Holt RA, Moore R, Schein JE, Birol I, Horsman DE, Jones SJ, Hirst M, Connors JM, Gascoyne RD, Marra MA. Identification of Genes Frequently Mutated in FL and DLBCL with Transcriptome, Genome and Exome Sequencing.

346. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2010. Mendez-Lago M, Morin RD, Mungall AJ, Chan S, Chittaranjan S, Severson TM, Goya R, Mungall K, Johnson NA, Boyle M, Woolcock B, Zeng T, McDonald H, An J, Yakovenko O, Tam A, Zhao YJ, Hirst M, Moore R, Schein JE, Jones SJ, Horsman DE, Gascoyne RD, Connors JM, Marra MA. Mutations in MLL2 and MEF2B Genes in Follicular Lymphoma and Diffuse Large B-Cell Lymphoma.

347. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2010. Morrissy S, Marra MA. Prognostic Value of Antisense-Correlated Splicing Events to Glioblastoma Multiforme.

348. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2010. Mungall AJ, Morin RD, An J, Yakovenko O, Boyle M, Johnson NA, Woolcock B, Leach S, Mayo M, Mendez-Lago M, Munro S, Zeng T, Zhao YJ, Hirst M, Holt RA, Moore RA, Schein JE, Gascoyne RD, Horsman DE, Connors JM, Jones SJ, Marra MA. Recurrent DNA Mutations In Non-Hodgkin Lymphomas Reveal Candidate Therapeutic Targets.

349. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2010. Morozova O, Hansford L, Mungall K, Attiyeh E, Corbett R, Thiessen N, Varhol R, Zhao YJ, Chiu R, Maslova A, Birol I, Jones S, Hirst M, Maris JM, Kaplan DR, Marra MA. Comparative Analysis of Primary Tumors and Metastases-Derived Tumor-Initiating Cells Provides Insights into Neuroblastoma Progression.

350. The American Society of Human Genetics Annual Meeting. Washington, DC. Nov 2010. du Souich C, Nowaczyk MJM, König A, Raymond FL, McLarren KW, Larstone R, Livesley J, Friedlander R, Marra MA, Boerkoel CF. Linking cholesterol biosynthesis and human behavior.

351. The American Society of Human Genetics Annual Meeting. Washington, DC. Nov 2010. Rupps R, van Karnebeek CD, Fejes A, Morimoto M, Shuen C, Markello T, Delaney A, Jones S, Marra M, Boerkoel CF. Progressive Systemic And Stenotic Vasculopathy: Candidate Genes Identified by Comparative Whole Exome Sequencing.

352. ImmunoVancouver 2010 Meeting. Vancouver, BC. June 2010. Nielsen JS, Macpherson N, Wick DA, Gascoyne RD, Connors JM, Marra MA, Webb JR, Nelson BH. Development of a platform to rapidly translate genomic discoveries into therapeutic cancer vaccines.

353. European Human Genetics Conference. Gothenburg, Sweden. June 2010. du Souich C, McClarren K, Larstone R, Friedlander R, Livesley J, Severson TM, Stockton DW, Raymond FL, Marra MA, Boerkoel CF. Linking cholesterol metabolism and human behavior.

354. Advances in Neuroblastoma Research. Stockholm, Sweden. June 2010. Vojvodic M, Morozova O, Blakely KM, Grinshtein N, Hansford LM, Smith KM, Tong J, Taylor P, Irwin M, Moffatt J, Moran MF, Marra MA, Kaplan DR. Identification of signaling pathways and drug candidates using primary neuroblastoma cancer stem cells by phosphoproteomics and transcriptome sequencing.

355. 15th Congress of European Hematology Association. Barcelona, Spain. June 2010. Kuchenbauer F, Petriv OI, Delaney A, Lecault V, White A, Kent D, Marmolejo L, Heuser M, Berg T, Copley M, Ruschmann J, Sekulovic S, Antignano F, Kuroda E, Ho V, Benz C, Halim T, Giambra V, Krystal G, Eaves CJ, Takei F, Weng AP, Piret J, Marra MA, Humphries RK, Hansen CL. Profiling of microRNA Expression in Purified Hematopoietic Populations and in Single Cells.

356. 15th Congress of European Hematology Association. Barcelona, Spain. June 2010. Heuser M, Yun H, Argiropoulos B, Yung E, Kuchenbauer F, Park G, Lai C, Leung M, Lin G, Hamwi I, Thiessen N, Robertson G, Hirst M, Marra M, Ganser A, Humphries R. MEIS1 Controls Susceptibility to MN1-Induced Leukemic Transformation.

357. HUGO's 13th Human Genome Meeting, Montpellier, France. May 2010. Rose AM, O'Neil NJ, Bilenky M, Butterfield YS, Malhis N, Flibotte S, Jones MR, Marra M, Baillie DL, Jones SJ. Accumulated Changes in a Genome of a Strain with a Highly Modified Reciprocal Exchange Distribution. **(Oral presentation)**

358. Canadian Society of Immunology Annual Meeting. Niagara Falls, ON. Apr 2010. Nielsen JS, Connors JM, Gascoyne RD, Webb JR, Marra MA, MacPherson N, Nelson BH. Development of a platform to rapidly translate genomic discoveries into therapeutic cancer vaccines.

359. 9th Annual UT-ORNL-KBRIN Bioinformatics Summit. Cadiz, KY. Mar 2010. Jones SJM*, Laskin J, Li YY, Griffith OL, An J, Bilenky M, Butterfield YS, Cezard T, Chuah E, Corbett R, Fejes A, Griffith M, Yee J, Martin M, Mayo M, Melnyk N, Morin RD, Pugh TJ, Severson T, Shah SP, Sutcliffe M, Tam A, Terry J, Thiessen N, Thomson T, Varhol R, Zeng T, Zhao YJ, Moore RA, Huntsman DG, Birol I, Hirst M, Holt RA, Marra MA. Genomic analysis of a rare human tumor. ***(BMC Bioinformatics. 2010 Jul 23;11 Suppl 4:03)***

360. 11th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. Feb 2010. Mungall AJ, Chu A, Chiu R, Corbett R, Field MA, Jackman SD, Mungall KL, Wong K, Boyle M, Carlsen R, Chan SY, Coope RJN, Hirst CA, Johnson N, Krzywinski MI, Lee D, Lin JB, Mayo M, Munro S, Severson T, Simpson JT, Steidl C, Zeng T, Zhao Y, Birol I, Hirst M, Holt RA, Jones SJ, Moore R, Gascoyne RD, Horsman DE, Connors JM, Schein JE, Marra MA. Base-Pair Resolution of Somatic and Germline-Derived Genome Rearrangement Breakpoints in Follicular Lymphoma. **(Oral presentation)**

361. 11th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. Feb 2010. Birol I, Robertson G, Schein JE, Jackman S, Chiu R, Field M, Qian J, Raymond A, Mungall K, Nielsen C, Butterfield Y, Cézard T, Newsome R, Thiessen N, Griffith M, Varhol R, Zhao YJ, Hirst M, Moore R, Marra MA, Pamela A Hoodless, Steven JM Jones. High-Throughput Analysis of Transcriptome Assemblies. **(Oral presentation)**

362. 11th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. Feb 2010. Morin RD, Johnson NA, Severson TM, Mungall AJ, An J, Paul JE, Boyle M, Woolcock BW, Kuchenbauer F, Goya G, Yap D, Humphries RK, Griffith OL, Shah S, Zhu H, Kimbara M, Shashkin P, Charlot JF, Tcherpakov M, Corbett R, Tam A, Varhol R, Smailus D, Moksa M, Zhao YJ, Delaney A, Qian H, Birol I, Schein J, Moore R, Holt R, Horsman DE, Connors JM, Jones S, Aparicio S, Hirst M, Gascoyne RD, Marra MA. Identifying recurrent somatic mutations in Follicular and Diffuse Large B-cell Lymphomas using second-generation sequencing.

363. 11th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. Feb 2010. Zhao YJ, Zeng T, Varhol R, Li I, Mayo M, Tam A, Chuah E, Wong T, Miller D, Smailus D, Stazyk G, Delaney A, Moore R, Birol I, Roscoe R, Holt R, Jones S, Hirst M, Marra MA. Production scale next generation sequencing.

364. 11th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. Feb 2010. Goya R, Morin R, Wong T, Zhao YJ, Hirst M, Pilarski LM, Belch A, Reiman T, Marra MA. Detection of Changes in Tumor Heterogeneity Using Next-Generation Sequencing of Transcriptomes.

365. 11th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. Feb 2010. Morrissy AS, Marra MA. The role of antisense transcription in the regulation of alternative splicing.

366. 11th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. Feb 2010. Morozova O, Hansford L, Smith L, Maslova S, Cezard T, Morin R, Thiessen N, Varhol R, Zhao YJ, Jones S, Hirst M, Kaplan D, Marra M. Using sequence census data from cancer tissue compendia to discover novel drug targets for refractory neuroblastoma.

367. 11th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. Feb 2010. Butterfield YS, Jones SJM, Laskin J, Li Y, Griffith O, An J, Bilenky M, Cezard T, Chuah E, Corbett R, Fejes A, Griffith M, Yee J, Martin M, Mayo M, Melnyk N, Morin RD, Pugh TJ, Severson T, Shah SP, Sutcliffe M, Tam A, Terry J, Thiessen N, Thomson T, Varhol R, Zeng T, Zhao Y, Moore R, Huntsman DG, Birol I, Hirst M, Holt RA, Marra MA. Evolution of an adenocarcinoma in response to selection by targeted kinase inhibitors.

368. 11th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. Feb 2010. Fejes AP, Leach S, Zhao YJ, Varhol R, Hirst M, Marra MA, Brooks-Wilson A, Jones SJM. RNA-Seq Determination of Non-Synonymous Coding Mutations in 5 Breast Cancer Cell Lines and a Matched Cancer/Normal Set.

369. 51st American Society of Hematology Annual Meeting and Exposition. New Orleans, LA. Dec 2009. Mungall AJ, Chu A, Chiu R, Corbett R, Field MA, Jackman SD, Mungall KL, Wong K, Boyle M, Carlsen R, Chan SY, Coope RJN, Hirst CA, Hirst M, Johnson N, Krzywinski M, Lee D, Lin JB, Moore R, Severson T, Simpson JD, Steidl C, Zeng T, Zhao YJ, Birol I, Holt RA, Jones SJ, Gascoyne RD, Horsman DE, Connors JM, Schein JE, Marra MA. Base-Pair Resolution of Somatic and Germline-Derived Genome Rearrangement Breakpoints in Follicular Lymphoma. **(Oral presentation)**

370. 51st American Society of Hematology Annual Meeting and Exposition. New Orleans, LA. Dec 2009. Mullighan CG, Morin RD, Zhang J, Hirst M, Zhao YJ, Yan C, Finney R, Edmonson M, Su X, Buetow K, Carroll WL, Chen I-M, Devidas M, Gerhard DS, Harvey RC, Hu J, Loh ML, Reaman GH, Relling MV, Smith M, Downing JR, Hunger SP, Willman CL, Marra M. Next generation transcriptomic resequencing identifies novel genetic alterations in high-risk (HR) childhood acute lymphoblastic leukemia (ALL): A Report from the Children's Oncology Group (COG) HR ALL TARGET Project.

371. 51st American Society of Hematology Annual Meeting and Exposition. New Orleans, LA. Dec 2009. Reiman T, Morin R, Goya R, Wong T, Zhao YJ, Hirst M, Pilarski LM, Belch A, Marra M. Comparative Whole Transcriptome Shotgun Sequencing (WTSS) of Myeloma at Diagnosis and at Drug-Resistant Relapse. **(Oral presentation)**

372. 51st American Society of Hematology Annual Meeting and Exposition. New Orleans, LA. Dec 2009. Cheung KJ, Johnson N, Affleck J, Severson T, Steidl C, Ben-Neriah S, Schein J, Morin DR, Moore R, Shah SP, Qian H, Paul J, Tlenius A, Lai B, Relander T, Lam WL, Savage KJ, Connors JM, Brown C, Marra M, Gascoyne RD, Horsman DE. TNFRSF14 is mutated in a subset of follicular lymphoma and correlated with inferior prognosis.

373. Joint Meeting of the Society for Neuro-Oncology/American Association of Neurological Surgeons/Congress of Neurological Surgeons. New Orleans, LA. Oct 2009. Nagarajan RP, Wang T, Johnson BE, Hong CB, Fouse S, Haussler D, Hirst M, Marra MA. Costello J. Deep sequencing of the DNA methylome of glioblastoma.

374. Human Proteome Organization Annual World Meeting, Toronto, ON. Sep 2009. Vojvodic M, Tong J, Morozova O, Smith KM, Hansford LM, Taylor P, Marra M, Moran MF, Kaplan DR. Phospho-Proteomic Analysis of Neuroblastoma Cancer Stem Cells Identifies B-Cell Receptor Signaling and SRC Family for Drug Targeting. **(Oral presentation)**

375. 38th Annual Scientific Meeting of the International Society for Hematology and Stem Cells. Athens, Greece. Sep 2009. Humphries K, Kuchenbauer F, Mah S, McPherson A, Berg T, Lai D, Murani AL, Hogge D, Starczynowski D, Karsan A, O'Connor M, Eaves C, Watahiki A, Wang Y, Aparicio S, Ganser A, Krauter J, Johnnidis J, Marra M, Carmargo F. Differential expression of miRNAs in cancer and a possible role in acute myeloid leukemia.

376. 38th Annual Scientific Meeting of the International Society for Hematology and Stem Cells. Athens, Greece. Sep 2009. Heuser M, Argiropoulos B, Yung E, Kuchenbauer F, Park G, Lai C, Chan S, Thiessen N, Robertson G, Hirst M, Marra M, Ganser A, Humphries AK. Transcriptional program defining cellular susceptibility to MN1-induced transformation.

377. International Society for Stem Cell Research (ISSCR) 7th Annual Meeting. Barcelona, Spain. July 2009. O'Connor MD, Yap D, Fee J, Zhao YJ, McDonald H, Zeng T, Hirst M, Marra MA, Aparicio S, Eaves CJ. High-throughput siRNA screening of human embryonal carcinoma cells reveals novel genes required for maintenance of human embryonic and induced pluripotent stem cells.

378. 42nd Annual Meeting of the Society for the Study of Reproduction. Pittsburgh, PA. July 2009. Ahn HW, Zhao H, Harris RA, Coarfa C, Milosavljevic A, Morin RD, Marra MA, Rajkovic A. Massive Parallel Sequencing of Small RNAs from Newborn Mouse Ovaries Identifies Novel miRNAs Preferentially Expressed in the Ovaries. **(Poster presentation)**

379. MicroRNA and Cancer Keystone Symposium. Keystone, CO. June 2009. Kuchenbauer F, Mah SM, Heuser M, Argiropoulos B, McPherson A, Morin RD, Rosten P, Berg T, Lai D, Starczynowski D, Karsan A, O'Connor MD, Eaves CJ, Aparicio SA, Ganser A, Krauter J, Johnnidis JB, Marra MA, Carmargo FD, Humphries RK. Emerging evidence of differential expression of miRNA*s and its contribution to the development of acute myeloid leukemia.

380. ASCO Annual Meeting. Orlando, FL. May-June 2009. Laskin JJ, Pugh TJ, Jackson C, Sutcliffe M, Ionescu D; Melosky B, Ho C, Sun S, Murray NR; Marra MA. Transcriptome-wide mutation discovery in patients in a phase II clinical trial of first-line erlotinib for clinically selected patients with advanced non-small cell lung cancer.

381. Canadian Human Genetics Conference. Harrison Hot Spring, BC. May 2009. Yang SW, Hitz M-P, Provost S, Chetaille P, Thibeault M, Bureau N, Riopel K, Bigras J-L, Richter A, Severson T, Marra M, Dubé M-P, Andelfinger G. Septal defects and left ventricular outflow tract obstruction: a novel syndrome mapping to Xq28.

382. Genome BC Genomics Forum and Research Exchange. Vancouver, BC. Apr 2009. Zeng T, Deng M, Ma K, Mah DG, McDonald H, Moksa M, Pandoh P, Tse K, Zhao YJ, Hirst M, Marra MA, Technology Development For Next-Generation Sequencing Platforms.

383. Genome BC Genomics Forum and Research Exchange. Vancouver, BC. Apr 2009.McDonald H, Pandoh P, Zeng T, Tse K, Hirst M, Marra MA. Massively Parallel Yeast Two Hybrid.

384. 10th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. Feb 2009. Birol I, Jackman S, Wong K, Chan S, DiGuistini S, Simpson J, Woodsworth D, Liao N, Krzywinski M, Schein J, Marra MA, Jones SJM. Second Generation *de Novo* Assembly and Finishing.

385. 10th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. Feb 2009. Hoodless PA, Wederell E, Bilenky M, Robertson G, Cullum R[1], Lee S, Hoffman B, Thiessen N, Tam A, Varhol R, Zhao YJ, Hirst M, Marra MA, Jones SJM. Deciphering Transcriptional Networks *in vivo* in the Mammalian Liver.

386. 10th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL Feb 2009. Griffith OL, Li Y, Leach S, Mungall AJ, Griffith M, Fejes A, Lee H, Stratford A, Marra MA. Dunn SE, Brooks-Wilson A, Jones SJM. Identification of Novel Iressa Synergists by Illumina Sequencing and Drug Screening in Breast Cancer.

387. 10th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. Feb 2009. Mungall AJ, Boyle M, Carlsen R, Chan SY, Corbett R, Chiu R, Chu A, Field M, Hirst C, Hirst M, Jackman S, Johnson N, Krzywinski MI, Lee D., Mungall K, Simpson J, Steidl C, Severson T, Wong K, Zeng T, Zhao Y, Birol I, Gascoyne RD, Horsman DE, Connors JM, Schein JE, Marra MA. Massively Parallel Sequencing of Genome Rearrangements in Follicular Lymphoma Patients Reveals Novel Somatic Mutations.

388. 10th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. Feb 2009. Morozova O, Morin RD, Hansford L, Hirst M, McDonald H, Zhao Y, Kaplan DR, Marra MA. Defining the identity of neuroblastoma tumor initiating cells via massively parallel transcriptome sequencing.

389. 10th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. Feb 2009. Pugh TJ, Laskin JJ, Asano J, Barclay L, Chan S, Morin RD, Sutcliffe M, Yang C, Ho C, Ionescu D, Jackson C, Lam S, Lee C, McWilliams A, Melosky B, Murray NR, Sun S, Marra MA. Transcriptome-wide mutation detection in pre-treatment lung cancers from individuals likely to benefit from erlotinib treatment.

390. 50th American Society of Hematology Annual Meeting & Exposition. San Francisco, CA. Dec 2008. Kuchenbauer F, Petriv OI, Delaney A, Kent D, Heuser M, Mah SM, Copley M, Ruschmann J, Antignano F, Kuroda E, Ho V, Benz C, Halim T, Giambra V, Krystal G, Eaves CJ, Takei F, Weng AP, Marra MA,

Hansen CL, Humphries RK. Comprehensive profiling of microRNAs in murine hematopoietic stem cells and lineages using a microfluidics approach. ***(Blood. 2008 Nov 16;112(11):857)***

391. 50th American Society of Hematology Annual Meeting & Exposition. San Francisco, CA. Dec 2008. Kent DG, Copley MR, Benz C, Wöhrer S, Dykstra BJ, Ma E, Cheyne J, Zhao Y, Bowie M, Zhao Y, Gasparetto M, Delaney A, Smith C, Marra M, Eaves CJ. New Candidate Regulators of Hematopoietic Stem Cells with High Self-renewal Activity. ***(Blood. 2008 Nov 16;112(11): 854-855)***

392. 50th American Society of Hematology Annual Meeting & Exposition. San Francisco, CA. Dec 2008. Zhao Y, Delaney A, Raouf A, Raghuram K, Li HYI, Schnerch A, Jiang XY, Eaves AC, Marra MA. Differentially Expressed and Novel Transcripts in Highly Purified Chronic Phase CML Stem Cells. ***(Blood. 2008 Nov 16;112(11): 79)***

393. 50th American Society of Hematology Annual Meeting & Exposition. San Francisco, CA. Dec 2008. Starczynowski DT, Kuchenbauer F, Argiropoulos B, Sung S, Morin R, Muranyi AL, Hirst M, Hogge DE, Marra M, Wells RA, Lam W, Humphries RK, Karsan A. Identification of Mir-145 and Mir-146a as microRNAs involved in the pathogenesis of 5q-syndrome. ***(Blood. 2008 Nov 16;112(11): 316)***

394. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2008. Griffith M, Pugh TJ, Tang MJ, Morin RD, Asano JK, Ally A, Chan SY, Taylor G, Morin GB, Tai IT, Marra MA. Genomic analysis of uridine monophosphate synthetase reveals novel mRNA isoforms associated with fluorouracil resistance in colorectal cancer.

395. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2008. Morozova O, Morozov V, Hirst M, Marra MA. Defining expression signatures of known cancer genes using seriation analysis of SAGE libraries from Cancer Genome Anatomy Project (CGAP).

396. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2008. Mungall, AJ, Boyle M, Carlsen R, Chan SY, Corbett R, Chiu, R, Chu A, Field M, Hirst C, Johnson N, Krzywinski MI, Lee D, Mungall K, Simpson J, Steidl C, Severson T, Wong K, Zeng T, Birol I, Hirst M, Schein JE, Gascoyne RD, Horsman DE, Connors JM, Marra MA. Sequence Validation Of Candidate Genome Rearrangements in Follicular Lymphoma Patients Reveals Novel Gene Fusion Events.

397. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2008. Paul J, Severson T, Cheung JK, Schein J, Horsman D, Marra M. Detailed Characterization Of The Lymphoma 1p36 Deletion.

398. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2008. Morrissy S, Morin R, Delaney A, Zeng T, McDonald H, Hirst M, Jones S, Marra M. Exploring The Transcriptome Of Cancer And Normal Tissues Using A Novel Tag Sequencing Approach.

399. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2008. McPherson A. Morin R, Wu D, Aparicio S, Marra M. An investigation into microRNA profiles and microRNA editing in breast cancer cells using next generation sequencing.

400. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2008. Farnoud N, Delaney A, Li I, Schein J, Marra M. Characterization of DNA Copy Number Variations in Lymphoma Genomes.

401. Genome Informatics. Hinxton, UK. Sep 2008. Krzywinski M, Schein J, Birol I, Jones S, Marra M. Circos: an Information Aesthetic for Comparative Genomics.

402. 10th International Conference on Malignant Lymphoma (ICML). Lugano, Switzerland. June 2008. Schein J, Krzywinski M, Hirst C, Chiu R, Chu A, Corbett R, Field M, Simpson J, Wong K, Carlsen R, Lee D, Boyle M, Chan S, Cheung KJ, Coope R, Delaney A, Flibotte S, Li I, Moore R, Severson T, Steidl C, Qian H, Wye N, Johnson N, Birol I, Jones S, Gascoyne R, Horsman D, Connors J, Marra A. Structural Rearrangement Discovery in Follicular Lymphoma Genomes. ***(Annals of Oncology. 2008 Jun; 19:178-129 Suppl 4)***

403. 10th International Conference on Malignant Lymphoma (ICML). Lugano, Switzerland. June 2008. Cheung KJ, Shah S, Steidl C, Johnson N, Relander T, Telenius A, Lai B, Qian H, Murphy K, Lam W, Marra M, Connors JM, Ng R, Gascoyne RD, Horsman D. Genome-wide profiling of follicular lymphoma by array comparative genomic hybridization reveals prognostically significant DNA copy number imbalances. ***(Annals of Oncology. 2008 Jun; 19:94 Suppl 4)***

404. 44th ASCO Annual Meeting. Chicago, Il. May-June 2008. Laskin JJ, Pugh T, Jackson C, Barclay L, Sutcliffe M, Ionescu D, Lam S, McWilliams A; Melosky B Ho C, Murray NR; Marra M. Genomic sequencing in a phase II clinical trial of first-line therapy of erlotinib for clinically selected patients with advanced non-small cell lung cancer.

405. Digestive Disease Week. San Diego, CA, USA. May 2008. Griffith M, Tang MJ, Chan S, Asano J, Ally A, Pugh T, Tai IT and Marra MA. Identification of differentially expressed alternative mRNA isoforms associated with chemotherapy resistance in colon cancer cell lines. ***(Gastroenterology*. *2008 Apr;134(4):A444-A444(1))***

406. 99th Annual Meeting of the American Association for Cancer Research. San Diego, CA. Apr 2008. Romanuik TL, Delaney MD, Marra MA, Sadar MD. Gene expression signatures associated with progression of prostate cancer to androgen-independence. (***Proceedings of the AACResearch Annual Meeting. 2008 Apr; 49: 400)***

407. Canadian Breast Cancer Research Alliance Conference. Vancouver, BC. Apr 2008. Eaves C, Eirew P, Raouf A, Stingl J, Turashvili G, Delaney A, Emerman J, Marra M, Aparicio S. Stem Cells in the Mammary Gland.

408. Genomic Disorders Conference. Hinxton, Cambridgeshire, UK, Mar 2008. Zahir FR, Adam S, Armstrong L, Delaney AD, Eydoux P, Marra MA, Van-Allen M, Friedman JM. Assessing pathogenicity of *de novo* CNVs in children with idiopathic mental retardation.

409. The 9th Annual AGBT Conference. Marco Island, FL. Feb 2008. Delaney A, Li I, Zhao Y, McDonald H, Zeng T, Hirst M, Hoodless PJ, Marra MA. An Illumina sequencing approach for tag-based transcriptome analysis. **(Platform presentation)**

410. The 9th Annual AGBT Conference. Marco Island, FL. Feb 2008. Hirst M, Delaney A, Zhao Y, Zeng t, Varhol R, Ingham M, Tam A, Prabhu A-L, Dhalla N, Pandoh P, Kamoh B, Kirk H, Ma K, Moksa M, Mah D, Lee S, Deng M, Li I, Charters A, Wong T, Robertson G, Bilenky M, Guin R, Jones S, Marra MA. A production scale next generation sequencing platform. **(Platform presentation)**

411. The 9th Annual AGBT Conference. Marco Island, FL. Feb 2008. Birol I, Simpson J, Wong K, Schein J, Marra M, Jones S. .De Novo Assembly of Short Sequence Reads. **(Platform presentation)**

412. Pacific Symposium of Biocomputing. Kohala Coast, HI, USA. Jan 2008. Griffith M, Tang M, Griffith O, Morin R, Chan S, Asano J, Zeng T, Flibotte S, Ally A, Baross A, Hirst M, Jones S, Morin G, Tai I and Marra MA. ALEXA – A microarray design platform for alternative expression analysis.

413. UBC Genetics and Bioinformatics Graduate Retreat. Vancouver, BC. Dec 2007. Morozova O, Morozov Y, Chikatamarla A, Bilenky M, Robertson G, Marra M. From pottery styles to mouse development: a method for delineating mammalian transcriptional regulatory networks. **(Best Poster Award - Bioinformatics category)**

414. UBC Genetics and Bioinformatics Graduate Retreat. Vancouver, BC. Dec 2007. Hou YC, Chittaranjan S, Marra MA, Gorski SM. Common regulators of apoptosis and autophagy-an analysis of known cell death genes in starvation-induced autophagy**. (Best Poster Award – Genetics category)**

415. 49th American Society of Hematology Annual Meeting and Exposition. Atlanta, GA. Dec 2007. Zhao YJ, Delaney A, Marra MA, Jiang XY, Eaves AC, Eaves CJ. Comparative transcriptome analysis of different

subsets of CD34(+) normal and chronic myeloid leukemia cells identifies novel perturbations in the CML stem cell population. (***Blood. 2007 Nov 110(11):19a-19A Part 1)***

416. 49TH American Society of Hematology Annual Meeting and Exposition. Atlanta, GA. Dec 2007. Kuchenbauer F, Morin R, Staaf J, Borg A, Argiropoulos B, Delaney A, Zeng T, McDonald H, Hirst M, Rovira C, Marra M, Humphries RK. Accurate Detection of the microRNA Transcriptome in a Leukemia Progression Model. (***Blood. 2007 Nov 16;110(11):265A Part 1)***

417. 49TH American Society of Hematology Annual Meeting and Exposition. Atlanta, GA. Dec 2007. Cheung K-J, Telenius A, Lai B, Johnson N, Relander T, Steidl C, Baross A, Qian H, Schein J, Marra M, Connors JM, Gascoyne RD, Horsman DE. High Frequency of 1p36.32 Deletion or Loss of Heterozygosity in Follicular Lymphoma (FL). (***Blood*. *2007 Nov 110(11):61A Part 1)***

418. 49TH American Society of Hematology Annual Meeting and Exposition. Atlanta, GA. Dec 2007. Kent D, Zhao Y, Bowie M, Dykstra B, Cheyne J, Zhao YJ, Delaney A, Hirst M, Marra M, Eaves CJ. Differences in the Transcriptomes of Highly Purified Fetal Liver and Adult Bone Marrow Hematopoietic Stem Cells Revealed by Long Serial Analysis of Gene Expression (LongSAGE). (***Blood*. *2007 Nov 110(11):384A Part 1)***

419. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2007. Bosdet I, Marra M, Gorski S. Programmed cell death in the drosophila retina – characterizing the echinus locus.

420. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2007. Petrescu A, Delaney A, Marra M. Tag Sequencing Approaches for the Detection of Cis-Encoded Antisense Transcription.

421. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2007. Farnoud N, Chan S, Flibotte S, Delaney A, Friedman JM, Marra M. DLOH: A novel bioinformatics tool for detection of CN deletions using LOH data.

422. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2007. Griffith M, Tang MJ, Griffith OL, Chan SY, Asano JK, Zeng T, Flibotte S, Ally A, Baross A, Morin RD, Hirst M, Jones SJM, Morin GB, Tai IT, Marra MA. ALEXA –a microarray design platform for alternative expression analysis.

423. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2007. Pugh TJ, Keyes M, Moore RA, Barclay L, Thomas D, Yang C, Pickles T, Mckenzie M, Morris JW, Agranovich A, Marra MA. Discovery of variants in DNA repair genes associated with late side-effects in prostate brachytherapy patients.

424. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2007. Pugh TJ, Delaney AD, Farnoud N, Flibotte S, Griffith M, Li I, Farinha P, Gascoyne RD, Marra MA. Two wrongs make a right: the use of whole genome amplification for pair-wise genome-wide copy number analysis of limited patient material.

425. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2007. Moore RA, Mayo MR, Wagner SA, Pugh TP, Axam HJ, Cruz KL, Matsuo C, Sze WK, Tam B, Thomas, D, Tomescu A, Trinh EK, Wilton JM, Marra MA, Holt RA. High-throughput amplicon sequencing platform at the BCCA, Genome Sciences Centre.

426. UBC Medical Genetics Research Day. Vancouver, BC. Oct 2007. Griffith M, Tang MJ, Griffith OL, Chan SY, Asano JK, Zeng T, Flibotte S, Ally A, Baross A, Morin RD, Hirst M, Jones SJM, Morin GB, Tai IT, Marra MA. ALEXA – A microarray design platform for alternative expression analysis.

427. The American Society of Human Genetics 57th Annual Meeting. San Diego, CA. Oct 2007. Friedman JM, Adam S, Arbour L, Armstrong L. Baross A, Birch P, Boerkoel C, Chan S, Delaney AD, Eydoux P, Flibotte S, Gibson WT, Langlois S, Li H, MacLeod P, McGilliray B, Michaud J, Patel M, Qian H, Rouleau G, Schein J, Van Allen M, Yong S-L, Zahir F, Marra M. Frequent detection of both pathogenic

and apparently benign *de novo* copy number variants by Affymetrix 500K GeneChip® array genomic hybridization in children with idiopathic mental retardation.

428. 36th Annual Meeting of the International Society for Experimental Hematology. Hamburg, Germany. Sep 2007. Kuchenbauer F, Morin R, Delaney A, Zeng T, McDonald H, Hirst M, Marra M, Humphries K. Comprehensive and quantitative detection of microRNAs in a leukemia progression model using a high throughput Solexa™ based sequencing platform. (***Exp Hematol*. *2007 Sep;35(9):77 Suppl.2)***

429. 36th Annual Meeting of the International Society for Experimental Hematology. Hamburg, Germany. Sep 2007. Zhao Y, Delaney A, Marra MA, Eaves AC, Eaves CJ. Comparative transcriptome analysis of normal and chronic myeloid leukemia stem cells.

430. 12th IASLC World Conference on Lung Cancer. Seoul, Korea. Sep 2007. Laskin JJ, Pugh T, Keogh C, Barclay L, Sutcliffe M, Ionescu D, Lam S, Melosky B, Ho C, Murray NR, Lee CW, Marra M. Correlative genetics in a phase II clinical trial of first-line therapy of erlotinib for clinically selected patients with advanced non-small cell lung cancer. **(Poster presentation) (*J Thoracic Oncol. 2007 Aug; 2(8):S442-S443 Suppl.S)***

431. 12th IASLC World Conference on Lung Cancer. Seoul, Korea. Sep 2007. Pugh TJ, Delaney AD, Flibotte S, Farnoud N, Li I, Farinha P, Gascoyne RD, Marra MA. Two Wrongs Make A Right: The Use of Whole-Genome Amplification for Pair-Wise Genome-wide Copy Number Analysis of Limited Patient Material.

432. 50th Annual Conference of the Canadian Society of Biochemisty, Molecular and Cellular Biology. Montreal, QC. Jul 2007. Morozova O and Marra MA. From cytogenetics to next-generation sequencing technologies: advances in the detection of genome rearrangements in tumors. (***Biochem Cell Biol*. *2008 Apr;86(2):81-91)***

433. 66th Society of Developmental Biology Annual Meeting. Cancun, Mexico. June 2007 Hoffman B, Kok D, Witzsche J, Hirst M, Robertson G, Hoodless PA, Jones S, Marra M, Helgason CD. Genome-wide analysis of Nkx2.2 binding sites using ChIP- tag sequencing (ChIP-TS). (***Develop Biol*. *2007 June 1,306 (1):354)***

434. 5th ISSCR Annual Meeting. Cairns, Queensland, Australia. June 2007. Morin RD, Delaney A, O'Connor M, Prabhu A-L, Zhao Y, McDonald H, Zeng T, Hirst M, Eaves C, Marra MA. Identification of small RNAs important in embryonic stem cells and their differentiation.

435. 5th ISSCR Annual Meeting. Cairns, Queensland, Australia. June 2007. Salvagiotto G, Vodyanik M, Ruotti V, Stewart R, Zhao Y, Marra M, Thomson J, Eaves C, Slukvin I. Molecular Profiling of Human Embryonic Stem Cell (ESC)-Derived Lymphohematopoietic Progenitors Reveal Altered Expression of Genes Associated with Hematopoietic Stem Cell (HSC) Self-Renewal and Survival.

436. 1st Michael Smith Laboratories Poster Event, University of British Columbia. Vancouver, BC. May 2007. Pugh TJ, Delaney AD, Flibotte S, Farnoud N, Li I, Farinha P, Gascoyne RD, Marra MA. Copy Number Biases Induced by Whole Genome Amplification & the Use of Amplified Material for Pair-Wise Analysis.

437. 1st Michael Smith Laboratories Poster Event, University of British Columbia. Vancouver, BC. May 2007. Petrescu A, Delaney A, Marra M. Massively Parallel Sequencing Approaches for the Detection of Cis-Encoded Antisense Transcription.

438. HUGO's 12th Human Genome Meeting. Montreal, QC. May 2007. **Morozova O**, Morozov V, Bilenky M, Robertson G, Marra M. From pottery styles to mouse development: a method for delineating mammalian transcriptional regulatory networks.

439. 3rd International DECIPHER Symposium, Wellcome Trust Conference Programme. Hinxton, UK. May 2007. Friedman JM, Delaney A, Adam S, Arbour L, Armstrong L, Baross A, Birch P, Boerkoel C, Chan

S, Gibson WT, Qian H, Langlois S, McGillivray BC, Patel M, Van Allen MI, Yong S-L, Zahir F, Eydoux P, Marra M. Affymetrix 500K GeneChip® Array Genomic Hybridiation in Children with Idiopathic Mental Retardation: The Vancouver Experience.

440. Seventh International Workshop on Molecular Aspects of Myeloid Stem Cell Development and Leukemia. May 2007. Annapolis, MD. Zhao Y, Jiang X, Delaney A, Marra M, Eaves A, Eaves C. Comparative transcriptome analysis of normal and CML stem cell populations.

441. Keystone Symposia (Autophagy in Health and Disease). Monterey, CA. Apr 2007. Chittaranjan S, McConechy M, Hou YC, Freeman JD, Marra MA, Gorski SM. Steroid hormone control of cell death and cell survival: molecular insights using RNAi.

442. Keystone Symposia (Autophagy in Health and Disease). Monterey, CA. Apr 2007. Hou YC, Chittaranjan S, Marra MA, Gorski SM. Common regulators of apoptosis and autophagy – an analysis of known cell death genes in starvation-induced autophagy.

443. 2007 IEEE International Symposium on Biomedical Imaging: From Nano to Macro. Washington, DC. Apr 2007. Furhmann DR, Corbett R, Birol I, Schein J, Qu Y, Mathewson C, Lee D, Johnson L, Saeedi P, Krzywinski M, Field M, Marra M. Large-insert clones as markers in DNA fingerpringing gels.

444. The 8th Annual AGBT Conference. Marco Island, FL. Feb 2007. Delaney AD, Hirst M, Schroth G, Zeng T, Zhao Y, Moore R, Holt RA, Jones S, Marra MA. First Steps towards the use of High Throughput Tag Sequencing: SAGE Libraries using Solexa Sequencing. **(Platform presentation)**

445. The 8th Annual AGBT Conference. Marco Island, FL. Feb 2007. Delaney AD, Baross A,Li HI, Nayar T, Flibotte S, Chan SY, Asano J, Ally A, Birch P, Brown-John M, Cao M, Fernandes N, Go A, Kennedy G, Langlois S, Eydoux P, Friedman JM, Marra MA. Assessment of Algorithms for Detection of Genomic Copy Number Variation in Oligonucleotide Microarray Data. **(**

446. The 8th Annual AGBT Conference. Marco Island, FL. Feb 2007. Hirst M, Zeng T, Tse K, Delaney A, Pang J, Wang J, Taylor G, Deng A, Moksa M, Fichter K, Mah D, Go A, Morin RD, Baross A, Wagner L, Jang W, Shenmen C, Temple G, Gerhard DS , Holt R, Jones S, Marra MA. Directed cloning of human and mouse genes by RT-PCR reveals a large collection of alternatively spliced transcripts.

447. The 8th Annual AGBT Conference. Marco Island, FL. Feb 2007. Schein J, Krzywinski M, Birol I, Chiu R, Field M, Wong K, Johnson L, Lee D, Mathewson C, Ali J, Baross A, Bosdet I, Chan S, Corbett R, Delaney A, Li I, Pugh T, Warren R, Yang G, Johnson N, Relander T, Holt R, Jones S, Gascoyne R, Horsman D, Connors J, Marra M. Multi-Patient High-Resolution Genome Rearrangement Discovery in Follicular Lymphoma.

448. The 8th Annual AGBT Conference. Marco Island, FL. Feb 2007. Pugh TJ, Farnoud N, Li HI, Farinha P, Gascoyne RD, Marra MA. Copy number biases induced by whole genome amplification are related to genome location and GC content.

449. The 8th Annual AGBT Conference. Marco Island, FL. Feb 2007. Chun HJE, Ralph SG, Cooper D, Kirkpatrick R, Palmquist D, Wynhoven B, Kolosova N, Oddy C, Jancsik S, Douglas CJ, Yang G, Holt, RA, Jones SJM, Marra MA, Ritland K, Bohlmann J. The poplar transcriptome: Analysis of 4,664 sequence-verified full-length cDNAs.

450. The 8th Annual AGBT Conference. Marco Island, FL. Feb 2007. Petrescu A, Delaney A, Marra M. An assessment of the utility of LongSAGE in detecting Cis-encoded sense-antisense transcription.

451. The 8th Annual AGBT Conference. Marco Island, FL. Feb 2007. Griffith M, Tang M, Chan S, Asano J, Griffith O, Zeng T, Flibotte S, Baross A, Hirst M, Tai I, Marra M. ALEXA – A computational platform for alternative expression analysis.

452. Lab Automation 2007. Palm Springs, CA. Jan 2007. Coope R, Guggenheimer K, Eugster P, Mathewson C, Schein J, Marra M. Automation for Agarose Based Clone Fingerprinting.

453. University of British Columbia, Medical Genetics Research Day. Vancouver, BC. Dec 2006. Griffith M, Tang M, Chan S, Asano J, Baross A, Tai I, Marra M. Identification Of Differentially Expressed Exons Associated With Chemotherapy Resistance In Colon Cancer Cell Lines.

454. Stem Cell Network 2006 Annual General Meeting. Ottawa, ON. Nov 2006. Hirst M, Delaney A, Rogers SA, Schnerch A, O'Connor MD, Zeng T, Moksa M, Fichter K, Mah D, Go A, Zhao Y, Khattra J, Prabhu A-L, Pandoh P, McDonald H, Dhalla N, Ma K, Lee S, Ally A, Chahal N, Siddiqui A, Holt R, Jones S, Gerhard DS, Thomson JA, Eaves CJ, Marra MA. A novel transcript identified by LongSAGE is a specific transcriptional marker of pluripotency in human embryonic stem cells.

455. BC Cancer Annual Cancer Conference. Vancouver, BC. Nov 2006. Khattra J, Morin R, Schnerch A, O'Connor M, Hirst M, Eaves C, Marra M. Characterization of novel protein-coding genes enriched in human ES cells.

456. BC Cancer Annual Cancer Conference. Vancouver, BC. Nov 2006. Qadir MA, Le D, Kwok B, To KH, Oomah S, McConechy M, Marra MA, Gorski SM. siRNA Mediated Chemosensitization of Breast Cancer Cells by Inhibiting Autophagy.

457. BC Cancer Annual Cancer Conference. Vancouver, BC. Nov 2006. Petrescu A., Delaney A., Marra M. An assessment of the utility of LongSAGE in detecting cis-encoded sense-antisense transcription.

458. BC Cancer Annual Cancer Conference. Vancouver, BC. Nov 2006. Hirst M, Delaney A, Rogers SA, Schnerch A, O'Connor MD, Zeng T, Moksa M, Fichter K, Mah D, Go A, Zhao Y, Khattra J, Prabhu A-L, Pandoh P, McDonald H, Dhalla N, Ma K, Lee S, Ally A, Chahal N, Siddiqui A, Holt R, Jones S, Gerhard DS, Thomson JA, Eaves CJ, Marra MA. A novel transcript identified by LongSAGE is a specific transcriptional marker of pluripotency in human embryonic stem cells.

459. BC Cancer Annual Cancer Conference. Vancouver, BC. Nov 2006. Chittaranjan S, Sandhu H, Wilton J, Ling I, Kuzyk M, Morin G, Marra M, Gorski S. Characterization of a novel autophagy-related gene in *Drosophila*.

460. BC Cancer Annual Cancer Conference. Vancouver, BC. Nov 2006. Griffith M, Tang M, Chan S, Asano J, Baross A, Tai I, Marra M. Identification of differentially expressed exons associated with chemotherapy resistance in colon cancer cell lines.

461. BC Cancer Annual Cancer Conference. Vancouver, BC. Nov 2006. Baross A, Delaney AD, Li HI, Nayar T, Flibotte S, Chan SY, Asano J, Ally A, Birch P, Brown-John M, Cao M, Fernandes N, Go A, Kennedy G, Langlois S, Eydoux P, Friedman JM, Marra MA. Assessment of Algorithms for Detection of Genomic Copy Number Variation in Oligonucleotide Microarray Data.

462. Cancer Genomics and Emerging Technologies 2006 Conference. Cambridge, MA. Oct 2006. Marra MA, Krzywinski M, Chiu R, Field M, Birol I, D'Souza B, Bosdet I, Mathewson C, Lee D, Baross A, Pugh T, Gascoyne R, Horsman D, Holt R, Relander T, Johnson N, Schein J, Connors JM. Mapping genome rearrangements in follicular lymphoma.

463. Cancer Genomics and Emerging Technologies 2006 Conference. Cambridge, MA. Oct 2006. Delaney AD, Li HI, Nayar T, Baross Á, Chan SY, Asano J, Ally A, Birch P, Langlois S, Eydoux P, Friedman JM, Marra MA Searching for Copy Number Polymorphism using Affymetrix GeneChip® Mapping Arrays. **(Platform presentation)**

464. Cancer Genomics and Emerging Technologies 2006 Conference. Cambridge, MA. Oct 2006. Baross A, Delaney AD, Li HI, Nayar T, Flibotte S, Chan SY, Asano J, Ally A, Birch P, Brown-John M, Cao M, Fernandes N, Go A, Kennedy G, Langlois S, Eydoux P, Friedman JM, Marra MA. Assessment of Algorithms for Detection of Genomic Copy Number Variation in Oligonucleotide Microarray Data.

465. Cancer Genomics and Emerging Technologies 2006 Conference. Cambridge, MA. Oct 2006. Pugh TJ, Li HI, Farinha P, Gascoyne RD, Marra MA. Genome Structural Fidelity of Whole Genome Amplification & Tissue Archival.

466. ASHG 56th Annual Meeting. New Orleans, LO. Oct 2006. Delaney AD, Li I, Nayar T, Baross A, Ally A, Asano J, Bailey D, Birch P, Brown-John M, Cao M, Chan S, Eydoux P, Fernandes N, Flibotte S, Go A, Holt RA, Kennedy G, Langlois S, Friedman JM, Marra MA. Gene copy number variation and the limits of detection using Affymetrix Genechip® Human Mapping 100k and 500k Arrays.

467. ASHG 56th Annual Meeting. New Orleans, LO. Oct 2006. Zahir, Baross A, Delaney AD, Eydoux P, Firth HV, Gibson WT, Langlois S, Martin H, Marra M, Thuresson A-C, Vermeesch J, Willat J, Yong SL, Friedman JM. Genotype-phenotype correlations for sub-microscopic copy number variants.

468. 4th Annual Meeting of the International Society for Stem Cell Research. Toronto, ON. June 2006. Hirst M, Delaney A, Rogers SA, Schnerch A, Persaud DR, Zeng T, Zhao Y, Morin R, Siddiqui A, Thomson JA, Eaves CJ, Marra MA. Characterizing the Expressed Genome of Human Embryonic Stem Cells through Deep LongSAGE Profiling Coupled with High-Throughput Race Rescue of Novel Transcripts.

469. 4th Annual Meeting of the International Society for Stem Cell Research. Toronto, ON. June 2006. Raouf A, Zhao Y, To K, Stingl J, Delaney A, Schnerch A, Asano J, Jones S, Emerman J, Marra M, Eaves C. Molecular Characterization of Highly Purified Human Mammary Epithelial Progenitor Subsets.

470. 42nd Annual Meeting of the American Society of Clinical Oncology. Atlanta, GA. June 2006. Bebb G, Pugh T, Sutcliffe M, Barclay L, Fee J, O’Connor R, Vielkind J, Ho C, Murray N, Laskin, J, Marra M. Previously Documented Mutations in the Epidermal Growth Factor Receptor (EGFR) Gene in a Non-Small Cell Lung Cancer (NSCLC) Population Treated with Gefitinib Are Not Associated with Response. (***J Clin Oncol. 2006 Jun 20;24(18):404S 7163 Par 1 Suppl. S)***

471. 8th Annual Meeting of the International Behavioural and Neural Genetics Society (IBANGS). May 2006. Vancouver, BC. Xie Y-Y, Bohacec S, Lee LLC, Delaney A, Khattra J, Holt R, Siddiqui A, Jones SJM, Marra MA, Simpson EM. Knowing your behavioural model: LCM-LongSAGE-Lite established for the developing mouse brain.

472. Beyond HapMap 3rd Annual International HapMap Project Community Analysis Meeting. Cambridge, MA. May 2006. Belmont J, Wheeler D, Song X-Z, Nazareth LV, Worley K, Fu Q, Weinstock G, Gibbs R, and the Bovine Genome Sequencing Consortium. A Dense Bovine Snp Map: Snp Discovery and Implications of Breed Divergence.

473. “Finishing in the Future” Meeting. Santa Fe, NM. May 2006. Ali J, Palmquist D, Wynhoven B, Huang P, Kirkpatrick R, Liu J, Chun E, Liao N, Siddiqui A, Holt R, Marra M, Jones S. A high throughput bovine full length cDNA sequencing pipeline.

474. “Finishing in the Future” Meeting. Santa Fe, NM. May 2006. Palmquist D, Huang P, Wynhoven B, Chun E, Kirkpatrick R, Ali J, Sidiqqui A, Holt R, Marra M, Jones S. Ensuring Transparent and Consistent High Quality in cDNA Finishing.

475. The Biology of Genomes Meeting. Cold Spring Harbor Laboratory, NY. May 2006. Schein J, Krzywinski M, Barber S, Brown-John M, Chan S, Chand S, Chiu R, Corbett R, D’Souza B, Featherstone R, Field M, Griffith M, Johnson L, Li I, Langlois N, Marcadier J, Mayo M, O’Connor K, Piche R, Pugh T, Del Rio L, Roger J, Tsai M, Wong D, Wye N, Yang G, Zeng T, Baross A, Flibotte S, Hirst M, Lee D, Mathewson C, Bosdet I, Birol I, Siddiqui A, Jones S, Holt R, Horsman D, Gascoyne R, Connors J, Marra M. Physical Map of a Follicular Lymphoma Genome: Identification and Sequencing of Genomic Rearrangements.

476. The Biology of Genomes Meeting. Cold Spring Harbor Laboratory, NY. May 2006. Hirst M, Delaney A, Rogers SA, Schnerch A, Persaud DR, O’Connor M, Zeng T, Moksa M, Fitcher K, Mah D, Ma K, Menzies S, Khattra J, Morin R, Siddiqui A, Holt R, Jones S, Thomson JA, Eaves CJ, Marra MA.

Characterizing the Expressed Genome of Human Embryonic Stem Cells Through Deep LongSAGE Profiling Coupled With High-Throughput Race Rescue of Novel Transcripts.

477. The Biology of Genomes Meeting. Cold Spring Harbor Laboratory, NY. May 2006. Baross A, Delaney AD, Ally A, Arbour L, Asano J, Bailey D, Birch P, Brown-John M, Cao M, Chan S, Charest DL, Eydoux P, Farnoud N, Fernandes N, Flibotte S, Go A, Gibson WT, Holt RA, Jones S, Kennedy G, Krzywinski M, Langlois S, Li HI, McGillivray BC, Nayar T, Schein J, Schnerch A, Siddiqui A, Yong S-L, Friedman JM, Marra MA. Genome Copy Number Analysis of Idiopathic Mental Retardation Using High-Density Oligonucleotide Microarrays.

478. The Biology of Genomes Meeting. Cold Spring Harbor Laboratory, NY. May 2006. Delaney AD, Li I, Nayar T, Baross A, Bailey D, Birch P, Brown-John M, Cao M, Chan S, Eydoux P, Fernandes N, Flibotte S, Go A, Holt RA, Jones S, Kennedy G, Krzywinski, M, Langlois S, Schein J, Siddiqui A, Friedman JM, Marra MA. Gene Copy Number Variants, the Limits of Detection Using Affymetrix SNP Genotype Chips.

479. The Biology of Genomes Meeting. Cold Spring Harbor Laboratory, NY. May 2006. Griffith M, Flibotte S, Zheng T, Hirst M, Marra M. Characterization of Alternative Splicing Events in the Druggable Genome Using Splicing Microarrays.

480. The Biology of Genomes Meeting. Cold Spring Harbor Laboratory. NY. May 2006. Gibbs R, Weinstock G on behalf on the Bovine Genome Sequencing Consortium. The Bovine Genome Project.

481. Canadian Breast Cancer Research Alliance Meeting. Montreal, QC, May 2006. Raouf A, Zhao Y, To K, Stingl J, Delaney A, Schnerch A, Asano J, Jones S, Emerman J, Marra M, Eaves C. Characterization Of Primitive Human Mammary Epithelial Cells.

482. Genomics Forum and Research Exchange 2006. Vancouver, BC. Apr 2006. Hirst M, Delaney A, Rogers SA, Schnerch A, Persaud DR, O'Connor M, Zeng T, Moksa M, Fitcher K, Mah D, Ma K, Lee S, Menzies S, Khattra J, Morin R, Siddiqui A, Holt R, Jones S, Thomson JA, Eaves CL, Marra MA. Characterizing the Expressed Genome of Human Embryonic Stem Cells Through Deep LongSAGE Profiling Coupled with High-Throughput Race Rescue of Novel Transcripts.

483. Genomics Forum and Research Exchange 2006. Vancouver, BC. Apr 2006. Krzywinski M, Ali J, Barber S, Brown-John M, Chand S, Chiu R, D'Souza B, Featherstone R, Field M, Johnson L, Langlois N, Marcadier J, Mayo M, O'Connor K, Piche R, Del Rio L, Roger J, Tsai M, Wong D, Wong K, Zeng T, Hirst M, Lee D, Mathewson C, Yang G, Wye N, Bosdet I, Birol I, Siddiqui A, Schein J, Holt R, Jones S, Horsman D, Gascoyne R, Connors J, Marra. A Sequence-Ready Physical Map of a Follicular Lymphoma Genome.

484. Genomics Forum and Research Exchange 2006. Vancouver, BC. Apr 2006. Morin RD, Chang E, Petrescu A, Liao N, Griffith M, Kirkpatrick R, Butterfield YS, Young AC, Stott J, Barber S, Babakaiff R, Dickson MC, Matsuo C, Wong D, Yang GS, Smailus DE, Wetherby KD, Kwong PN, Grimwood J, Brinkley III CP, Brown-John M, Reddix-Dugue N, Mayo M, Schmutz J, Beland J, Park M, Gibson S, Olson T, Bouffard GG, Tsai M, Featherstone R, Chand S, Siddiqui AS, Jang M, Lee E, Klein SL, Blakesley RW, Zeeberg BR, Sudarshan N, Weinstein JN, Pennacchio CP, Myers RM, Green ER, Wagner L, Gerhard DS, Marra MA, Jones SJM, Holt RA. Sequencing and analysis of 10,967 full-length cDNA clones from *Xenopus laevis* and *Xenopus tropicalis*.

485. Genomics Forum and Research Exchange 2006. Vancouver, BC. Apr 2006. Pugh T, Bebb G, Barclay L, Sutcliffe M, Fee J, Salski C, O'Connor R, Ho C, Murray N, Melosky B, English J, Vielkind J, Horsman D, Laskin J, Marra M. EGFR Mutations in Archival Specimens from Gefitinib-Treated Lung Cancer Patients.

486. Genomics Forum and Research Exchange 2006. Vancouver, BC. Apr 2006.Ali J, Wynhoven B, Palmquist D, Chun H-J E, Liu J, Kirkpatrick R, Stott J, Barber S, Yang G, Babakaiff R, Beland J, Chand

S, Del Rio L, Dreolini L, Featherstone R, Gibson S, Matsuo C, Mayo M, Roger J, Tsai M, Wong D, Moore SS, Guan LL, Lobo S, Meng Y, Taniguchi M, Wang Z, Schreiber K, Prange K, Shapiro N, Shenmen C, Wagner L, Alexander L, MacNeil M, Brownstein MJ, Siddiqui A, Holt R, Jones S, Marra M. An Efficient Strategy for Full Length cDNA Sequence Finishing in *Bos Taurus.*

487. Genomics Forum and Research Exchange 2006. Vancouver, BC. Apr 2006. Li I, Delaney A, Baross A, Nayar T, Schnerch A, Friedman J, Marra M. Hemizygous Deletions Identified by Affymetrix GeneChip™ SNP Genotype Arrays.

488. Genomics Forum and Research Exchange 2006. Vancouver, BC. Apr 2006. Farnoud N, Baross A, Chan S, Flibotte S, Taylor MD, Friedman JM, Marra M. A novel bioinformatics approach for detection of chromosome copy number changes using oligonucleotide level intensity distribution.

489. Genomics Forum and Research Exchange 2006. Vancouver, BC. Apr 2006. Chun EHJ, Kirkpatrick R, Liu J, Palmquist D, Wynhoven B, Ali J, Shenmen C, Wagner L, Howe K, Searle S, Siddiqui A, Holt R, Marra M, Jones S. An Effective Strategy of Full-Length Clone Selection in *Bos taurus.*

490. Genomics Forum and Research Exchange 2006. Vancouver, BC. Apr 2006. Bainbridge MN, Warren RL, Hirst M, Romanuik T, Zeng T, Go A, Delaney A, Griffith M, Hickenbotham M, Magrini V, Mardis ER, Sadar MD, Siddiqui AS, Marra MA, Jones SJM. Analysis of the prostate cancer cell line LNCaP transcriptome using a sequencing-by-synthesis approach.

491. Genomics Forum and Research Exchange 2006. Vancouver, BC. Apr 2006. Wang G, Jones S, Marra, M, Sadar MD. Genes targeted by both the androgen and pka signalling pathways that are dependent upon androgen receptor.

492. 3rd Canadian Developmental Biology Conference. Mont-Tremblant, QC. Apr 2006. Hoodless PA, Vrljicak P, Hou J, Cullum R, McKnight KD, Montpetit R, Rupert JL, Wu MK, Charters A, Siddiqui A, Helgason CD, Simpson EM, Jones S, Marra M. The Mouse Atlas of Gene Expression.

493. The 7th Annual AGBT Conference. Marco Island, FL. Feb 2006. Marra M, Krzywinski M, Brown-John M, Chand S, Chiu R, D’Souza B, Featherstone R, Field M, Johnson L, Langlois N, Marcadier J, Mayo M, O’Connor K, Piche R, Del Rio L, Roger J, Tsai M, Wang G, Wong D, Lee D, Mathewson C, Wye N, Bosdet I, Birol I, Siddiqui A, Jones S, Holt R, Horsman D, Gascoyne R, Connors J, Schein J. A Physical Map of a Follicular Lymphoma Genome.

494. The 7th Annual AGBT Conference. Marco Island, FL. Feb 2006. Baross A, Delaney AD, Asano J, Bailey D, Birch P, Brown-John M, Cao M, Chan S, Charest DL, Eydoux P, Farnoud N, Fernandes N, Flibotte S, Go A, Holt RA, Jones S, Kennedy G, Krzywinski M, Langlois S, Li I, Nayar T, Schein J, Siddiqui A, Friedman JM, Marra MA. Genome Copy Number Analysis of Idiopathic Mental Retardation Using High-Density Oligonucleotide Microarrays.

495. The 7th Annual AGBT Conference. Marco Island, FL. Feb 2006. Pugh T, Farinha P, Gascoyne R, Marra M. Application of Fresh, Archival, and Whole-Genome-Amplified Materials to High-Resolution CGH Microarrays.

496. The 7th Annual AGBT Conference. Marco Island, FL. Feb 2006. Pugh T, Barclay L, Sutcliffe M, Fee J, O’Connor R, Ho C, Murray N, Melosky, B, English, J, Bebb G, Vielkind J, Laskin J, Marra M. EGFR Mutations in Archival Specimens from Gefitinib-Treated Lung Cancer Patients.

497. The 7th Annual AGBT Conference. Marco Island, FL. Feb 2006. Birol I, Krzywinski M, Brown-John M, Chand S, Chiu R, Corbett R, D’Souza B, Featherstone R, Field M, Johnson L, Langlois N, Marcadier J, Mayo M, O’Connor K, Piche R, Del Rio L, Roger J, Saeedi P, Tsai M, Yang G, Wong D, Lee D, Mathewson C, Wye N, Bosdet I, Siddiqui A, Jones S, Holt R, Horsman D, Gascoyne R, Connors J, Fuhrmann D, Liu M, Schein J, Marra M. Construction and Analysis of Physical Genomic Maps Using Double-Enzyme Digests of BAC Clones.

498. The 7th Annual AGBT Conference. Marco Island, FL. Feb 2006. Hirst M, Zeng T, Moksa M, Mah D, Fichter K, Go A, Ma K, Pang J, Delaney A, Morin R, Wang J, Chuah E, Kirkpatrick R, Smailus DE, Barber S, Baross A, Siddiqui A, Holt R, Jones SJM, Marra MA. The Mammalian Gene Collection: Closing the Gap.

499. The 7th Annual AGBT Conference. Marco Island, FL. Feb 2006. Hirst M, Delaney A, Rogers SA, Schnerch A, Persaud DR, O'Connor M, Zeng T, Moksa M, Menzies S, Baross A, Khattra J, Siddiqui A, Holt R, Jones S, Thomson JA, Eaves CJ, Marra MA. LongSAGE Transcriptome Analysis of Nine Human Embryonic Stem Cell Lines Reveals Novel Transcripts and an Over Representation of RNA Binding Proteins.

500. The 7th Annual AGBT Conference. Marco Island, FL. Feb 2006. Siddiqui A, Delaney A, Schnerch A, Griffith O, Jones S, Marra M. An Examination of Sequence Biases in Large Scale Gene Expression Profiling Data.

501. The 7th Annual AGBT Conference. Marco Island, FL. Feb 2006. Morin RD, Chang E, Petrescu A, Liao N, Griffith M, Kirkpatrick R, Butterfield YS, Young AC, Stott J, Barber S, Babakaiff R, Dickson MC, Matsuo C, Wong D, Yang GS, Smailus DE, Wetherby KD, Kwong PN, Grimwood J, Brinkley III CP, Brown-John M, Reddix-Dugue N, Mayo M, Schmutz J, Beland J, Park M, Gibson S, Olson T, Bouffard GG, Tsai M, Featherstone R, Chand S, Siddiqui AS, Jang M, Lee E, Klein SL, Blakesley RW, Zeeberg BR, Sudarshan N, Weinstein JN, Pennacchio CP, Myers RM, Green ER, Wagner L, Gerhard DS, Marra MA, Jones SJM, Holt RA. Sequencing and analysis of 10,967 full-length cDNA clones from *Xenopus laevis* and *Xenopus tropicalis*.

502. The 7th Annual AGBT Conference. Marco Island, FL. Feb 2006. Chun EHJ, Kirkpatrick R, Liu J, Palmquist D, Wynhoven B, Ali J, Shenmen C, Wagner L, Howe K, Birney E, Siddiqui A, Holt R, Marra M and Jones S. An Efficient Strategy of Full-Length Clone Selection in *Bos taurus*.

503. Pacific Symposium on Biocomputing (PSB) 2006. Maui, HI. Jan 2006. Griffith M, Flibotte S, Hirst M, Morin G, Tai I, Tang M, Marra MA. A Microarray Design for the Detection of Alternate Protein Isoforms: Application to a Model of Chemotherapy Resistance.

504. Plant and Animal Genome XIV Conference. San Diego, CA. Jan 2006. Moore SS, Guan L, Lobo S, Meng Y, Taniguchi M, Wang Z, Stott J, Ali J, Kirkpatrick K, Siddiqui A, Barber S, Babakaiff R, Beland J, Chand S, Chun HJE, Del Rio L, Dreolini L, Featherstone R, Gibson S, Liu J, Matsuo C, Mayo M, Palmquist D, Roger J, Tsai M, Wong D, Wynhoven B, Yang G, Schreiber K, Prange C, Shapiro N, Shenmen C, Wagner L, Alexander L, MacNeil M, Brownstein MJ, Holt R, Jones S, Marra M. Bovine Genome Sequencing Program: Full-length cDNA Sequencing.

505. Plant and Animal Genome XIV Conference. San Diego, CA. Jan 2006. Kirkpatrick R, Liu J, Chun E, Palmquist D, Wynhoven B, Ali J, Shenmen C, Wagner L, Howe K, Birney E, Siddiqui A, Holt R, Jones S, Marra M. An Efficient Strategy for Full Length Clone Selection in *Bos taurus*.

506. Plant and Animal Genome XIV Conference. San Diego, CA. Jan 2006. Ali J, Wynhoven B, Palmquist D, Chun HJE, Liu J, Kirkpatrick R, Stott S, Barber S, Yang G, Babakaiff R, Beland J, Chand S, Del Rio L, Dreolini L, Featherstone R, Gibson S, Matsuo C, Mayo M, Roger J, Tsai M, Wong D, Moore SS, Guan L, Lobo S, Meng Y, Taniguchi M, Wang Z, Schreiber K, Prange K, Shapiro N, Shenmen C, Wagner L, Alexander L, MacNeil M, Brownstein MJ, Siddiqui A, Holt R, Jones S, Marra M. An Efficient Strategy for Full Length cDNA Sequence Finishing in *Bos taurus*.

507. Plant and Animal Genome XIV Conference. San Diego, CA. Jan 2006. Everts-van der Wind A, Larkin DM, Green CA, Elliott JS, Olmstead CA, Chiu R, Schein JE, Marra MA, Womack JE, Lewin HA. A high-resolution whole-genome cattle-human comparative map reveals new details of mammalian chromosome evolution.

508. Plant and Animal Genome XIV Conference. San Diego, CA. Jan 2006. Larkin DM, Everts-van der Wind A, Chiu R, Schein JE, Elliott JS, Marra MA, Womack JE, Lewin HA. Integration of High-Resolution Cattle Radiation Hybrid and Fingerprint Contig Maps.

509. 47th American Society of Hematology Annual Meeting. Atlanta, GA. Dec 2005. Marra MA, Krzywinski M, Chiu R, Field M, Birol I, D'Souza B, Bosdet I, Mathewson C, Lee D, Baross A, Gascoyne RD, Horsman D, Holt R, Schein J, Connors JM. Towards the Human Cancer Genome Project: A sequence-ready physical map of a follicular lymphoma genome. ***(Blood. 2005 Nov; 106:605)***

510. 5th Annual ORFeome Meeting. Boston, MA. Nov 2005. Hirst M, Zeng T, Moksa M, Mah D, Fichter K, Go A, Ma K, Pang J, Delaney A, Morin R, Wang J, Chuah E, Kirkpatrick R, Smailus DE, Barber S, Baross A, Griffith M, Holt R, Jones SJM, Marra MA. The Mammalian Gene Collection: Closing the Gap.

511. Stem Cell Network AGM 2005. Calgary, AB. Nov 2005. Hirst M, Delaney A, Rogers SA, Schnerch A, Persaud DR, O'Connor M, Zeng T, Moksa M, Menzies S, Baross A, Khattra J, Siddiqui A, Holt R, Jones S, Thomson JA, Eaves CJ, Marra MA. LongSAGE Transcriptome Analysis of Nine Human Embryonic Stem Cell Lines Reveals Novel Transcripts and an Over Representation of RNA Binding Proteins.

512. Stem Cell Network AGM 2005. Calgary, AB. Nov 2005. Schnerch A, Delaney A, Rogers S, O'Connor M, Zhao Y, SAGE Library Production Group, Pera MF, Robins A, Thomson JA, Verfaillie CM, Marra M, Eaves C. Is a common repertoire of pluripotency genes expressed in multipotent adult progenitor cells and human embryonic stem cells?

513. Stem Cell Network AGM 2005. Calgary, AB. Nov 2005. Persaud DR, Hirst M, Schnerch A, Rogers S, O'Connor M, Eaves C, Thomson JA, Marra M. Characterization of a previously undescribed gene expressed in undifferentiated human embryonic stem cells: potential role in the mechanism that regulates their self- renewal and maintenance of the stem cell state.

514. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2005. Hou YCC, McConechy M, Marra MA, Gorski SM. A Screen for Novel Transcriptional Regulators of Ecdysone Mediated Cell Death.

515. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2005. Romanuik T, Holt R, Jones S, Marra M, Sadar M. Discovery of Genes Involved in Cross-Talk Between the Androgen and PKA Pathways in Prostate Cancer Using Long Serial Analysis of Gene Expression.

516. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2005. Persaud DR, Hirst M, Schnerch A, Rogers S, O'Connor M, Eaves C, Thomson J, Marra M. Characterization of a Previously Undescribed Gene Expressed in Undifferentiated Human Embryonic Stem Cells: Potential Role in the Mechanism that Regulates their Self- Renewal.

517. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2005. Pugh T, Barclay L, Sutcliffe M, Fee J, O'Connor R, Ho C, Murray N, Melosky B, English J, Bebb G, Laskin J, Marra M. Identification of EGFR Mutations in Archival Specimens from Nsclc Patients Treated with Gefitinib.

518. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2005. Baross A, Chan S, Go A, Li HI, Nayar T, Farnoud N, Brown-John M, Khattra J, Asano J, Schein J, Charest DL, Delaney AD, Friedman JM, Marra MA. Gene Copy Number Analysis Using High-Density Oligonucleotide Microarrays.

519. BC Cancer Annual Cancer Conference. Vancouver, BC. Nov 2005. Krzywinski M, Brown-John M, Chand S, Chiu R, D'Souza B, FeatherstoneR, Field M, Johnson L, Langlois N, Marcadier J, Mayo M, O'Connor K, Piche R, Del Rio L, Roger J, Tsai M, Wong D, Lee D, Mathewson C, Wye N, Bosdet I, Birol I, Siddiqui A, Schein A, Jones S, Horsman D, Gascoyne R, Connors J, Marra M. A sequence-ready physical map of a follicular lymphoma genome.

520. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2005. Schnerch A, Delaney A, Rogers S, O'Connor M, Zhao Y, SAGE Library Production Group, Pera MF, Robins A, Thomson JA, Verfaillie CM, Marra M, Eaves C. Is a common repertoire of pluripotency genes expressed in multipotent adult progenitor cells and human embryonic stem cells?

521. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2005. Qadir MA, To KH, Yung T, Marra MA, Gorski SM. Sensitization of Breast Cancer Cells to Chemotherapy by Inhibiting Autophagy.

522. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2005. Griffith M, Hirst M, Morin R, Flibotte S, Connors J, Marra M. Development of a Method for the Study of Alternative Splicing in Cancer.

523. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2005. Chittaranjan S, Marra M, Gorski S. The Role of Innate Immunity Signaling in *Drosophila* Salivary Gland Autophagic Cell Death.

524. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2005. Halaschek-Wiener J, Oliveira L, Madden K, Jones S, Connors J, Lee ND, Meneilly G, Marra MA, Brooks-Wilson A. Genetics of Healthy Aging: A Population-Based Study.

525. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2005. Petrescu A, Delaney A, Hoodless P, Marra M. Large-Scale High-Throughput Characterization of Gene Regulation via Antisense Transcription using SAGE.

526. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2005. Bosdet I, Marra M, Gorski S. Programmed cell death in the *Drosophila* retina – characterizing the *echinus* locus.

527. Genome Informatics Meeting, Cold Spring Harbor Laboratory, NY. Oct 2005. Moerman D, Johnsen R, Newbury R, Anastis D, Fang L, Lee D, Lin J, Wong K, McKay S, Mills C, Okada M, Sonnhammer E, Tu D, Viveiros R, Wong K, Marra M, Schnabe R, Jones S, Baillie D. An interactive database of *C. elegans* promoter::GFP expression constructs.

528. Genome Informatics Meeting, Cold Spring Harbor Laboratory, NY. Oct 2005. Warren RL, Varabei D, Platt D, Huang X, Messina D, Hillier L, Yang S-Y, Wallis J, Chinwalla A, Siddiqui AS, Schein JE, Marra MA, Jones SJM. Real-Time Contiguity Improvement of Whole-Genome Shotgun Assemblies Using Physical Maps.

529. Genome Informatics Meeting, Cold Spring Harbor Laboratory, NY. Oct 2005. Siddiqui AS, Khattra J, Delaney AD, Zhao Y, Robertson G, Bilenky M, Astell C, Asano J, Babakaiff R, Barber S, Beland J, Bohacec S, Brown-John M, 53 more authors, Marra MA. A Fine-Scale Dissection of Developing Mouse Tissues for Gene Expression Profiling.

530. 55th Annual Meeting of The American Society of Human Genetics. Salt Lake City, Utah. Oct 2005. Friedman JM. Arbour L, Armstrong L, Bailey D, Baross A, Birch P, Brown-John M, Cao M, Chan S, Charest DL, Delaney A, Eydoux P, Farnoud N, Fernandes N, Flibotte S, Gibson W, Go A, Hanson R, Holt R, Jones S, Kennedy G, Krzywinski M, Langlois, Li HI, McGillivray B, Nayar T, Rajcan-Separovic E, Schein J, Siddiqui A, Van Allen M, Yong S-L, Marra M. High-Resolution Analysis of Genomic Imbalance in Children with Mental Retardation.

531. 55th Annual Meeting of The American Society of Human Genetics. Salt Lake City, Utah. Oct 2005. Eydoux P, Yong SL, Akbarli NA, Bailey D, Baross A, Brown-John M, Cao M, Chan S, Charest DL, Delaney A, Farnoud N, Garbutt K, Go A, Kennedy G, Krzywinski M, Li HI, Langlois S, Schein J, Marra MA, Friedman J. Microdeletion 13q12: a possible new syndrome identified by whole genome SNP screening.

532. American Medical Informatics Association (AMIA) 2005 Annual Symposium. Washington, DC. Oct 2005. Lonergan K, Lam W, Marra M, MacAulay C, Follen M, Richards-Kortum R, Markey MK. Identification of Biomarkers for Cervical Pre-Cancer using SAGE.

533. Programmed Cell Death Conference, Cold Spring Harbor Laboratory, NY. Sep 2005. Hou YC, McConechy M, Marra M, Gorski SM. A Screen for Novel Transcriptional Regulator of Ecdysone Mediated Cell Death.

534. Programmed Cell Death Conference, Cold Spring Harbor Laboratory, NY. Sep 2005. McConechy M, Chittaranjan S, Hou YC, Marra M, Gorski SM. A functional genomics approach using RNAi for the discovery of novel cell death genes.

535. Programmed Cell Death Conference, Cold Spring Harbor Laboratory, NY. Sep 2005. McConechy M, Chittaranjan S, Hou YC, Marra M, Gorski SM. Functional analysis of genes associated with Drosophila salivary gland death.

536. 26th Annual David W. Smith Workshop, Iowa City, IA. Aug 2005. Friedman JM, Farnoud N, Arbour L, Armstrong L, Bailey D, Birch P, Brown-John M, Cao M, Chan S, Charest DL, Eydoux P, Fernandes N, Flibotte S, Gibson W, Go A, Kennedy G, Langlois, McGillivray B, Rajcan-Separovic Van Allen M, Yong S-L, Marra M. High-resolution analysis of genomic imbalance related to mental retardation (MR).

537. 64th Annual Meeting of the Society for Developmental Biology. San Francisco, CA. Jul-Aug 2005. Wu MK, Cullum R, Rupert JL, Siddiqui A, Delaney A, Charters A, Khattra J, Jones S, Marra M, Hoodless PA. The mouse atlas of gene expression: SAGE analysis of preimplantation stages. (***Develop Biol. 2005 Jul 15;283(2):612-612 180)***

538. 11th World Conference on Lung Cancer. Barcelona, Spain. July 2005. Bebb G, Pugh T, Ho C, Laskin J, Murray N, van Niekirk D, Sutcliffe M, Fee J, Brooks-Wilson A, Marra M. Asian ethnicity, somatic epidermal growth factor receptor (EGFR) mutations and response to gefitinib in non-small cell lung cancer patients treated in a North American setting. (***Lung Cancer**. **2005 Jul 2;49:S61)***

539. Plant Biology 2005. Seattle, WA. July 2005. Lund S, Reid K, Liao N, Kirkpatrick R, Stott J, Peng F, Schlosser J, Shukin R, Bowen P, Holt R, Jones S, Marra M, Bohlmann J. Development of an EST Database for Gene Discovery in Wine Grape.

540. DECIPHER Symposium 2005. Hinxton, England. June 2005. Friedman JM, Farnoud N, Arbour L, Armstrong L, Bailey D, Birch P, Brown-John M, Cao M, Chan S, Charest DL, Eydoux P, Fernandes N, Gibson W, Go A, Kennedy G, Langlois S, McGillivray B, Rajcan-Separovic E, Van Allen M, Yong S-L, Marra M. High-resolution analysis of genomic imbalance related to mental retardation.

541. 15th Biennial International *C. elegans* Conference. Los Angeles, CA. June 2005. Wong K, McKay SJ, Huang P, Ruzanov P, Hogan M, Pofahl N, Green R, Mills C, Baillie DL, Jones SJM, Marra MA, Moerman DG. Transcription profiling of *C. elegans* developmental stages: A comparison of different platforms.

542. 15th Biennial International *C. elegans* Conference. Los Angeles, CA. June 2005. Rankin A, Lau J, Edgley M, Stott J, Holt R, Marra M, Moerman D. Is resequencing a viable cost effective strategy for obtaining *C. elegans* mutations?

543. 15th Biennial International *C. elegans* Conference. Los Angeles, CA. June 2005. Perkins J, Wong K, Warren R, Schein J, Stott J, Holt R, Jones S, Marra M, Moerman D. A *Caenorhabditis elegans* fosmid library.

544. 15th Biennial International *C. elegans* Conference. Los Angeles, CA. June 2005. Blacque O, Perens E, Boroevich K, Inglis P, Li C, Warner A, Khattra J, Jones S, Marra M, Baillie D, Moreman D, Shaham S, Leroux M. SAGE and bioinformatics identifies novel cilia-related genes, including a new IFT gene, dyf-13.

545. 15th Biennial International *C. elegans* Conference. Los Angeles, CA. June 2005. Wong K, McKay S, Khattra J, Charest D, Asano J, Chan S, Goszczynski B, Huang P, Lorch P, McGhee J, Mills C, Tian H,

Zapf R, Zhao Y, Stott J, Holt R, Baillie DL, Jones S, Marra M, Moerman D. SAGE on specific cells and tissues during *C. elegans* embryogenesis.

546. 3rd Annual Meeting of the International Society for Stem Cell Research. San Francisco, CA. June 2005. O'Connor M, Schnerch A, Khattra J, Asano J, Chan S, SAGE Library Production Group, Thomson J, Marra M, Eaves C. Gene Expression Profiling of Undifferentiated Human Embryonic Stem Cells.

547. 3rd Annual Meeting of the International Society for Stem Cell Research. San Francisco, CA. June 2005. Raouf A, Zhao Y, Kent D, Sting J, Khattra J, Delaney A, Schnerch A, Asano J, Jones S, Marra M, Eaves C. Purification and Molecular Characterization of Primitive Human Mammary Epithelial Cells.

548. 34th Annual Meeting of the American Aging Association. Oakland, CA, June 2005. Halaschek-Wiener J, Oliveira L, Madden K, Jones S, Connors J, Lee ND, Meneilly G, Marra MA, Brooks-Wilson A. Genetics of Healthy Aging: A Population-Based Study.

549. The 5th International Cell Death Symposium. Maynooth, Ireland. June 2005. Chittaranjan S, Marra M, Gorski S. The Role of a Novel Gene Involved in Autophagic Cell Death.

550. The Biology of Genomes. Cold Spring Harbor Laboratory, NY, May 2005. Hansen N, Park M, Portnoy M, Idol J, Maduro V, Lee-Lin S-Q, Hu P, Schein J, Marra M, Bouffard G, Green ED, NISC Comparative Sequencing Program. Evolution of a Targeted Comparative Mapping and Sequencing Pipeline.

551. The Biology of Genomes. Cold Spring Harbor Laboratory, NY, May 2005. Krzywinski M, Bosdet I, Mathewson C, Chiu R, Field M, Lee D, Saeedi P, Volik S, Wye N, Yang G, Siddiqui A, Holt R, Jones S, Collins C, Gascoyne R, Schein J, Marra M. Fingerprint Profiling: Whole-Genome Balanced Aberration Discovery in Cancer using Restriction Digest BAC Fingerprints.

552. The Biology of Genomes. Cold Spring Harbor Laboratory, NY, May 2005. Hirst M, Zeng T, Moksa M, Mah D, Fichter K, Pang J, Delaney A, Morin R, Wang J, Chuah E, Kirkpatrick R, Smailus DE, Stott J, Baross A, Griffith M, Holt R, Jones SJM, Marra MA. The Mammalian Gene Collection: Closing the Gap.

553. The Biology of Genomes. Cold Spring Harbor Laboratory, NY, May 2005. Holt RA, Wilson GM, Flibotte S, Missirlis PI, Krzywinski M, Marra MA, Jones S, Clark AG. Identification by Full Coverage BAC Array CGH of DNA Segments Gained in the Human Lineage Since Divergence from the Human/Chimp Common Ancestor.

554. The Biology of Genomes. Cold Spring Harbor Laboratory, NY, May 2005. Delaney A, Siddiqui A, Khattra J, Varhol R, Leung D, Marra M. Progress in SAGE Bioinformatics.

555. The Biology of Genomes. Cold Spring Harbor Laboratory, NY, May 2005. Schnerch A, Khattra J, Asano J, Chan S, SAGE Library production Group, Thomson J, Eaves C, Marra M. Global Transcriptome Analysis of Undifferentiated Human Embryonic Stem Cells.

556. The Biology of Genomes. Cold Spring Harbor Laboratory, NY, May 2005. Farnoud N, Arbour L, Armstrong L, Bailey D, Birch P, Brown-John M, Cao M, Chan S, Charest DL, Eydoux P, Fernandes N, Gibson N, Go A, Kennedy G, Langlois S, McGillivray B, Rajcan-Separovic E, Van Allen M, Yong S-L, Marra M, Friedman JM. High-Resolution Analysis of Genomic Imbalance Related to Mental Retardation (MR).

557. The Eight Canadian Drosophila Research Conference (CanFly 2005). Simon Fraser University. Burnaby, BC. May 2005. Hou YC, McConechy M, Marra M, Gorski SM. Characterization of a Novel Transcriptional Regulator of Autophagic Programmed Cell Death.

558. The Eight Canadian Drosophila Research Conference (CanFly 2005). Simon Fraser University. Bunaby, BC. May 2005. **C**hittaranjan S, Sandhu H, Wilton J, Marra M, Gorski S. Characterization of a novel autophagy or autophagic cell death related gene in Drosophila.

559. Gordon Research Conference on Autophagy in Stress, Development and Disease. Il Ciocco, Barga, Italy. Apr 2005. Qadir MA, To KH, Marra MA, Gorski SM. Quantifying Autophagy in Complex Systems.

560. Gordon Research Conference on Autophagy in Stress, Development and Disease. Il Ciocco, Barga, Italy. Apr 2005. Chittaranjan S, Sandhu H, Wilton J, Marra M, Gorski S. Characterization of a novel autophagy-related gene in Drosophila.

561. Genomics Forum, Research Exchange 2005. Vancouver, BC. Apr 2005. Krzywinski M, Bosdet I, Mathewson I, Chiu R, Field M, Lee D, Saeedi P, Volik S, Wye N, Yang G, Siddiqui A, Holt R, Jones S, Gascoyne R, Collins C, Schein J, Marra M. Fingerprint Profiling: Detecting Balanced Rearrangements in Tumor Genomes.

562. Genomics Forum, Research Exchange 2005. Vancouver, BC. Apr 2005. Butterfield YS, Griffith M, Griffith O, Guin R, Kirkpatrick R, Liao N, Liu J, Palmquist D, Petrescu AS, Stott JM, Yang GS, Barber SA, Brown-John M, Chand SS, Mayo MR, Olson T, Smailus DE, Holt RA, Siddiqui AS, Jones S, Marra M. Full Length cDNA Sequencing Bioinformatics Pipeline.

563. Genomics Forum, Research Exchange 2005. Vancouver, BC. Apr 2005. Mathewson C, Lee D, Bosdet I, Smailus D, Krzywinski M, Brown-John M, Chand S, Chiu R, Del Rio L, Featherstone R, Field M, Johnson L, Langlois N, Marcadier J, O’Connor K, Roger J, Gascoyne R, Horsman D, Osoegawa K, de Jong PJ, Pinkel D, Albertson D, Holt R, Schein J, Marra M. Whole Genome High Throughput Methods for Detection of Chromosomal Reaarrangements.

564. Genomics Forum, Research Exchange 2005. Vancouver, BC. Apr 2005. Morin RD, Wang J, Pang J, Hirst M, Chuah E, Butterfield Y, Delaney A, Griffith M, Zeng T, Moksa M, Mah D, Fichter K, Kirkpatrick R, Smailus DE, Stott J, Baross A, Holt R, Jones SJM, Marra MA. Completing the Mammalian Genome Collection: An Automated Sequencing and Validation Pipeline.

565. Genomics Forum, Research Exchange 2005. Vancouver, BC. Apr 2005. Pleasance ED. Gorski SM, Marra M, Jones SJM. SAGE Dataset Analysis of Programmed Cell Death in *Drosophila melanogaster* and Cancer.

566. Genomics Forum, Research Exchange 2005. Vancouver, BC. Apr 2005. Ruzanov P, MacAulay C, Lonergan K, Lam S, Lam W, Marra M, Jones S. Deriving the Transformation Events in Tumorigenesis Using Data from Serial Analysis of Gene Expression.

567. Genomics Forum, Research Exchange 2005. Vancouver, BC. Apr 2005. Taylor GA, Warren RL, D’Souza CA, Barber S, Stott JM, Smailus D, Yang G, Schein JE, Siddiqui AS, Holt R, Jones SJM, Marra MA, Kronstad JW. Genomics of the Fungal Pathogen *Cryptococcus neoformans* Serotype B: WGS Assembly, Finishing and Large-Scale Comparative Genomics Studies.

568. Genomics Forum, Research Exchange 2005. Vancouver, BC. Apr 2005. Varhol R, Robertson N, Oveisi-Fordorei M, Fjell C, Leung D, Siddiqui A, Marra M, Jones S. DiscoverySpace: A Tool for Gene Expression Analysis and Biological Discovery.

569. Genomics Forum, Research Exchange 2005. Vancouver, BC. Apr 2005. Wong K, McKay Steven Jones, Baillie DL, Jones SJM, Marra MA, Mills C, Huang P, Ruzanov P, Moerman DG. Transcription Profiling of *C. elegans* Developmental Stages Using Serial Analysis of Gene Expression and Microarrays.

570. Genomics Forum, Research Exchange 2005. Vancouver, BC. Apr 2005. Balasundaram M, Stott JM, Barber SA, Yang GS, Smailus D, Babakaiff R, Beland J, Del Rio L, Featherstone R, Gibson S, Matsuo C, Mayo M, Tsai M, Wong D, Marra MA, Holt RA. Quality Management System: A Practical Application to the High Throughput Sequencing Platform.

571. Genomics Forum, Research Exchange 2005. Vancouver, BC. Apr 2005. Zeng T, Hirst M, Baross A, Griffith M, Moksa M, Mah D, Fichter K, Pang J, Delaney A, Morin R, Wang J, Chuah E, Kirkpatrick R,

Smailus DE, Stott J, Holt R, Butterfield YSN, Jones SJM, Marra MA. The Mammalian Gene Collection: Closing the Gap.

572. 35th International Congress of Physiological Sciences. San Diego, CA. Mar-Apr 2005. Rupert JL, Wu M, Cullum R, Charters A, Marra M, Hoodless PA. Serial analysis of gene expression (SAGE) in the developing mouse lung: Perinatal lung transcriptomes.

573. AGBT/AMS Conference. Marco Island, FL. Feb 2005. Holt RA , Wilson GM, Missirlis P, Marra MA, Jones S, Clark AG, Flibotte S. A Full Coverage BAC Array CGH Screen for DNA Copy Number Differences Between Human and Chimp.

574. AGBT/AMS Conference. Marco Island, FL. Feb 2005. Schein J, Bosdet I, Lee D, Astakhov V, Brown-John M, Chand S, Chiu R, Cloutier A, Del Rio L, Featherstone R, Field M, Johnson L, Krzywinski M, Marcadier J, Mason A, Matsuo C, Mayo M, Moran J, O’Connor K, Olson T, Prabhu A, Roger J, Saeedi P, Shin H, Tsai M, Varabei D, Wong D, Wye N, Fuhrmann D, Siddiqui A, Jones S, Marra M. Advances in Applications of Restriction Digest Fingerprinting to Physical Mapping and Whole-Genome Analysis.

575. AGBT/AMS Conference. Marco Island, FL. Feb 2005. Siddiqui AS, Delaney A, Khattra J, Hirst M, Rupert J, Astell C, Asano J, Bohacec S, Chan S, Cullum R, Hirst M, Hoffman B, Kuo B, Landry A, Leung D, Lee L, Moksa M, Ruiz de Alagara T, Teague K, Varhol R, Wu M, Xie YX, Zeng T, Zhang I, Jones S, Simpson EM, Helgason CD, Hoodless P, Marra M. The Mouse Atlas Project: A Study of Gene Expression in Mouse Development.

576. AGBT/AMS Conference. Marco Island, FL. Feb 2005. Krzywinski M, Bosdet I, Mathewson C, Chiu R, Field M, Lee D, Saeedi R, Volik S, Wye N, Yang G, Siddiqui A, Holt R, Jones S, Collins C, Gascoyne R, Schein J, Marra M. Application of Restriction Digest BAC Fingerprints to Whole-Genome Chromosomal Aberration Profiling in Cancer.

577. AGBT/AMS Conference. Marco Island, FL. Feb 2005. Hirst M, Baross A, Zeng T, Griffith M, Moksa M, Mah D, Pang J, Delaney A, Morin R, Wang J, Chuah E, Kirkpatrick R, Smailus DE, Stott J, Holt R, Jones SJM, Marra MA. The Mammalian Gene Collection: Closing the Gap.

578. AGBT/AMS Conference. Marco Island, FL. Feb 2005. Khattra J, Zhao Y, McDonald H, Asano J, Pandoh P, Girn N, Ma K, Prabhu A, Lee S, Rogers S, Charest D, Delaney A, Jones S, Marra M. Advances in high-throughput transcriptome profiling: SAGE platform at the BC Cancer Research Centre.

579. AGBT/AMS Conference. Marco Island, FL. Feb 2005. Delaney A, Siddiqui A, Rogers S, Khattra J, Marra M. Advances in SAGE Bioinformatics.

580. AGBT/AMS Conference. Marco Island, FL. Feb 2005. Yang GS, Stott JM, Smailus D, Barber SA, Balasundaram M, Marra MA, Holt RA. High throughput sequencing: A failure mode analysis.

581. Keystone Symposia. Molecular Regulation of Stem Cells. Banff, AB. Feb 2005. Zhao Y, Raouf A, Delaney A, Khattra A, Jones S, Marra M, Eaves C. Transcriptome profiling of normal adult human bone marrow Lin^- $CD34^+$ cells using a novel PCR-SAGE technique.

582. BC Cancer Agency Annual Cancer Conference 2004. Vancouver, BC. Nov 2004. Siddiqui AS, Delaney A, Khattra J, Hirst M, Rupert J, Astell C, Asano J, Bohacec S, Chan S, Cullum R, Hoffman B, Kuo B, Landy A, Leung D, Lee L, Moksa M, Ruiz de Alagara T, Teague K, Varhol R, Wu M, Xie R, Zeng T, Zhang I, Jones S, Simpson EM, Helgason C, Hoodless P, Marra M. Uncovering transcriptional complexity in the Mouse Atlas Project: A Study of Gene Expression in Mouse Development.

583. BC Cancer Agency Annual Cancer Conference 2004. Vancouver, BC. Nov 2004. Krzywinski M, Volik S, Bosdet I, Brebner J, Mathewson C, Wye N, Brown-John M, Chiu R, Cloutier A, Featherstone R, Lee D, Marcadier J, Masson A, Matsuo C, Moran J, O’Connor K, Olson T, Del Rio L, Tsai M, Wong D, Siddiqui A, Schein J, Jones S, Collins C, Marra M. High resolution and rapid profiling of chromosomal aberrations in cancer genomes using restriction digest fingerprinting.

584. BC Cancer Agency Annual Cancer Conference 2004. Vancouver, BC. Nov 2004. Barber SA, Stott JM, Yang GS, Tsai M, Wong D, Marra MA, Tai I, Holt RA. Exon Sequencing at the Genome Sciences Centre Sequencing Group: PTEN Mutation in Cowden's Disease.

585. BC Cancer Agency Annual Cancer Conference 2004. Vancouver, BC. Nov 2004. Bebb W, Marra M. 180!? EGFR Mutations and TKIs in Non Small Cell Lung Cancer: Hitting the Target?

586. BC Cancer Agency Annual Cancer Conference 2004. Vancouver, BC. Nov 2004. Pleasance ED, Gorski SM, Marra MA, Jones SJM. Identification of Programmed Cell Death Genes by Analysis of Gene Expression in Drosophila Melanogaster and Human Cancer Progression.

587. BC Cancer Agency Annual Cancer Conference 2004. Vancouver, BC. Nov 2004. Qadir MA, To T, Marra M, Gorski SM. Implications of Autophagy in Cancer Treatment.

588. BC Cancer Agency Annual Cancer Conference 2004. Vancouver, BC. Nov 2004. Zeng T, Hirst M, Baross A, Griffith M, Moksa M, Mah D, Pang J, Delaney A, Morin R, Wang J, Chuah E, Kirkpatrick R, Smailus DE., Stott J, Holt R, Jones SJM, Marra MA. The Mammalian Gene Collection: Closing the Gap.

589. BC Cancer Agency Annual Cancer Conference 2004. Vancouver, BC. Nov 2004. Halaschek-Wiener J, Khattra JS, McKay S, Pouzyrev A, Stott JM., Yang GS, Holt RA, Jones SJM, Marra MA, Brooks-Wilson AR, Riddle DL. Analysis of Long-lived C. elegans daf-2 Mutants using Serial Analysis of Gene Expression.

590. BC Cancer Agency Annual Cancer Conference 2004. Vancouver, BC. Nov 2004. Khattra J, Chan S, Zhao Y, Asano J, Pandoh P, McDonald H, Girn N, Ma K, Prabhu A-l, Lee S, Rogers S, Delaney A, Charest D, Jones S, Marra M. Large Scale Transcriptome Profiling: Sage And DNA Microarray Platforms at Canada's Michael Smith Genome Sciences Centre.

591. BC Cancer Agency Annual Cancer Conference 2004. Vancouver, BC. Nov 2004. Freeman JD, Leung A, Ma K, Cagan RL, Marra MA, Gorski SM. The Drosophila Ortholog of Human Rcc1 is Required for Programmed Cell Death.

592. BC Cancer Agency Annual Cancer Conference 2004. Vancouver, BC. Nov 2004. Chittaranjan S, Wilton J, Sandhu H, Marra M, Gorski S. The Role of a Novel Gene Involved in Autophagic Cell Death.

593. BC Cancer Agency Annual Cancer Conference 2004. Vancouver, BC. Nov 2004. Siddiqui AS, Delaney A, Khattra J, Hirst M, Astell C, Marra M. Technology Development in SAGE, Choice of Anchor Enzyme, Tagging Enzyme, and Tag Length.

594. BC Cancer Agency Annual Cancer Conference 2004. Vancouver, BC. Nov 2004. Hirst M, Astell CR, Griffith M, Coughlin SM, Moksa M, Zeng T, Smailus DE, Holt RA, Jones S, Marra MA, Petric M, Krajden M, Lawrence D, Mak A, Chow R, Skowronski DM, Tweed SA, Goh SH, Brunham RC, Robinson J, Bowes V, Sojonky K, Byrne SK, Li Y, Konasa D, Booth T, Paetzel M. A Novel Avian Influenza H7n3 Strain Associated with an Avian Influenza Outbreak in British Columbia.

595. BC Cancer Agency Annual Cancer Conference 2004. Vancouver, BC. Nov 2004. Bosdet I, Marra MA, Gorski SM. Programmed Cell Death in the Drosophila retina – Characterizing the Echinus locus.

596. BC Cancer Agency Annual Cancer Conference 2004. Vancouver, BC. Nov 2004. McConechy M, Hou C, Marra MA, Gorski SM. A Functional Genomics Approach Using RNAi for the Discovery of Novel Cell Death Genes.

597. Genome Canada: National Genomics & Proteomics Symposium. Vancouver, BC. Nov 2004. Simpson EM, Xie YY, Bohacec S, Lee L, Khattra J, Delaney A, Jones SJM, Marra MA. Two Terrific Technologies Together: LCM-SAGE Expression Profiling of the Developing Brain.

598. Genome Canada: National Genomics & Proteomics Symposium. Vancouver, BC. Nov 2004.Smailus D, Krzywinski M, Stott J, Mathewson C, Lee D, de Jong PJ, Albertson D, Friedman J, Marra M, Schein J,

Holt R. Large-scale Production of BAC Clone Representations for Microarray Comparative Genome Hybridization.

599. 54th Annual Meeting of the American Society of Human Genetics. Toronto, ON. Oct 2004. Smailus D, Krzywinski M, Stott J, Mathewson C, Lee D, de Jong PJ, Albertson D, Friedman J, Marra M, Schein J, Holt R. Large-scale Production of BAC Clone Representations for Microarray Comparative Genome Hybridization.

600. 54th Annual Meeting of the American Society of Human Genetics. Toronto, ON. Oct 2004. Krzywinski M, Volik S, Bosdet I, Brebner J, Mathewson C, Chiu R, Lee D, Siddiqui A, Jones S, Collins C, Schein J, Marra M. Application of Restriction Digest BAC Fingerprints to Detect Chromosomal Aberrations in Cancer.

601. 18th International Mouse Genome Conference. Seattle, WA. Oct 2004. Bohacec S, Xie Y, Kuo B, Khattra J, Siddiqui A, Helgason CD, Hoodless PA, Jones S, Marra M, Simpson EM. Comprehensive SAGE Atlas of Murine Gene Expression Throughout Development.

602. Neuroscience 2004. The Society for Neuroscience 34th Annual Meeting. San Diego, CA. Oct 2004. Xie Y, Bohacec S, Lee L, Khattra J, Delaney A, Jones S, Marra M, Simpson EM. SAGE libraries constructed from murine neural tissue harvested by laser capture microdissection (LCM).

603. SAGE 2004 Conference. Boston, MA. Sep 2004. Marra M, Khattra J, Varhol R, Leung D, Simpson EM, Helgason C, Jones S, Firpo M, Pera M, Eaves C, Thomson J, Riggins G, Hoodless P, Siddiqui A, Delaney A. Quantitative and Comprehensive Gene Expression Profiles in Developing Mouse Tissues and in Human Embryonic Stem Cells Lines.

604. SAGE 2004 Conference. Boston, MA. Sep 2004. Kronstad JW, Lian TS, Simmer M, D’Souza CD, Steen BR, Zuyderduyn S, Jones S, Marra M. Iron-regulated transcription and capsule formation in the fungal pathogen *Cryptococcus neoformans*.

605. Mouse Molecular Genetics Annual Meeting. Cold Spring Harbor Laboratory, NY. Sep 2004. Hoodless PA, Rupert JL, Siddiqui A, Wu MK, Delaney A, Callum R, Lee L, Charters A, Khattra J, Jones S, Marra M. SAGE Analysis of Tissues in Mouse Development.

606. Functional Genomics – from birth to death. Göttenberg, Sweden. Aug 2004. Siddiqui A, Khattra J, Schnerch A, Delaney A, Pera M, Firpo M, Thomson J, Eaves C, Marra M. Large Scale Comparative Transcriptome Analysis of Multiple Undifferentiated Human Embryonic Stem Cell Lines.

607. West Coast Worm Meeting 2004. Santa Barbara, CA. Aug 2004. Ruzanov R, McKay SJ, Jones SJM, Marra M, Moerman DG, Baillie DL, Riddle DL. Annotation of *C. elegans* genes associated with longevity using serial analysis of gene expression (SAGE).

608. West Coast Worm Meeting 2004. Santa Barbara, CA. Aug 2004. Fox RM, Von Stetina SE, Ruff SJ, McDermott J, Brodigan T, Krause M, Wong K, McKay SJ, Johnsen R, Khattra J, Anastis D, Baillie DL, Jones SJM, Newbury R, Viveiros R, Warner A, Zhpf R, Marra M, Moerman D, Miller, III DM. A Gene Expression Profile of Body wall Muscle Cells.

609. West Coast Worm Meeting 2004. Santa Barbara, CA. Aug 2004. Johnsen R, Chen L, Mah A, McKay S, Newbury R, Tang E, Tu D, Wong K, Zhao Z, Jones S, Marra M, Moerman D, Sonnhammer E, Baillie D. Expression in *C. elegans* of Promoter::GFP Constructs For Genes with Human Orthologs.

610. West Coast Worm Meeting 2004. Santa Barbara, CA. Aug 2004. Moerman DG, McKay SJ, Johnsen R, Khattra J, Asano J, Baillie D, Chan S, Dube N, Fang L, Goszczynski B, Ha E, Halfnight E., Hollebakken R, Huang P, Hung K, Jensen V, Jones SJM, Li D, Mah A, McGhee J, Newbury R, Pouzyrev A, Riddle DL, Rogalski T, Tian H, Tu D, Tyson JR, Vatcher G, Warner A, Wong K, Zhao Z, Marra M. Gene Expression Profiling of Cells, Tissues and Development Stages of the Nematode *C. elegans.*

611. West Coast Worm Meeting 2004. Santa Barbara, CA. Aug 2004. Hwang BJ, Muller HM, Stenberg PW, McKay S, Huang P, Sternberg P, Jones SJ, Riddle DL, Pouzyrev AT, Velculescu VE, Marra MA, Moerman D, Baillie D. Experimental annotation of *C. elegans* and *C. briggsae* Genomes by the TEC-RED technique.

612. West Coast Worm Meeting 2004. Santa Barbara, CA. Aug 2004. Wong K, McKay SJ, Baillie DL, Jones SJM, Marra M, Mills C, Huang P, Ruzanov P, Moerman DG. Transcription Profiling of *C. elegans* developmental stages using Serial Analysis of Gene Expression and Microarrays.

613. 11th International Cereal Rusts and Powdery Mildews Conference. Norwich, UK. Aug 2004. Bakkeren G, Hu G, Linning R, Kamp A, Joseph C, McCallum B, Banks T, Cloutier S, Butterfield Y, Liu J, Kirkpatrick R, Stott J, Yang G, Smailus D, Jones S, Marra M, Schein J, Pei J, Westwood T. Generation of a wheat leaf rust, *Puccinia triticina*, EST database and microarray from stage-specific cDNA libraries.

614. 63rd Annual Meeting for the Society for Developmental Biology, Calgary, AB. July 2004. Mah A, Asano J, Bilenky M, Boroevich K, Chan S, Dube N, Fang L, Goszczynski B, Halfknight E, Hassel M, Hollebakken R, Huang P, Jensen V, Johnsen R, Jones S, Khattra J, Lee A, Marra M, McGhee J, McKay S, Mills C, Moerman D, Newbury R, Ouellette F, Riddle D, Robertson G, Ruzanov P, Sonnhammer E, Tian H, Tu D, Tyson J, Warner A, Wong K, Wong S, Zhao Z, Baillie DL. Multi-Approach Expression Profiling of Human Orthologous genes in *C. elegans*.

615. The First Northern Lights Summer Conference, CFBS 47th Annual Meeting. Vancouver BC. June 2004. Quayle S, Hare H, Hwang D, Jones S, Schein J, Marra M, Sadar M. A Custom Microarray for Profiling Gene Expression Changes in Advanced Prostate Cancer.

616. The First Northern Lights Summer Conference, CFBS 47th Annual Meeting. Vancouver BC. June 2004. Romanuik T, Quayle S, Hwang D, Marra M, Sadar M. Serial Analysis of Gene Expression with Androgen-Independent Prostate Cancer.

617. The First Northern Lights Summer Conference, CFBS 47th Annual Meeting. Vancouver BC. June 2004. Zhao Y, Raouf A, Khattra J, Schnerch A, Asano J, Jones S, Marra M, Eaves C. Amplification of RNA for Serial Analysis of Gene Expression (SAGE) Applications to Small Cell Samples.

618. Poplar Symposium Sponsored by the German Science Foundation, Understanding Poplar: From Genes to Functions. Göttingen, Germany. May 2004. Bohlmann J, Ralph S, Kelleher C, Yueh H, Jancsik S, Oddy C, Marra M, Schein J, Holt R, Jones S, Siddiqui A, Butterfield Y, Kirkpatrick R, Ritland C, Douglas C, Ellis B, Ritland K. Canada's contribution to the international poplar genome sequencing project and mining for insect-defense genes in the poplar genome.

619. 46th Annual Thomas L. Petty Lung Conference: Lung Cancer: Early Events, Early Interventions. Aspen, CO. May 2004. Garnis C, Coe B, Henderson L-J, Ishkanian A, Watson S, Marra M, Minna J, Lam S, MacAulay C, Lam W. Construction and Optimization of Chromosome Arm-Specific Comparative Genomic Hybridization Arrays for Identifying Genetic Alterations In Preinvasive Lung Cancers.

620. 46th Annual Thomas L. Petty Lung Conference: Lung Cancer: Early Events, Early Interventions. Aspen, CO. May 2004. MacAulay C, Lonergan K, Chi B, Zuyderduyn Z, Schein J, Tsao M, LeRiche J, Jones S, Marra M, Lam S, Lam W. Serial Analysis of Gene Expression Profiles of Developmental Stages in Non-small Cell Lung Carcinoma.

621. The Biology of Genomes. Cold Spring Harbor Laboratory, NY. May 2004. Butterfield YSN, Griffith M, Griffith O, Guin R, Kirkpatrick R, Liao N, Morin R, Chow W, Liu J, Palmquist D, Petrescu A, Warren R, Santos JR, Chan A, Stott JM, Yang GS, Barber SA, Brown-John M, Chand SS, Mayo MR, Olson T, Smailus D, Holt RA, Siddiqui A, Jones S, Marra MA. Full length cDNA sequencing and analysis pipeline.

622. The Biology of Genomes, Cold Spring Harbor Laboratory, NY. May 2004. McKay SJ, Johnsen R, Khattra J, Asano J, Baillie DL, Bilenky M, Chan S, Dube N, Fang L, Goszczynski B, Ha E, Halfnight E,

Hassel M, Hollebakken R, Huang P, Hung K, Jensen V, Jones SJM, Li D, Mah A, Marra M, Mills C, McGhee J, Newbury R, Pouzyrev A, Riddle DL, Rogalski T, Robertson G, Ruzanov P, Tian H, Tu D, Warner A, Wong K, Zhao Z, and Moerman DG. Gene Expression Profiling of Cells, Tissues and Developmental Stages of the Nematode *C. elegans.*

623. The Biology of Genomes, Cold Spring Harbor Laboratory, NY. May 2004. Krzywinski M, Volik S, Bosdet I, Brebner J, Mathewson C, Wye C, Brown-John M, Chiu R, Cloutier A, Featherstone R, Lee D, Marcadier J, Masson A , Matsuo C, Moran J, O'Connor K, Olson T, Del Rio L, Tsai M, Wong D, Siddiqui A, Schein J, Jones S, Collins C, Marra M. Application of Multiple Digest BAC Fingerprints to Detect Chromosomal Aberrations in Cancer.

624. The Biology of Genomes, Cold Spring Harbor Laboratory, NY. May 2004. Delaney A, Marra M, Gerhardt D, Simpson E, Hoodless P, Jones S, Riggins G, Helgason C. The Atlas of Gene Expression in Mouse Development.

625. The Biology of Genomes, Cold Spring Harbor Laboratory, NY. May 2004. Kirkpatrick R, Ralph S, Liu J, Palmquist D, Butterfield Y, Stott J, Babakaiff R, Barber S, Brown-John M, Chand S, Cloutier A, Featherstone R, Girn N, Lee D, Masson A, Mayo M, Moran J, Olson T, Prabhu A-L, Tsai M, Yang G, Cooper D, Gunter L, Tuskan J, Bohlmann J, Ritland K, Ellis B, Douglas C, Siddiqui A, Holt R, Jones S, Marra M. Gene Discovery in Poplar.

626. The Biology of Genomes, Cold Spring Harbor Laboratory, NY. May 2004. Schnerch A, Khattra K, Delaney A, Pera M, Firpo M, Thomson J, Eaves C, Marra M. Large scale comparative transcriptome analysis of multiple undifferentiated human embryonic stem cell lines.

627. The Biology of Genomes. Cold Spring Harbor Laboratory, NY. May 2004. Siddiqui A, Astakhova T, Bilenky M, Griffith O, Hassel M, Kennedy J, Lin K, Montgomery S, Robertson G, Sleumer M, Tsang E, Fu T, Marra M, Jones S. A unified platform for *CIS*-regulatory element detection.

628. The Biology of Genomes. Cold Spring Harbor Laboratory, NY. May 2004. Griffith M, Baross A, Butterfield YSN, Coughlin SM, Zeng T, Griffith OL, Petrescu AS, Smailus DE, Khattra J, McDonald HL, McKay SJ, Moksa M, Holt RA, Marra MA. Targeted large scale generation and analysis of Full-ORF human cDNA clones.

629. The Biology of Genomes. Cold Spring Harbor Laboratory, NY. May 2004. Varhol R, Leung D, Robertson N, Oveisi-Fordoei M, Fjell C, Zuyderduyn S, Siddiqui A, Marra M, Jones S. DISCOVERYspace: A platform for gene expression analysis.

630. Gordon Research Conferences - Mammary Gland Biology. Barga, Italy. May 2004. Raouf A, Zhao Y, Tegzes A, Stingl J, Khattra J, Marra M, Emerman J, Eaves C. Differential Expression of Breast Cancer Genes in Highly Enriched Populations of Normal Human Breast Epithelial Progenitors.

631. 104th General Meeting for the American Society of Microbiology. New Orleans, LO. May 2004. Tangen KL, Steen BR, Lian TS, Zuyderduyn S, Jones SJM, Marra M, Kronstad JW. Iron Regulated Transcription and Virulence in the Pathogenic Fungus Cryptococcus neoformans using Serial Analysis of Gene Expression (SAGE).

632. Annual Canadian Developmental Biology Symposium. Banff, AB. Apr 2004. Rupert JL, Wu MK, Cullum R, Lee L, Charters A, Khattra J, Helgason CD, Simpson EM, Jones S, Marra M and Hoodless PA. The Atlas of Gene Expression in Mouse Development: a SAGE Project.

633. 2004 Genomics Forum: Genomics and the Science of Life. Vancouver, BC. Mar 2004. Leung D, Teague K, Zuyderduyn S, Varhol R, Pleasance E, Warren R, Siddiqui A, Jones S, Marra M. A comprehensive approach to SAGE tag to gene mapping and an overview of the architecture of the Mouse Atlas of Gene Expression web site.

634. 2004 Genomics Forum: Genomics and the Science of Life. Vancouver, BC. Mar 2004. Nayar T, Delaney A, Marra M. Microarray Data Analysis: Which Software is Best?

635. 2004 Genomics Forum: Genomics and the Science of Life. Vancouver, BC. Mar 2004. McConechy M, Mansfield B, Leung A, Marra M, Gorski S. A Functional Genomics Approach to the Discovery of Novel Cell Death Genes.

636. 2004 Genomics Forum: Genomics and the Science of Life. Vancouver, BC. Mar 2004. Kirkpatrick R, Liu J, Palmquist D, Butterfield Y, Siddiqui A, Jones S, Marra M. EST Sequencing Bioinformatics Pipeline.

637. 2004 Genomics Forum: Genomics and the Science of Life. Vancouver, BC. Mar 2004. Pleasance E, Gorski SM, Marra M, Jones S. Identification of novel programmed cell death genes using large-scale gene expression data and comparative genomics approaches.

638. 2004 Genomics Forum: Genomics and the Science of Life. Vancouver, BC. Mar 2004. Schnerch A., Khattra J, Delaney A, Pera M, Firpo M, Thomson J, Jones S, Eaves C, Marra M. Large scale comparative transcriptome analysis of multiple undifferentiated human embryonic stem cell lines.

639. 2004 Genomics Forum: Genomics and the Science of Life. Vancouver, BC. Mar 2004. Petrescu A Butterfield Y, Griffith M, Griffith O, Guin R, Kirkpatrick R, Liao N, Liu J, Palmquist D, Stott J, Yang G, Barber S, Brown-John M, Chand S, Mayo M, Olson T, Smailus D, Holt R, Siddiqui A, Jones S, Marra M. Full length cDNA sequencing bioinformatics pipeline.

640. 2004 Genomics Forum: Genomics and the Science of Life. Vancouver, BC. Mar 2004. Stott J, Smailus D, Babakaiff R, Barber S, Butterfield Y, Brown-John M, Chan A, Guin R, Chand S, Featherstone R, Kirkpatrick R, Liao N, Liu J, Masson A, Mayo M, Moran J, Olson TE, Palmquist D, Petrescu AS, Santos JR, Varhol R, Warren R, Wong D, Yang GSH, Marra M and Robert A Holt. Accelerating Discovery - The Genome BC Sequencing Platform at Canada's Michael Smith Genome Sciences Centre.

641. 2004 Genomics Forum: Genomics and the Science of Life. Vancouver, BC. Mar 2004. Astakhova T, Bilenky M, Fu T, Griffith O, Hassel M, Kennedy J, Lin K, Montgomery S, Robertson G, Sleumer M, Tsang E, Siddiqui A, Marra M, Jones S. Sockeye: A 3D workspace for comparative genomics and cis-regulatory element detection.

642. 2004 Genomics Forum: Genomics and the Science of Life. Vancouver, BC. Mar 2004. Sleumer M, Astakhova T, Bilenky M, Griffith O, Hassel M, Kennedy J, Lin K, Montgomery S, Pleasance E, Robertson G, Tsang E, Fu T, Siddiqui A, Marra M, Jones S. Sockeye: A platform for cis-regulatory element discovery.

643. 2004 Genomics Forum: Genomics and the Science of Life. Vancouver, BC. Mar 2004. Warren R, Myhre M, Dosanjh M, Petrescu A, Yang G, Scott J, Butterfield Y, Schein J, Shin H, Latreille P, Khattra J, Smailus D, Siddiqui A, Holt R, Jones S, Marra M, Mohn W, Fukuda M, Davies J, Eltis L. Whole genome shotgun assembly and characterization of rhodococcus sp. rha1, a pcb-degrading actinomycete.

644. 2004 Genomics Forum: Genomics and the Science of Life. Vancouver, BC. Mar 2004. Griffith M, Baross A, Butterfield Y, Coughlin S, Zeng T, Griffith O, Petrescu A, Smailus D, Khattra J, McDonald H, McKay S, Moksa M, Holt R, Marra M. Targeted large scale generation and analysis of full-ORF human cDNA clones.

645. 2nd Annual Canadian Gene Expression Conference. Vancouver, BC. Mar 2004. Jones S, Griffith O, Pleasance E, Fulton D, Oveisi M, Astakhova T, Hassel M, Sleumer M, Kennedy J, Li Y, Lin K, Robertson G, Montgomery S, Fu T, Marra M, Siddiqui A. Utility of large expression datasets from SAGE, Affymetrix and cDNA microarrays for identifying genes under similar regulatory control.

646. 2nd Annual Canadian Gene Expression Conference. Vancouver, BC. Mar 2004. Kirkpatrick R, Liu J, Palmquist D, Butterfield Y, Siddiqui A, Jones S, Marra M. EST Sequencing Bioinformatics Pipeline.

647. 2nd Annual Canadian Gene Expression Conference. Vancouver, BC. Mar 2004. Kent D, Zhao Y, Raouf A, Dykstra B, Khattra J, Schnerch A, Marra M, Eaves C. Development of a Strategy for Gene Expression Profiling of Biologically Pure Populations of Adult Murine Hematopoietic Stem Cells.

648. 2nd Annual Canadian Gene Expression Conference. Vancouver, BC. Mar 2004. Baross A, Butterfield YSN, Coughlin SM, Zeng T, Griffith M, Griffith O, Petrescu AS, Smailus DE, Khattra J, McDonald HL, McKay SJ, Moksa M, Siddiqui A, Jones SJM, Holt RA, Marra MA. Systematic Recovery and Analysis of Full-ORF Human cDNA Clones.

649. 2nd Annual Canadian Gene Expression Conference. Vancouver, BC. Mar 2004. Pleasance E, Gorski SM, Marra MA, Jones SJM. Identification of novel programmed cell death genes using large-scale gene expression data and comparative genomics approaches.

650. Keystone Symposia: Biological Discovery Using Diverse High-Throughput Data. Steamboat Springs, Colorado. Mar 2004. Quayle S, Hare H, Hwang D, Jones S, Schein J, Marra M, and Sadar M. A custom microarray for profiling gene expression changes in advanced prostate cancer.

651. Keystone Symposia: Signaling in Vertebrate Organogenesis (C4). Santa Fe, NM. Mar 2004. Rupert JL, Wu MK, Cullum R, Lee L, Landry A, Helgason CD, Simpson EM, Jones S, Marra M, Hoodless PA. The Atlas of Gene Expression in Mouse Development.

652. ASI Exchange 2004. Vancouver, BC. Mar 2004. Montgomery S, Astakhova T, Bilenky M, Griffith O, Hassel M, Kennedy J, Lin K, Robertson G, Sleumer M, Tsang E, Fu T, Siddiqui A, Marra M, Jones S. Sockeye: A platform for cis-regulatory element discovery.

653. Systems Biology: Genomic approaches to transcriptional regulation. Cold Spring Harbor Laboratory, NY. Mar 2004. McGhee J, Robertson G, Khattra J, Moerman D, Baillie D, Jones S, Marra M, McKay S. The Transcription Factor Network Regulating Development of the Caenorhabditis elegans Intestine.

654. Systems Biology: Genomic approaches to transcriptional regulation. Cold Spring Harbor Laboratory, NY. Mar 2004. Astakhova T, Bilenky M, Fu T, Griffith O, Hassel M, Kennedy J, Lin K, Montgomery S, Robertson G, Sleumer M, Tsang E, Siddiqui A, Marra M, Jones S. SOCKEYE: a 3D workspace for comparative genomics and cis-regulatory element detection.

655. 2004 AGBT Meeting, Marco Island, FL. Feb 2004. Marra M, Khattra J, Schnerch A, Delaney A, Pera M, Firpo M, Thompson J, Eaves C. Large Scale Comparative Transcriptome Analysis of Multiple Undifferentiated Human Embryonic Stem Cell Lines.

656. 2004 AGBT Meeting, Marco Island, FL. Feb 2004. Marra MA, Chittaranjan S, McConechy M, Pleasance ED, Mansfield BA, Gorski SM. A Functional Genomics Approach to Autophagic Cell Death Gene Discovery.

657. 2004 AGBT Meeting, Marco Island, FL. Feb 2004. Krzywinski M, Bosdet I, Smailus D, Chiu R, Mathewson C, Wye N, Asano J, Barber S, Brown-John M, Chan S, Chand S, Chittaranjan S, Cloutier A, Fjell C, Girn N, Gray C, Kutsche R, Lee D, Lee S, Masson A, Mayo M, McLeavy C, Olson T, Pandoh P, Prabhu A-L, Shin H, Spence L, Stott J, Taylor S, Tsai M, Yang G, Albertson D, Lam W, Choy C-O, Osoegawa K, Zhao S, de Jong PJ, Schein J, Jones S, Marra M. Whole Genome Mammalian Clone Sets for High-Resolution BAC Arrays.

658. 2004 AGBT Meeting, Marco Island, FL. Feb 2004. Jones S, Astakhova T, Bilenky M, Griffith O, Hassel M, Kennedy J, Lin K, Montgomery S, Robertson G, Sleumer M, Tsang E, Fu T, Siddiqui A, Marra M. Sockeye: A platform for cis-regulatory element discovery.

659. 2004 AGBT Meeting, Marco Island, FL. Feb 2004. Siddiqui AS, Khattra J, Zuyderduyn S, Simpson E, Helgason C, Jones S, Hoodless P, Marra M. A Quantitative and Comprehensive Atlas of Gene Expression in Mouse Development.

660. 2004 AGBT Meeting, Marco Island, FL. Feb 2004. Butterfield YS, Griffith M, Griffith O, Guin R, Kirkpatrick R, Liao N, Liu J, Palmquist D, Petrescu AS, Stott JM, Yang GSH, Brown-John M, Chand SS, Mayo MR, Olson TE, Smailus DE, Holt RA, Siddiqui A, Jones S, Marra M. Full length cDNA sequencing bioinformatics pipeline.

661. 2004 AGBT Meeting, Marco Island, FL. Feb 2004. Baross A, Schertzer M, Zuyderduyn S, Jones SJM, Marra MA, Lansdorp PM. The Effect of Telomerase (hTERT) and Ataxia Telangiectasia Mutated (ATM) on Gene Expression Profiles in Human Fibroblasts.

662. 2004 AGBT Meeting, Marco Island, FL. Feb 2004. Baross A, Butterfield YSN, Coughlin SM, Griffith M, Griffith O, Khattra J, McDonald HL, Petrescu AS, Smailus DE, Zeng T, Jones SJM, Holt RA, Marra MA. Completing the Mammalian Gene Collection: Targeted Large Scale Generation and Analysis of Full-ORF Human cDNA Clones.

663. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2003. Quayle S, Hare H, Hwang D, Jones S, Schein J, Marra M, and Sadar M. Subtractive hybridization for identifying novel expressed sequences in prostate cancer.

664. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2003. Romanuik T, Quayle S, Hwang, D, Marra M, Sadar MD. SAGE analysis of androgen-independent prostate cancer.

665. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2003. Zhao Y, Raouf A, Khattra J, Schnerch A, Marra M, Eaves C. A novel method to amplify RNA extracts from small numbers of cells for Serial Analysis of Gene Expression (SAGE).

666. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2003. Mansfield BA, McConechy M, Marra MA, Gorski SM. A Functional Genomics Approach to the Discovery of Novel Cell Death Genes.

667. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2003. Baross Á, Butterfield Y, Coughlin S, Griffith M, Griffith OL, Khattra J, McDonald HL, Petrescu AS, Smailus DE, Zeng T, Jones SJM, Holt RA, Marra MA. Completing the Mammalian Gene Collection: Targeted large scale generation and analysis of full-ORF human cDNA clones.

668. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2003. Schnerch A, Asano J, Baross A, Khattra J, Pleasance E, Zuyderduyn S, Eaves C, Thomson J, Jones S, Marra M. Investigations of the Transcriptome of human embryonic stem cells using high throughput expression profiling and the characterization of enriched transcripts.

669. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2003. Butterfield Y, Khattra J, Griffiths O, Montgomery S, Petrescu A, Smailus D, Stott J, Yang G, Asano J, Barber S, Chan S, Cloutier A, Coughlin S, Freeman D, Girn N, Hanson R, Leach S, Mayo M, McDonald H, Pandoh P, Robertson A, Schein J, Siddiqui A, Astell C, Brooks-Wilson A, Holt R, Jones S, Marra M. The Genome Sequence of the SARS-associated Coronavirus –past, present, and future.

670. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2003. Chittaranjan S, Marra M, Gorski S. The Role of a Novel Gene Involved in Autophagic Cell Death.

671. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2003. Khattra J, Chan S, Asano J, Pandoh P, Coughlin S, McDonald H, Girn N, Baross A, Zeng T, Ma K, Lee S, McKay S, Schnerch A, Zuyderduyn S, Teague K, Delaney A, Zhao Y, Raouf A, Eaves C, Siddiqui A, Jones S, Marra M. Transcriptome profiling technologies: Nanogram sampling and large scale processing.

672. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2003. Halaschek-Wiener J, Collins J, Le N, Connors J, Meneilly G, Jones S, Riddle D, Marra M, Brooks-Wilson A. Identification of genes and genetic variation underlying healthy aging.

673. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2003. Bosdet I, Mathewson C, Lee D, Chiu R, Cloutier A, Featherstone R, Fjell C, Krzywinski M, Matsuo C, O'Connor K, Osoegawa K, Shin H, Tsai M, Wong D, Wye N, Prasad A, Portnoy M, Hoskins R, Celniker S, deJong PJ, Rubin G, Green E, Jones S, Schein J, Marra M. Applications for Fingerprinted BAC Clones.

674. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2003. Freeman JD, Ma K, Cagan R, Marra M, Gorski S. The Drosophila Ortholog of human RCCI is required for programmed cell death.

675. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2003. Pleasance E, Gorski S, Griffith O, Marra M, Jones S. Programmed Cell Death in Cancer: Expression patterns of genes involved in apoptosis and autophagic cell death.

676. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2003. Hou C, Chittaranjan S, Marra M, Gorski S. The role of AKAP200 in programmed cell death.

677. 17th International Mouse Genome Conference. Brauschweig, Germany. Nov 2003. Nagaraja R, Brathwaite M, Waeltz P, Schroeder M, Jefferson J, Schein J, Marra M, Abe K, Roe B. Physical map and sequence analysis in mouse t-complex.

678. 9th International Conference on Applied Genomics. Amsterdam, The Netherlands. Oct 2003. Quayle S, Hare H, Hwang D, Jones S, Schein J, Marra M, and Sadar M. Subtractive hybridization for identifying novel expressed sequences in prostate cancer.

679. 15th International Genome Sequencing and Analysis Conference. Savannah, GA. Sep 2003. Holt RA, Astell CR, Jones SJM, Brooks-Wilson A, Marra MA. The Genome Sequence of the SARS Associated Coronavirus.

680. The Second Annual General Meeting of the Stem Cell Network. Vancouver, BC. Sep 2003. Zhao Y, Raouf A, Khattra J, Schnerch A, Marra M, Eaves C. A novel method to amplify RNA extracts from small numbers of cells for Serial Analysis of Gene Expression (SAGE).

681. 1st Canadian Plant Genomics Workshop. Saskatoon, SK. Aug 2003. Jones SJM, Zuyderduyn S, Varhol R, Oveisi M, Fjell C, Leung D, Robertson N, Rusaw S, Ruzanov P, Pleasance ED, Schnerch A, Vatcher G, Siddiqui A, Marra M. Integrated genomic approaches to interpreting gene expression.

682. 10th World Congress on Lung Cancer. Vancouver, BC. Aug 2003. Ruzanov P, MacAulay C, Lonergan K, Lam S, Lam W, Marra M, Jones S. Deriving the transformation events in tumorogenesis using data from Serial Analysis of Gene Expression.

683. 10th World Congress on Lung Cancer. Vancouver, BC. Aug 2003. Coe BP, Garnis C, Zhu C, Krzywinski M, Marra M, Minna J, Lam S, Tsao M, MacAulay C, Lam W. Construction of a high resolution CGH array for chromosome 5p and analysis of SCLC and NSCLC Cell Lines.

684. 10th World Congress on Lung Cancer. Vancouver, BC. Aug 2003. Zuyderduyn S, Oveisi M, Varhol R, Vatcher G, Fjell C, Robertson N, Lam WL, Lam S, Lonergan K, MacAulay C, Siddiqui A, Marra M, Jones SJM. Exploring the molecular basis of non-small cell early-stage lung cancer with the DISCOVERY platform.

685. 10th World Congress on Lung Cancer. Vancouver, BC. Aug 2003. Chan THW, MacAulay C, Lam W, Lam S, Lonergan K, Jones S, Marra M, Ng RT. Using the permutation test to analyze lung cancer sage libraries.

686. 11th Conference of the International Society for Molecular Plant-Microbe Interactions. St. Petersburg, Russia. July 2003. Bakkeren G, Hu GG, Linning R, McCallum B, Banks T, Cloutier S, Butterfield Y, Liu J, Kirkpatrick R, Stott J, Yang G, Smailus D, Jones S, Marra M, Schein J. Generation of a wheat leaf rust fungus, Puccinia triticina, EST database from stage-specific cDNA libraries.

687. 14th International C. elegans Meeting, University of California. Los Angeles, CA. July 2003. Johnsen R, Fang L, Ha E, Mah A, McKay S, Tu D, Zhao Z, Jones S, Marra M, Moerman D, Ouellette F, Sonnhammer E, Baillie D. Expression of promoter-GFP constructs in *C. elegans.*

688. 14th International C. elegans Meeting, University of California. Los Angeles, CA. July 2003. McKay S, Jones S, Khattra J, Marra M, Moerman D, McGhee J, Asano J, Chan S, Coughlin S, Girn N, Huang P, Kai H, McDonald H, Pandoh P, Varhol R, Vatcher G, Warner A, Wong K, Zuyderduyn S, Baillie D. Evaluation of SAGE for the study of developmental gene expression profiles in *C. elegans.*

689. 14th International C. elegans Meeting, University of California. Los Angeles, CA. July 2003. S McKay, R Johnsen, S Jones, J Khattra, M Marra, D Moerman, F Ouellette, T Burglin, E Sonnhammer, A Vas Gomes, C Wahlestedt, J Asano, S Chan, S Coughlin, L Fang, N Girn, E Ha, P Huang, H Kai, A Mah, H McDonald, P Pandoh, D Tu, A Warner, K Wong , D Baillie. Gene expression profiles in cells, tissues and development of *C. elegans.*

690. 46th Annual Thomas L. Petty Aspen Lung Conference. Aspen, CO. June 2003. MacAulay C, Lonergan K, Chi B, Zuyderduyn S, Schein J, Tsao M, LeRiche J, Jones S, Marra M, Lam S, Lam W. Serial analysis of gene expression profiles of developmental stages in non-small cell lung carcinoma.

691. IUFRO Tree Biotechnology Meeting. Umea, Sweden. June 2003. Tuskan GA, DiFazio S, Wullschleger S, Ritland K, Bohlmann J, Douglas C, Ellis B, Marra M, Chapman J, Richardson P, Rokhsar D. The Populus Genome: Development of an Information Resource.

692. Gordon Research Conference on Autophagy, in Stress, Development and Disease. Waterville, ME. June 2003. Gorski S, Chittaranjan S, Hou YC, Pleasance E, Ma K, Varhol R, Marra M. Discovery and Functional Analysis of Genes Associated with Autophagic Cell Death.

693. Congress on In Vitro Biology. Portland, OR. May-June 2003. Tuskan GA, DiFazio S, Wullschleger S, Ritland K, Bohlmann J, Douglas C, Ellis B, Marra M, Chapman J, Richardson P, Rokhsar D. The Populos genome: Development of the information resource.

694. Pathology Day. Vancouver, BC. May 2003. Quayle S, Hare H, Akopian V, Hwang D, Jones S, Schein J, Tung S, Marra M, and Sadar M. Discovery of new genes differentially expressed in androgen independent prostate cancer.

695. 12th Annual Canadian Genetic Diseases Network Scientific Meeting. Kananaskis, AB. May 2003. Campbell G, Bosdet I, Butland S, Devon R, Hayden M, Leavitt B, Marra M, Wilkinson A, Ouellette F. GeMS DB: A database integrating clinical and experimental data for the study of Genomic Mutational Signature Sequences.

696. The Genome of Homo Sapiens. Cold Spring Harbor Laboratory, NY. May 2003. The Genome Canada C. elegans II Consortium. Preliminary analysis of expression profiles of human ortholog genes in *C. elegans.*

697. The Genome of Homo Sapiens. Cold Spring Harbor Laboratory, NY. May 2003. Osoegawa K, Choy C-O, Lammer E, Iovannisci D, Krzywinski M, Marra M, Schoenmakers E, de Jong PJ. High-resolution mapped BAC-arrays for use in CGH.

698. The Genome of Homo Sapiens. Cold Spring Harbor Laboratory, NY. May 2003. Butland S, Bosdet I, Campbell G, Devon R, Hayden M, Leavitt B, Marra M, Wilkinson A, Ouellette F. Integrated bioinformatics and clinical approach to identify disease-gene associations.

699. Genome Informatics. Cold Spring Harbor Laboratory, NY. May 2003. Bilenky M, Astakhova T, Montgomery S, Rak M, Robertson G, Sleumer M, Siddiqui A, Marra M, Jones S. Sockeye: A 3D approach to multi-genome visualization.

700. Genome Informatics. Cold Spring Harbor Laboratory, NY. May 2003. Fjell C, Bosdet I, Chiu R, Flibotte S, Mathewson C, Shin H, Wye N, Schein J, Jones SJM, Marra M. Fingerprint mapping bioinformatics for sequencing the rat genome.

701. Genome Informatics. Cold Spring Harbor Laboratory, NY. May 2003. McKay S, Johnsen R, Mah A, Fang L, Tu D, Khattra J, Warner A, Kai H, Ha E, Huang P, Jones S, Marra M, Moerman D, Baillie D. Large-scale analysis of gene expression profiles of cells and tissues in *C. elegans.*

702. 1st Canadian Gene Expression Conference. Vancouver, BC. Mar 2003. Jones SJM, Zuyderduyn S, Varhol R, Oveisi M, Ruzanov P, Rusaw S, Pleasance ED, Schnerch A, Vatcher G, Marra M. Serial Analysis of Gene Expression in Cancer Research.

703. 1st Canadian Gene Expression Conference. Vancouver, BC. Mar 2003. Gorski SM, Chittaranjan S, Pleasance ED, Freeman JD, Anderson CL, Varhol RJ, Coughlin SM, Zuyderduyn SD, Jones SJM, Marra MA. A SAGE Approach to Discovery of Genes Involved in Autophagic Cell Death.

704. The ASI Exchange 2003. Vancouver, BC. Mar 2003. Saeedi P, Krzywinski M, Jones S, Marra MA. Automated lane tracking for DNA gel images.

705. Children's and Women's Health Centre of BC Student Research Forum. Vancouver, BC. Mar 2003. Campbell G, Bosdet I, Butland S, Devon R, Hayden M, Leavitt B, Marra M, Ouellette F. GeMS DB: A database of clinical and experimental data for the study of Genomic Mutational Signature Sequences.

706. Fifth European Symposium of the Protein Society (FASEB). Florence, Italy. Mar 2003. Jensen-Seaman MI, Lazar J, Shiozawa M, Barreto NE, Lemke A, Gibbs R, Weinstock G, Schein J, Marra M, Zhao S, de Jong P, Jacob HJ. A Comparative genomics approach to positionally cloning a gene for renal failure.

707. Molecular Mechanisms of Apoptosis meeting. Banff, AB. Feb 2003. Chittaranjan S, Marra M, Gorski S. Role of defense response genes in autophagic cell death of Drosophila salivary glands.

708. Advances in Genome Biology & Technology and Automation in Mapping & DNA Sequencing 4th Annual Meeting. Marco Island, FL. Feb 2003. Krzywinski M, Bosdet I, Smailus D, Mathewson C, Wye N, Barber S, Brown-John M, Chand S, Cloutier Al, Masson A, Mayo M, Olson T, MacAulay C, Lam W, Choy CO, Osoegawa K, Zhao S, de Jong PJ, Schein J, Jones S, Marra M. A set of rearrayed BAC clones spanning the human genome.

709. Advances in Genome Biology & Technology and Automation in Mapping & DNA Sequencing 4th Annual Meeting. Marco Island, FL. Feb 2003. Krzywinski M, Schein J, Chiu R, Bosdet I, Mathewson C, Wye N, Barber S, Brown-John M, Chand S, Cloutier A, Masson A, Mayo M, Olson T, Jones S, Hoskins R, Celniker S, Rubin G, Marra M. Verification of Drosophila melanogaster sequence assembly using restriction digest BAC fingerprints derived from multiple enzymes.

710. Advances in Genome Biology & Technology and Automation in Mapping & DNA Sequencing 4th Annual Meeting. Marco Island, FL. Feb 2003. Jones S, Ruzanov P, MacAulay C, Lam W, Lonergan K, Lam S, Zuyderduyn S, Schein J, Oveisi M, Varhol R, Rusaw S, Schnerch A, Khattra J, Thomson J, Humphries K, Eaves C, Ling V, Marra M. High-throughput serial analysis of gene expression profiling of cancers.

711. Advances in Genome Biology & Technology and Automation in Mapping & DNA Sequencing 4th Annual Meeting. Marco Island, FL. Feb 2003. Butterfield Y, MacDonald K, Stott J, Yang G, Smailus D, Griffith O, Guin R, Barber S, Girn N, Lee D, Prabhu A-L, Miranda T, Schein J, Jones S, Marra M. An integrated approach to transposon-mediated full length cDNA sequencing.

712. Advances in Genome Biology & Technology and Automation in Mapping & DNA Sequencing 4th Annual Meeting. Marco Island, FL. Feb 2003. Khattra J, Chan S, Asano J, Pandoh P, Vatcher G, Schnerch A, Doug F, Zuyderduyn S, Leung D, Teague K, Jones S, Marra M. High-throughput gene expression analysis technologies at the British Columbia Cancer Agency.

713. TIGR/ASM Microbial Genomes 3rd Annual Conference. New Orleans, LA. Jan 2003. Eltis L, Butterfield Y, Dosanjh M, Goncalves E, Khattra J, Overton L, Patel R, Patrauchan M, Smailus D, Stott J, Warren R, Yang G, Jones S, Marra M, Schein J, Mohn W, Fukuda M, Davies J. Genomic Analysis of Rhodococcus sp. RHA1.

714. SAGE 2003. Amsterdam, Netherlands. Jan 2003. Lam W, Lonergan K, Zuyderduyn S, Schein J, Tsao M, LeRiche J, Jones S, Marra M, MacAulay C, Lam S. Gene expression profiles of developmental stages of non-small cell lung carcinoma.

715. SAGE 2003. Amsterdam, Netherlands. Jan 2003. Zuyderduyn S, Varhol R, Oveisi M, Ruzanov P, Rusaw S, Pleasance ED, Schnerch A, Vatcher G, Marra M, Jones SJM. The discovery platform: A database and software system for integration, interrogation and visualization of biological and SAGE data.

716. SAGE 2003. Amsterdam, Netherlands. Jan 2003. Schnerch A, Asano J, Chan S, Khattra J, Oveisi M, Pleasance E, Ruzanov P, Varhol R, Vatcher G, Zuyderduyn S, Eaves CJ, Humphries K, Thomson JA, Jones S, Marra M. Global gene expression profiling in murine and human embryonic stem cells using SAGE and Affymetrix genechips.

717. SAGE 2003. Amsterdam, Netherlands. Jan 2003. Pleasance ED, Varhol R, Zuyderduyn S, Marra MA, Jones SJM. Assessment of SAGE in transcript identification based on a new method of tag-to-gene mapping.

718. Comparative Plant Genomics Conference. Cold Spring Harbor Laboratory, NY. Dec 2002. Beavis B, Bohlmann J, Bradshaw HD, Douglas C, Ellis B, Grover A, Larimer F, Martin F, Marra M, Nilsson O, Richardson P, Rokhsar D, Ritland K, Sandberg G, Strauss SH, Tuskan G. Poplar genomics: Global collaboration to develop tools that revolutionize knowledge of tree development and wood quality.

719. University of British Columbia Medical Genetics Research Day. Vancouver, BC. Nov 2002. Gorski SM, Chittaranjan S, Pleasance ED, Freeman JD, Anderson CL, Varhol RJ, Coughlin SM, Zuyderduyn SD, Jones SJM, Marra MA. A SAGE Approach to Discovery of Genes Involved in Autophagic Cell Death.

720. University of British Columbia Medical Genetics Research Day. Vancouver, BC. Nov 2002. Pleasance ED, Chittaranjan S, Freeman JD, Varhol RJ, Zuyderduyn SD, Marra MA, Gorski SM, Jones SJM. Bioinformatics analysis of SAGE expression data and applications to cell death.

721. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2002. de Leeuw RJ, Pal A, Chhanabhai M, Karsan A, Connors JM, Klasa R, Marra MA, Horsman D, Lam WL. Serial Analysis of Gene Expression Profile of a Richter’s Transformation of Chronic Lymphocytic Leukemia.

722. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2002. Bosdet I, Gorski S, Marra M. Programmed cell death in the Drosophila melanogaster retina – cloning and characterizing the Echinus locus.

723. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2002. Chittaranjan S, Marra M, Gorski S. Role of defense response genes in autophagic cell death of Drosophila salivary glands.

724. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2002. Freeman D, Ma K, Rusconi JC, Cagan RL, Marra MA, Gorski SM. Characterization of inxs, a gene involved in programmed cell death in the developing Drosophila retina.

725. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2002. Yang G, Stott J, Smailus D, Barber S, Girn N, Lee D, MacDonald K, Prabhu A-L, Tsai M, Schein J, Marra M. SAGE and full length cDNA sequencing at the BCCA Genome Sciences Centre.

726. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2002. Quayle S, Hare H, Akopian1 V, Hwang D, Jones S, Schein J, Marra M, Sadar M. Discovery of new genes differentially expressed in androgen independent prostate cancer.

727. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2002. Gorski S, Chittaranjan S, Pleasance ED, Freeman JD, Anderson CL, Varhol RJ, Coughlin SM, Zuyderduyn SD, Jones SJM, Marco MA. A SAGE approach to discovery of genes involved in autophagic cell death.

728. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2002. Fjell C, Astakova V, Chiu R, Flibotte S, Saeedi P, Shin H, Schein J, Jones S, Marra M. Bioinformatics for genetic physical mapping.

729. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2002. Pleasance ED, Chittaranjan S, Freeman JD, Varhol RJ, Zuyderduyn SD, Marra MA, Gorski SM, Jones SJM. Bioinformatic analysis of SAGE expression data and applications to cell death.

730. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2002. Bosdet I, Chiu R, Fjell C, Fuhrmann D, Krzywinski M, Osoegawa K, Brown-John M, Chand S, Cloutier A, Masson A, Mathewson C, Mayo M, Olson T, Spence L, Wye N, deJong PJ, Schein J, Jones S, Marra M. Physical maps constructed from fingerprinted BAC clones.

731. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2002. Khattra J, Chan S, Asano J, Pandoh P, Vatcher G, Schnerch A, Zuyderduyn S, Leung D, Teague K, Jones S, Marra M. Application of high-throughput gene expression technologies at the Genome Sciences Centre.

732. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2002. Krzywinski M, Schein J, Chiu R, Bosdet I, Mathewson C, Wye N, Barber S, Brown-John M, Chand S, Cloutier A, Masson A, Mayo M, Olson T, Jones S, Hoskins R, Celniker S, Rubin G, Marra M. Verification of Drosophila Melanogaster sequence assembly using restriction digest BAC fingerprints derived from multiple enzymes.

733. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2002. Krzywinski M, Bosdet I, Smailus D, Mathewson C, Wye N, Barber S, Brown-John M, Chand S, Cloutier A, Masson A, Mayo M, Olson T, Lam W, MacAulay C, Osoegawa K, Zhao S, de Jong PJ, Schein J, Jones S, Marra M. A set of rearrayed BAC clones spanning the human genome.

734. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2002. Montgomery S, Astakhova T, Bilenky M, Rak M, Robertson G, Sleumer M, Marra M, Jones S. Mammalian gene expression platform.

735. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2002. Butterfield Y, Guin R, Macdonald K, Griffith O, Skalska U, Smailus D, Schein J, Jones S, Marra M. Sequencing bioinformatics at Canada’s Michael Smith’s Genome Sciences Centre.

736. Canadian Phytopathological Society - British Columbia Regional Meeting. Summerland, BC. Oct 2002. Hu GG, Linning R, Joseph C, McCallum B, Xing T, Walsh A, Banks T, Cloutier S, Jordan M, Matsalla C, Schein J, Butterfield Y, Jones S, Marra M, Bakkeren G. Generation of a database for expressed sequence tags of leaf rust (*Puccinia triticina)* of wheat from stage-specific cDNA libraries and construction of a corresponding microarray.

737. The 10th International Conference on Intelligent Systems for Molecular Biology. Edmonton, AB. Aug 2002. Butterfield Y, Guin R, Skalska U, Smailus D, Schnerch A, Teague K, Schein J, Marra M, Jones S and the Genome Sciences Centre. Software development for high-throughput DNA sequencing.

738. International Society for Animal Genetics Conference. Gottingen, Germany. Aug 2002. Larkin DM, Schein J, Green C, Dekoj TR, Bachman S, Schweitzer P, Rebeiz M, Everts-van der Wind A, Jones S, Bosdet I, Mathewson C, Wye N, Chiu R, Moore S, Keele JW, Kappes SM, Marra M, de Jong P, Womack JE, Lewin HA. Toward a comparatively anchored, sequence-ready whole genome physical map of the cattle genome.

739. 84th Annual Meeting of the Endocrine Society. San Francisco, CA. June 2002. Quayle S, Hare H, Akopian V, Hwang D, Jones S, Schein J, Marra M, Sadar M. Gene expression profiles associated with progression of prostate cancer to androgen-independence.

740. Genomics Workshop Wheat Genomics: narrow host range pathogens. London, UK. June 2002. Bakkeren G, Hu G, Linning R, McCallum B, Xing T, Walsh A, Cloutier S, Jordan M, Matsalla C, Schein J, Butterfield Y, Jones S, Marra M. Construction of cDNA libraries covering different life cycle stages of the wheat leaf rust fungus, Puccinia triticina (race BBB/Lr1) and generation of a database of 10,000 ESTs.

741. Gordon Conference on Cell Death. Waterville, ME. June 2002. Gorski S, Anderson C, Chittaranjan S, Freeman D, Garland E, Jones S, Varhol R, Zuyderduyn S, Marra M. Transcription profiling of autophagic cell death.

742. Gordon Conference on Cell Death. Waterville, ME. June 2002. Freeman JD, Rusconi JC, Cagan RL, Marra MA, Gorski SM. Characterization of inxs, a gene involved in Programmed Cell Death in the developing Drosophila retina.

743. Pathology Day. Vancouver, BC. May 2002. Quayle S, Hare H, Akopian V, Hwang D, Jones S, Schein J, Marra M, Sadar M. Identification of a novel gene differentially expressed in the progression of prostate cancer.

744. Genome Sequencing & Biology Conference. Cold Spring Harbor Laboratory, NY. May 2002. Nagaraja R, Waeltz P, Brathwaite M, Schein J, Marra M, Schlessinger D. Sequence analysis and physical map in mouse t-complex inversion 2 region and comparison to syntenic region in human.

745. Genome Sequencing & Biology Conference. Cold Spring Harbor Laboratory, NY. May 2002. Gregory SG, McPherson JD, Marra M, Zhao S, Osoegawa K, and others on behalf of the International Mouse Genome Mapping Consortium. A physical map of the mouse genome.

746. Genome Sequencing & Biology Conference. Cold Spring Harbor Laboratory, NY. May 2002. The Rat Genome Sequencing Consortium. Sequencing the Rat Genome.

747. Genome Sequencing & Biology Conference. Cold Spring Harbor Laboratory, NY. May 2002. Krzywinski M, Jones S, Bosdet I, Schein J, Marra M. A set of rearrayed BAC clones spanning the human genome.

748. Genome Sequencing & Biology Conference. Cold Spring Harbor Laboratory, NY. May 2002. Bosdet I, Barber S, Chan S, Chiu R, Fjell C, Krzywinski M, Leach S, Lee D, Mathewson C, Olson T, Osoegawa K, Prabhu A, Saeedi P, Shin H, Taylor S, Tsai M, Wye N, de Jong PJ, Schein J, Jones S, Marra M. Fingerprinted BAC clone physical maps.

749. Genome Sequencing & Biology Conference. Cold Spring Harbor Laboratory, NY. May 2002. Smailus D, Asano J, Butterfield Y, Girn N, Guin R, Krzywinski M, Lee S, MacDonald K, Olson T, Pandoh P, Saeedi P, Skalska U, Spence L, Stott J, Teague K, Yang G, Schein J, Jones S, Marra M. Transposon-mediated cDNA Sequencing at the BC Cancer Agency Genome Sequence Centre.

750. American Association for Cancer Research 93rd Annual Meeting. San Francisco, CA. Apr 2002. Lonergan K, MacAulay C, Smailus D, Zuyderduyn S, Jones S, Marra M, Lam S, Lam W. Comparing Expression Profiles of Lung Cancer Progression by SAGE.

751. Transcriptome 2002: From Functional Genomics to Systems Biology. Seattle, WA. Mar 2002. Matrubutham U, Mirchandani J, Liu J, Gleeson M, MacDonald K, Asano J, Butterfield Y, Girn N, Lee S, Olson T, Pandoh P, Skalska U, Smailus D, Spence L, Stott J, Yang G, Schein J, Marra M. A Novel Approach to Eliminate Vector Background and Increase Sequencing Efficiency of cDNA.

752. Physiological Genomics & Rat Models. Cold Spring Harbor Laboratory, NY. Dec 2001. Schein J , Bosdet I, Chiu R, Fjell C, Fuhrmann D, Girn N, Krzywinski M, Leach S, Lee D, Lee S, Mathewson C, Ness S, Osoegawa K, Prabhu A, Saeedi P, Spence L, Taylor S, Wye N, de Jong P, Jones S, Marra M. A BAC fingerprint map of the rat genome.

753. Northwest Urological Society 48th Annual Meeting. Vancouver, BC. Dec 2001. Quayle S, Hare H, Akopian V, Jones S, Schein J, Marra M, Sadar M. Gene expression analysis of androgen-independent prostate cancer.

754. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2001. Lonergan K, MacAulay C, Smailus D, Zuyderduyn S, Jones S, Marra M, Lam S, Lam W. Comparing Expression Profiles of Lung Cancer Progression by SAGE.

755. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2001. Bosdet I, Chiu R, Fjell C, Fuhrmann D, Girn N, Krzywinski S, Leach S, Lee D, Lee S, Mathewson C, Ness S, Osoegawa K, Prabhu A, Saeedi P, Spence L, Taylor S, Wye N, de Jong P, Schein J, Jones S, Marra M. Fingerprinted BAC clones for physical map construction.

756. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2001. Chittaranjan S, Garland E, Freeman D, Jones S, Marra M, Gorski S. Transcription profiling of cell death in drosophila melanogaster.

757. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2001. Smailus D, Asano J, Butterfield Y, Chan S, Guin R, Krzywinski M, MacDonald K, Olson T, Pandoh P, Skalska U, Schnerch A, Stott J, Tsai M, Yang G, Zuyderduyn S, Schein J, Jones S, Marra M. Full-length cDNA and SAGE sequencing at the British Columbia Cancer Agency Genome Sequence Centre.

758. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2001. Zuyderduyn S, Varhol R, Oveisi-Fordoei M, Garland E, Krzywinski M, Marra M, Jones S. SAGEdb: A computational platform for investigations using serial analysis of gene expression.

759. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2001. Awarded "Best Poster." Quayle S, Hare H, Akopian V, Jones S, Schein J, Marra M, Sadar M. Differential gene expression in a model of advanced prostate cancer.

760. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2001.Quayle S, Hare H, Akopian V, Jones S, Schein J, Marra M, Sadar M. Gene expression analysis of androgen-independent prostate cancer.

761. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. Nov 2001. Garland E, Chittaranjan S, Freeman D, Gorski S, Varhol R, Zuyderduyn S, Marra M, Jones S. A new method of tag to gene mapping allows more comprehensive analysis of data from Serial Analysis of Gene Expression.

762. University of British Columbia Medical Genetics Research Day. Vancouver, BC. Nov 2001. Garland E, Chittaranjan S, Freeman D, Gorski S, Varhol R, Zuyderduyn S, Marra M, Jones S. A new method of tag to gene mapping allows more comprehensive analysis of data from Serial Analysis of Gene Expression.

763. Functional Genomics, Satellite to the 8th International Conference on Environmental Mutagens. Seattle, WA. Oct 2001. Quayle S, Hare H, Akopian V, Jones S, Schein J, Marra M, Sadar M. Identification of new targets for the treatment of androgen-independent prostate cancer.

764. SAGE 2001 Frontiers in Transcriptome Exploration. Coronado, CA. Sep 2001. Lian T, Steen BR, Tangen K, MacDonald K, Zuyderduyn S, Marra M, Jones S, Kronstad J. Analysis of Virulence-Related Transcription in the Human Pathogenic Fungus Cryptococcus neoformans Using SAGE.

765. SAGE 2001 Frontiers in Transcriptome Exploration. Coronado, CA. Sep 2001. Jones SJM, Riddle DL, Pouzyrev AT, Velculescu VE, Hillier L, Eddy SR, Stricklin SL, Baillie DL, Waterston R, Marra M. Changes in Gene Expression Associated with Developmental Arrest and Longevity.

766. SAGE 2001 Frontiers in Transcriptome Exploration. Coronado, CA. Sep 2001. Garland E, Varhol R, Zuyderduyn S, Marra M, Jones S. Transcript construction for increased accuracy of tag to gene mapping in SAGE analysis.

767. SAGE 2001 Frontiers in Transcriptome Exploration. Coronado, CA. Sep 2001. Varhol R, Zuyderduyn S, Lypkie P, Krzywinski M, Garland E, Marra M, Jones S. SAGEdb: Integrated Database for Gene Expression Analysis.

768. SAGE 2001 Frontiers in Transcriptome Exploration. Coronado, CA. Sep 2001. Zuyderduyn S, Varhol R, Garland E, Krzywinski M, Marra M, Jones S. SAGEspace: Interrogating and Visualizing SAGEdb.

769. International Society for Trace Elements in Humans 2001 Meeting. Quebec City, PQ. Sep 2001. Mattman A, Vatcher G, Marra M, Jones S, Lockitch G, Huntsman D. Investigation of the transferrin receptor 2 (TFR2) gene in HFE C282Y negative patients with atypical hereditary Hemochromatosis (HH).

770. Joint Meeting of the American Phytopathological Society, the Mycological Society of America, and the Society of Nematologists. Salt Lake City, UT. Aug 2001. Kronstad J, Lee N, Wake K, Jiang G, Klose J, Schein J, Marra M, Jones S. Sex, signaling and morphogenesis in smut fungi. ***(Phytopathology 91 (6 Supplement): S165-S166 June 2001)***

771. 13th International C. elegans international meeting. Los Angeles, CA. June 2001. Riddle DL, Jones SJ, Pouzyrev AT, Velculescu VE, Hillier L, Eddy SR, Stricklin SL, Baillie DL, Waterston R, Marra MA. Changes in gene expression associated with developmental arrest and longevity in C. elegans.

772. Genome Sequencing and Mapping. Cold Spring Harbor Laboratory, NY. May 2001. Ness S, Fjell C, Chiu R, Saeedi P, Fuhrmann D, Schein J, Jones S, Marra M. Developing computational strategies for constructing and analyzine physical maps of large genomes.

773. Genome Sequencing and Mapping. Cold Spring Harbor Laboratory, NY. May 2001. Butterfield Y, Zuyderduyn S, Schnerch A, Guin R, Krzywinski M, Schein J, Smailus D, Jones S, Marra M. Bioinformatics for human full length cDNA sequencing at the BCCA Genome Sequence Centre.

774. Genome Sequencing and Mapping. Cold Spring Harbor Laboratory, NY. May 2001. Smailus D, Butterfield Y, Chan S, Guin R, Krzywinski M, Mathewson C, Prabhu A, Schnerch A, Stott J, Tsai M, Zuyderduyn S, Schein J, Jones S, Marra M. Full-length cDNA sequencing at the British Columbia Cancer Agency Genome Sequence Centre.

775. Genome Sequencing and Mapping. Cold Spring Harbor Laboratory, NY. May 2001. Schein J, Asano J, Bosdet I, Chiu R, Fjell C, Fuhrmann D, Gray C, Krzywinski M, Kutsche R, Lee S, Mathewson C, McLeavy C, Ness S, Osoegawa K, Pandoh P, Saeedi P, Spence L, van den Bosch N, Yang G, de Jong PJ, Jones S, McPherson J, Marra M. A fingerprinted BAC clone physical map of the mouse genome.

776. The Fifth Annual International Conference on Computational Molecular Biology. Montreal, PQ. Apr 2001. Thorne M, Marra M, Jones S. Cataloguing candidate elements involved in transcriptional regulation in the Caenorhabditis elegans genome.

777. Mouse Molecular Genetics. Cold Spring Harbor Laboratory, NY. Aug 2000. Marra M, Schein J, Bosdet I, Chan S, Chiu R, Fuhrmann D, Guin R, Krzywinski M, Kutsche R, Mathewson C, Pandoh P, Prabhu A, Smailus D, Sness S, Stott J, Tsai M, Yang G, Smith M, Jones S and McPherson J. Fingerprinted clones for the sequencing of the mouse genome.

778. The Third International Symposium on Fungal Genomics: Novel Developments in Functional, Evolutionary and Computational Genomics. Athens, GA. July 2000. Steen BR, Tangen K, MacDonald K, Marra M, Jones S, Kronstad J. Genome analysis and infection regulated gene expression in Cryptococcus neoformans.

779. Genome Sequencing and Mapping. Cold Spring Harbor Laboratory, NY. May 2000. Fuhrmann DR, Marra MA, Chinwalla A, Jones S, Waterston R. Automated image analysis for DNA restriction mapping.

780. 5th Annual International Human Genome Meeting. Vancouver, BC. Apr 2000. Schein J, Bosdet I, Chan S, Chittaranjan S, Chiu R, Krzywinski M, Prabhu A, Smailus D, Stott J, Thorne M, Zapala M, McPherson J, Smith M, Jones S, Marra M. Fingerprinted BAC clones for sequencing the genome of the mouse.