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CANADA’S MICHAEL SMITH GENOME SCIENCES CENTRE

## CURRICULUM VITAE

## STEVEN J.M. JONES

Canada’s Michael Smith Genome Sciences
Centre at BC Cancer
570 West 7th Avenue
Vancouver, British Columbia
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e-mail: sjones@bcgsc.ca

## AREAS OF EXPERTISE:

bioinformatics, genomics, cancer genomics, comparative genomics, computational drug design, epigenomics, gene prediction, DNA sequencing, gene expression, gene regulatory control

## EDUCATION:

| Degree | Institution | Subject of Degree | Supervisor | Start Date | End Date |
|---|---|---|---|---|---|
| Ph.D. | Sanger Institute, Cambridge, UK | Bioinformatics | Dr. Richard Durbin and Dr. John Sulston | 03/1995 | 06/1999 |
| M.Sc. | Simon Fraser University, Burnaby, Canada | Genetics | Dr. David Baillie | 01/1991 | 02/1994 |
| B.Sc.(Hons) | Bristol University, Bristol, UK | Biochemistry | | 10/1987 | 06/1990 |

## ACADEMIC EMPLOYMENT HISTORY:

| | | |
|---|---|---|
| 09/2019 | Present | Adjunct Professor, Molecular Biology & Biochemistry, Simon Fraser University |
| **04/2016** | **Present** | **Co-Director, Canada’s Michael Smith Genome Sciences Centre, BC Cancer** |
| 04/2015 | Present | Scientific Director, Canada’s Genomic Enterprise (CGEN.ca) |
| 05/2013 | Present | Adjunct Professor, School of Computing Science, Simon Fraser University |
| 07/2010 | Present | Distinguished Scientist, BC Cancer Research Institute, BC Cancer |
| 07/2010 | Present | Professor, Medical Genetics, University of British Columbia |
| 09/2006 | Present | Chair, Bioinformatics Graduate Program, University of British Columbia |
| 09/2006 | Present | Associate Member, Peter Wall Institute for Advanced Studies, University of British Columbia |
| 07/2002 | Present | Founding Director, CIHR/MSFHR Bioinformatics Training Program |
| 10/2001 | Present | Director Bioinformatics, Genome BC Bioinformatics Platform |
| 06/2000 | Present | Associate Member, Michael Smith Laboratories, University of British Columbia |
| **01/1999** | **Present** | **Head, Bioinformatics, Canada’s Michael Smith Genome Sciences Centre, BC Cancer** |
| 10/2008 | 08/2019 | Professor, Molecular Biology & Biochemistry, Simon Fraser University |

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|---|---|---|
| 11/2005 | 04/2016 | Associate Director, Genome Sciences Centre, BC Cancer |
| 01/1999 | 07/2010 | Senior Scientist, BC Cancer Research Centre, BC Cancer |
| 07/2005 | 06/2010 | Associate Professor, Medical Genetics, University of British Columbia, |
| 11/2005 | 06/2010 | Adjunct Professor, Medical Microbiology & Infectious Diseases, University of Manitoba |
| 04/2001 | 10/2008 | Adjunct Professor, Molecular Biology & Biochemistry, Simon Fraser University |
| 10/2002 | 01/2007 | Associate Director, University of British Columbia Bioinformatics Centre (UBiC) |
| 07/2002 | 07/2005 | Assistant Professor, Medical Genetics, University of British Columbia, |
| 02/2000 | 06/2002 | Adjunct Professor, Medical Genetics, University of British Columbia, |
| 03/1994 | 06/1998 | Bioinformatician, Bioinformatics Department, Sanger Centre, United Kingdom |

## HONOURS AND AWARDS:/

| | | |
|---|---|---|
| 2024 | Distinguished Honorary Affiliate | Canadian College of Medical Geneticists |
| 03/2024 | Outstanding Service in Bioinformatics Award | Bioinformatics Network Canada (BioNet) |
| 04/2023 to Present | Fellow | Royal College of Physicians, Edinburgh |
| 2022 | Assistant Deputy Minister (ADM) Distinction Award for 2022 | Ecosystems and Oceans Science Fisheries and Oceans Canada, Government of Canada |
| 06/2022 | Faculty of Medicine Distinguished Achievement Award | University of British Columbia |
| 10/2020 | Highly Cited Researcher for 2020 | Clarivate Analytics |
| 06/2020 | 2020 Team Science Award: TCGA | American Association for Cancer Research |
| 10/2019 | Highly Cited Researcher for 2019 | Clarivate Analytics |
| 06/2019 to 06/2026 | UBC Canada Research Chair in Computational Genomics | Canadian Institutes of Health Research ($1,400,000) |
| 11/2018 | Highly Cited Researcher for 2018 | Clarivate Analytics |
| 10/2017 | Named one of 40 (from 1200) UBC Science Co-op Supervisor Recognition Award | University of British Columbia Science Co-op Program |
| 09/2016 | Named one of Web of Science Highly Cited Researchers (Computer Science Division) | Thomson Reuters |
| 09/2015 | Named one of 50 (from 22,000) most Inspiring Alummi over the last 50 years | Simon Fraser University |
| 06/2014 | Named one of the World's Most Influential Scientific Minds (Computer Science Division) | Thomson Reuters |
| 06/2014 | Fellow | Canadian Academy of Health Sciences |
| 05/2014 | Faculty of Medicine Distinguished Achievement Award | University of British Columbia, Faculty of Medicine |
| 03/2014 | The Journal of Pathology Jeremy Jass Prize for Research Excellence in Pathology | Manuscript Winner: Concurrent CIC mutations, and 1p/19q loss distinguish oligodendrogliomas from other cancers. |
| 04/2012 | Killam Teaching Prize | University of British Columbia ($5000) |
| 06/2011 | Fellow | Life Sciences Division of Academy of Science<br>Royal Society of Canada |
| 03/2010 | Genome BC Award for Scientific Excellence | LifeSciences British Columbia |

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|---|---|---|
| 10/2009 | IEEE InfoVis 2009 | Best Paper Award – AbySS-Explorer: Visualizing Genome Sequence Assemblies. |
| 05/2008 | Michael Smith Foundation for Health Research | MSFHR Five Year Senior Scholar Award, Biomedical (July 2008 to June 2013 - $500,000) |
| 10/2007 | Department Teaching Award | Medical Genetics Department, University of British Columbia |
| 07/2006 | Faculty Merit Award | Medical Genetics Department, University of British Columbia |
| 09/2006 | Senior Early Career Scholar | Peter Wall Institute for Advances Studies ($5500) |
| 06/2006 | Spencer Award for IT Innovation | University of British Columbia ($1000) |
| 06/2006 | President's 40th Anniversary Award | Simon Fraser University |
| 05/2006 | Top 40 Under 40 Award | Canada's Caldwell Partners International |
| 01/2006 | Top 40 Under 40 Award | Business in Vancouver |
| 07/2005 | Faculty Merit Award | Medical Genetics Department, University of British Columbia |
| 11/2004 | Outstanding Alumni Awards 2004, Simon Fraser University | Outstanding Alumni Award for Academic Achievement |
| 03/2004 | BC Biotech Biotechnology Awards | Innovation and Achievement Award (to Michael Smith Genome Sciences Centre) |
| 12/2003 | Genome Technology Magazine | Voted one of the top 5 most innovative in Bioinformatics |
| 07/2003 | Faculty Merit Award | Medical Genetics Department, University of British Columbia |
| 07/2003 | Michael Smith Foundation for Health Research | MSFHR Five Year Scholar Award, Biomedical (July 2003 to June 2008- $400,000) |
| 07/2003 | Michael Smith Foundation for Health Research | Matching Funds to Five Year Scholar Award (July 2003 – March 2006 $50,000) |
| 07/2003 | Michael Smith Foundation for Health Research | Establishment Grant (July 2003 – March 2006 $75,000) |

## TEACHING EXPERIENCE:

| Year | University | Course Number | Scheduled Hours | Class Size | Hours Taught |
|---|---|---|---|---|---|
| 01/2023 | Simon Fraser University/ University of British Columbia | MBB505/ BIOF520 Problem Based Learning. | 44 | 18 | 44 |
| 01/2023 | University of British Columbia | MEDGEN 505 | 36 | 18 | 3 |
| 01/2022 | Simon Fraser University/ University of British Columbia | MBB505/ BIOF520 Problem Based Learning. | 40 | 19 | 40 |
| 01/2022 | University of British Columbia | MEDGEN 505 | 36 | 18 | 3 |
| 01/2021 | Simon Fraser University/ University of British Columbia | MBB505/ BIOF520 Problem Based Learning. | 40 | 30 | 40 |
| 01/2021 | University of British Columbia | MEDGEN 505 | 36 | 15 | 3 |
| 01/2020 | University of British Columbia | MEDGEN 505 | 36 | 15 | 3 |
| 01/2019 | University of British Columbia | MEDGEN 505 | 36 | 25 | 3 |
| 09/2018 | Simon Fraser University | MBB 440 Molecular Biology | 52 | 33 | 52 |
| 01/2018 | University of British Columbia | MEDGEN 505 | 3 | 15 | 3 |
| 08/2017 | Simon Fraser University/ University of British Columbia | MBB659/BIOF501A | 26 | 20 | 14 |

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|---|---|---|---|---|---|
| 01/2017 | Simon Fraser University/<br>University of British Columbia | MBB505/ BIOF520 Problem Based Learning. | 4 | 21 | 4 |
| 01/2017 | University of British Columbia | MEDGEN 505 | 3 | 15 | 3 |
| 10/2016 | Guest Lecturer<br>Simon Fraser University | MBB 438 Human Genetics | 2 | 80 | 2 |
| 09/2016 | Simon Fraser University/<br>University of British Columbia | MBB659/BIOF501A | 26 | 8 | 22 |
| 01/2016 | University of British Columbia | PBL in Bioinformatics | 4 | 12 | 4 |
| 01/2016 | University of British Columbia | MEDGEN 505 | 36 | 14 | 27 |
| 01/2015 | University of British Columbia | PBL in Bioinformatics | 4 | 14 | 4 |
| 01/2015 | University of British Columbia | MEDGEN 505 | 36 | 12 | 30 |
| 02/2014 | Simon Fraser University | MBB 435 Genome Biology | 2 | 27 | 2 |
| 01/2014 | University of British Columbia | PBL in Bioinformatics | 4 | 10 | 4 |
| 01/2014 | University of British Columbia | MEDGEN 505 | 36 | 20 | 33 |
| 06/2013 | Simon Fraser University | MBB 435 Genome Biology | 2 | 60 | 2 |
| 01/2013 | University of British Columbia | MEDGEN 505 | 36 | 18 | 30 |
| 01/2013 | University of British Columbia | PBL in Bioinformatics | 4 | 10 | 4 |
| 03/2012 | Simon Fraser University | MBB 446/746 | 2 | 50 | 2 |
| 01/2012 | University of British Columbia | MEDGEN 505 | 36 | 19 | 30 |
| 01/2012 | University of British Columbia | PBL in Bioinformatics | 4 | 10 | 4 |
| 01/2011 | University of British Columbia | MEDGEN 505 | 36 | 19 | 30 |
| 01/2011 | University of British Columbia | PBL in Bioinformatics | 4 | 10 | 4 |
| 11/2010 | Simon Fraser University | MBB 438 | 2 | 51 | 2 |
| 02/2010 | Simon Fraser University | MBB 440 | 2 | 52 | 2 |
| 01/2010 | University of Bristish Columbia | PBL in Bioinformatics | 4 | 9 | 4 |
| 01/2010 | University of British Columbia | MEDGEN 505 | 33 | 22 | 27 |
| 03/2009 | University of British Columbia | PBL in Bioinformatics | 2 | 12 | 2 |
| 02/2009 | University of British Columbia | PBL in Bioinformatics | 2 | 12 | 2 |
| 01/2009 | University of British Columbia | MEDGEN 505 | 3 | 21 | 3 |
| 01/2008 | University of Bristish Columbia | PBL in Bioinformatics | 4 | 15 | 4 |
| 01/2008 | University of British Columbia | MEDGEN 505 | 36 | 17 | 33 |
| 07/2007 | Canadian Bioinformatics Wkshp Lead Faculty Instructor - Genomics Vancouver 2007 | Genomics | n/a | n/a | n/a |
| 01/2007 | University of British Columbia | MEDGEN 505 | 36 | 18 | 30 |
| 05/2006 | Canadian Bioinformatics Workshop Lead Faculty Instructor - Genomics Vancouver 2006 | Genomics | n/a | n/a | n/a |

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|---|---|---|---|---|---|
| 01/2006 | University of British Columbia | MEDGEN 505 | 36 | 24 | 33 |
| 05/2005 | Canadian Bioinformatics Workshop Lead Faculty Instructor - Genomics Calgary 2005 | Genomics | n/a | n/a | n/a |
| 01/2005 | University of British Columbia | MEDGEN 505 | 36 | 20 | 33 |
| 08/2004 | Canadian Bioinformatics Workshop Lead Faculty Instructor - Genomics Vancouver 2004 | Genomics | n/a | n/a | n/a |
| 01/2004 | University of British Columbia | MEDGEN 505 | 36 | 30 | 36 |
| 08/2003 | Canadian Bioinformatics Workshop Instructor Lecturer - Genomics Calgary 2003 | Bioinformatics | n/a | n/a | n/a |
| 03/2003 | Simon Fraser University | MBB829 | 6 | 12 | 6 |
| 02/2003 | Canadian Bioinformatics Workshop Instructor Lecturer - Bioinformatics Vancouver 2003 | Bioinformatics | 3 | 50 | 3 |
| 10/2002 | Canadian Bioinformatics Workshop Panel Participant and Instructor Lecturer - Genomics Montreal 2002 | Genomics | n/a | n/a | n/a |
| 02/2002 | Canadian Bioinformatics Workshop Instructor Lecturer – Bioinformatics Vancouver 2002 | Bioinformatics | n/a | n/a | n/a |
| 01/2002 | University of British Columbia | MEDGEN 505 | 36 | 40 | 36 |
| 01/2001 | Canadian Bioinformatics Workshop Instructor Lecturer – Genomics Montreal 2001 | Genomics | n/a | n/a | n/a |
| 01/2001 | University of British Columbia | MEDGEN 505 | 36 | 53 | 36 |
| 01/2000 | Canadian Bioinformatics Workshop Instructor Lecturer – Genomics Vancouver 2000 | Genomics | n/a | n/a | n/a |

## SOCIETY MEMBERSHIPS:

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|---|---|---|
| 2013 | 2020 | Member, American Society of Hematology (ASH) |
| 2013 | 2020 | Member, American Association for Cancer Research (AACR) |
| 2009 | 2010 | Member, International Society for Computational Biology (ISCB) |
| 2006 | 2007 | Member, Canadian Society for Systems Biology (CSSB/SBSC) |
| 2006 | 2007 | Member, Association for Computing Machinery, Special Interest Group—Knowledge Discovery in Data |
| 2006 | 2006 | Member, International Society for Computational Biology (ISCB) |
| 2004 | 2004 | Member, International Society for Computational Biology (ISCB) |
| 1990 | 1992 | President, Simon Fraser University, Biology Graduate Student Society |

## COMMITTEE AND OTHER INVOLVEMENT:

| | | |
|---|---|---|
| 02/2024 | 03/2024 | Member, SickKids and CHU Sainte-Justine Precision Child Health Partnership (PCHP) Catalyst Program Adjudication Panel |
| 04/2023 | 05/2023 | Chair, Terry Fox Research Institute Marathon of Hope Cancer Centres Network, Review Committee for the Health Informatics & Data Science Competition |
| 12/2022 | Present | Member, Terry Fox Research Institute Marathon of Hope Cancer Centres Network, Steering Committee |
| 03/2022 | Present | Member, Medical Genetics (MEDG) Graduate Program Advisory Committee, UBC |

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| 2021 | Present | Member, CGEn Scientific Advisory Board, Canada's National Platform for Genome Sequencing & Analysis |
| 07/2021 | Present | Member, CRC Internal Review Committee, UBC |
| 05/2021 | Present | Member, BC COVID-19 Biobank Network (BCCBN) Scientific Review Committee |
| 12/2020 | Present | Member, Academy of Translational Medicine (ATM) Regulatory Advisory Council, UBC |
| 04/2020 | Present | Member, Precision Oncology Experimental Therapeutics (POET) Planning Committee |
| 2019 | Present | Co-Chair, Terry Fox Research Institute Marathon of Hope Cancer Centres Network, Data Policy and Standards Committee |
| 07/2017 | Present | Member, PROFYLE Executive Committee (PEC) |
| 03/2017 | Present | President & CEO, Ifowonco Informatics |
| 07/2012 | Present | Member, CIHR Canadian Epigenetic, Environment and Health Research Consortium (CEEHRC) |
| 10/2023 | 10/2023 | Session Chair, Precision Oncology Experimental Therapeutics (POET) Calgary, Alberta. AI in Cancer |
| 02/2023 | 02/2023 | Member, Canada Research Chairs Internal Review Committee, UBC |
| 05/2021 | 12/2022 | Member, CanCOGeN Data Sharing Committee, Genome Canada |
| 01/2021 | 12/2022 | Member, CanCOGeN Coordination Committee, Genome Canada |
| 01/2016 | 2022 | Member, Gairdner Medical Review Panel |
| 02/2009 | 03/2022 | Member, Genomic Sciences and Technology Graduate Program (GSAT), UBC |
| 03/2022 | 03/2022 | Participant, Opening Remarks, 2022 BIG Research day, 11th Annual Meeting, University of British Columbia, Vancouver, BC |
| 03/2022 | 03/2022 | Member, Canada Research Chairs Internal Review Committee, UBC |
| 11/2021 | 11/2021 | Session Chair, BC Cancer Summit, BC Cancer Research Stream, Virtual |
| 09/2021 | 09/2021 | Member, Canada Research Chairs Internal Review Committee, UBC |
| 10/2020 | 10/2020 | Session Chair, Pricision Oncology Experimental Therapeutics (POET) Virtual. Adoption of genomics for clinical decision making Across Canada |
| 02/2020 | 03/2020 | Member, Faculty of Medicine Killam Teaching Prizes Adjudication Committee, UBC |
| 05/2019 | 2020 | Reviewer, European EASI-Genomics Infrastucture, Sequencing & Bioinformatic Platforms |
| 12/2019 | 12/2019 | Member, Deutsche Forschungsgemeinschaft (DFG) "Medicine" Review Panel Bonn, Germany |
| 09/2019 | 2019 | Member, Bioinformatics & Machine Learning Recruitment Search Committee, Medical Genetics UBC/BC Cancer |
| 05/2019 | 2019 | Member, Search Committee, Computational Cancer, UBC |
| 09/2017 | 2018 | Member, Search Committee, Simon Fraser University, Cancer Biology Faculty Position |
| 03/2016 | 09/2018 | Member, Genome England-Genome BC Steering Committee. |
| 10/2016 | 09/2018 | Member, Population Sequencing Leadership Council Working Group (PLCWG) |
| 04/2018 | 04/2018 | Session Chair, Pricision Oncology Experimental Therapeutics (POET) Calgary, Alberta. Epigenetics as a Precision Biomarker in the Era of Immunotherapy |
| 01/2018 | 01/2018 | Participant and Panel Member, Life Sciences BC "Access to Innovation-Precision Health |
| 09/2017 | 11/2017 | Member, Terry Fox Research Institute (TFRI) New Investigator Review Committee |
| 09/2017 | 09/2017 | Participant, Genome Canada, Rare Disease and Implementation of Genomics in the Healthcare System, Ottawa, ON |
| 06/2017 | 06/2017 | Participant and **Keynote Speaker,** Cancer Genomics CBW Workshop, Toronto, ON |
| 05/2017 | 05/2017 | Participant and Invited Speaker, Canadian Foundation for Innovation Workshop and Princess Margaret Cancer Centre, Toronto, ON |
| 04/2017 | 04/2017 | Participant and Session Chair, Precision Oncology Exerimental Therapeutics (POET), Calgary, Alberta |
| 07/2013 | 2017 | Member, Research Advisory Committee, The Pancreas Centre BC |
| 12/2016 | 12/2016 | Participant and **Keynote Speaker**, Functional Genomics Symposium, Doha, Qatar |

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| 10/2016 | 10/2016 | Participant, Roundtable Research Leaders Discussion, Genome BC, Vancouver, BC |
| 10/2016 | 10/2016 | Participant, American Society of Human Genetics (ASHG), Vancouver, BC |
| 10/2016 | 10/2016 | Participant and Invited Speaker, Global Alliance for Genomics and Health, Vancouver,BC |
| 10/2016 | 10/2016 | Participant and Presenter, BioCanRx Board of Directors Meeting, Vancouver, BC |
| 09/2016 | 09/2016 | **Keynote Speaker**, Seven Bridges Graph Genome Day, London, UK |
| 09/2016 | 09/2016 | Participant, European Commission Workshop & The Blueprint/IHEC Conference, Brussels, Belgium |
| 07/2016 | 07/2016 | Participant, IEEE World Congress on Computational Intelligence Conference, Vancouver, BC |
| 06/2016 | 06/2016 | Participant and Presenter, Pediatric Oncology Conference, Vancouver, BC |
| 06.2016 | 06/2016 | Participant and Invited Speaker, Summit for Cancer Immunotherapy Conference, Halifax, Nova Scotia |
| 05/2016 | 05/2016 | Particpant, Terry Fox Research Institute (TFRI) Annual Scientific Meeting, Vancouver,BC |
| 05.2016 | 05/2016 | Participant and **Keynote Speaker**, 1st Annual Canadian Computational Biology Conference, Toronto, Ontario |
| 05/2016 | 05/2016 | Member, Peter Wall Theme Development Workshop Application, Calgary, Alberta |
| 03/2016 | 03/2016 | Participant, Science and Industry Advisory Committee (SIAC), Genome BC, Vancouver |
| 12/2015 | 12/2015 | Member, Peer Review Panel, Genetics Networks Program, Canadian Institute for Advanced Research (CIFAR) |
| 04/2015 | 07/2016 | Member, Local organizing committee, International Union of Biochemistry & Molecular Biology (IUBMB) |
| 02/2016 | 02/2016 | Session Chair, Advances in Genome Biology & Technology, Orlando, Florida |
| 01/2016 | 01/2016 | Session Chair, Computational Epigenomics, Epigenomics Conference, San Juan, Puerto Rico. |
| 01/2016 | 01/2016 | Panel Member, Shaping the Furture of Health, BCTECH Summit, Vancouver, BC. Moderator: Honourable Terry Lake, Minister of Health |
| 2012 | 2016 | Member, Biocomputing Scientific Advisory Board, Ontario Institute for Cancer Research |
| 02/2015 | 02/2015 | Participant, 10th Scientific Workshop of the International Cancer Genome Consortium (ICGC), Verona, Italy |
| 08/2011 | 12/2014 | Member, Scientific Advisory Board, Genome Alberta Bovine Genomics |
| 11/2013 | 10/2014 | Organizing Member, 2014 IHEC Symposium, Vancouver, BC |
| 06/2014 | 06/2014 | Participant, Genome Canada/CIHR Bioinformatics and Computational Biology Strategy Committee Meeting, Toronto, Ontario |
| 11/2013 | 11/2013 | Participant and Invited Speaker, EMBL Conference on Cancer Genomics, Heidelberg, Germany |
| 11/2013 | 11/2013 | Participant and Invited Speaker, IHEC Symposium, Berlin, Germany |
| 10/2013 | 10/2013 | Participant, IBM Research, Genomic Medicine Strategic Meeting, NY, NY |
| 07/2013 | 07/2013 | Participant, FSHD Genomics & Epigenomics Workshop, FHCRC, Seattle, Washington |
| 06/2013 | 06/2013 | Participant, Conifer Genome Sequencing Summit, Bjorkliden, Lapland, Sweden |
| 02/2013 | 02/2013 | Member, FOM, UBC Killam Teaching Prize Adjudication Committee |
| 01/2013 | 01/2013 | Participant & Speaker, McGill University, Systems Biology Workshop, Barbados |
| 01/2013 | 01/2013 | Session Chair, Genomic Applications, APBC, Vancouver, BC 2013 |
| 01/2013 | 01/2013 | Session Chair, **Keynote address**, APBC, Vancouver, BC, 2013 |
| 01/2012 | 01/2013 | Organizer, 11th Asia Pacific Bioinformatics Conference, Vancouver, BC, 2013 |
| 04/2006 | 01/2012 | Member, AGBT, Scientific Advisory Committee, Marco Island, Florida |
| 09/2012 | 09/2012 | Paticipant, International Human Epigentics Consortium, Seoul, Korea 2012 |
| 06/2012 | 06/2012 | Session Chair, 1st International Conference on Integrative Salmonid Biology, Oslo Norway |

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|---|---|---|
| 01/2012 | 01/2012 | Session Chair, Keynote 2, APBC 2012, Melbourne, Australia |
| 01/2012 | 01/2012 | Panel Member, Bioinformatics: Current Stratagies and Future Directions, APBC 2012, Melbourne, Australia |
| 11/2011 | 11/2011 | Session Chair, CSHL: Genome Informatics, CSHL, NY |
| 10/2011 | 10/2011 | Participant and Invited Speaker, Next-generation Sequencing Technology & Algorithms for Primary Data Analysis Workshop, IPAM, UCLA, Los Angeles, CA |
| 09/2011 | 09/2011 | Participant and Invited Speaker, CIHR Personalized Medicine Workshop, Luxembourg |
| 06/2011 | 06/2011 | iDEA Challenge Conference (Illumina's Data Excellence Award) San Diego, CA |
| 05/2011 | 05/2011 | iDEA Challenge Judging Meeting (Illumina's Data Excellence Award) Alexandria, VA |
| 04/2011 | 04/2011 | Review Panel Member, Alberta Innovates Health Solutions Grant Review Committee, Edmonton, AB |
| 03/2011 | 03/2011 | Invited Presenter: Student Biotechnology Network (SBN), Vancouver, BC. Title: "Next Generation Bioinformatics" |
| 01/2009 | 01/2011 | Member, International Cancer Genome Consortium (ICGC) Data Coordination and Management Working Group |
| 12/2010 | 12/2010 | Participant, 3rd Next Generation Sequencing Hinxton Retreat Workshop, Hinxton, UK |
| 11/2010 | 11/2010 | Invited Presenter: Year of Science, Vancouver, BC. Title: "The road to personalized medicine: the right treatment for the right person at the right time" |
| 09/2010 | 09/2010 | Co-Chair, CSHL, Personal Cancer Genomes, CSHL, NY |
| 07/2010 | 07/2010 | Committee Member, Illumina Sequencing Expert Panel, Toronto, Ontario |
| 06/2010 | 06/2010 | Chair, CIHR Emerging Team Grant Peer Review Committee, Ottawa |
| 05/2010 | 05/2010 | Panel Member, Genome BC Genomics Forum 2010, Vancouver, BC |
| 06/2009 | 06/2009 | Chair, CIHR Catalyst Grant:Bioinformatics Competition, Ottawa |
| 05/2009 | 05/2009 | Panel Member, Genome Canada Data Release Workshop, Toronto |
| 03/2009 | 03/2009 | Panel Member, High-Thruput Sequencing (HTP) Meeting, Medical Research Council, UK |
| 10/2008 | 10/2008 | Participant, CCRA/CPAC International Cancer Genome Consortium Workshop, Toronto |
| 04/2008 | 04/2008 | Ad-hoc Member, Genome Institute of Singapore External Scientific Review Committee |
| 04/2008 | 04/2008 | Participant, Genome Canada Cancer Stem Cell Workshop, Toronto |
| 04/2008 | 04/2008 | Participant & Speaker, McGill University rSNP's Workshop, Barbados |
| 05/2007 | 05/2007 | Co-Chair, 12th Human Genome Meeting, Human Genome Organization, Montreal, Qu. |
| 01/2007 | 02/2007 | Review Panel Member, Joint Genome Institute, Walnut Creek, California |
| 09/2002 | 01/2007 | Member, University of British Columbia, UBC Bioinformatics Centre (UBiC) Steering Committee |
| 04/2006 | 12/2006 | Member, Scientific Organizing Committee, The RegCreative Jamboree, Ghent, Belgium |
| 12/2004 | 12/2006 | Reviewer, MSFHR, Biomedical Research Committee |
| 11/2006 | 11/2006 | Review Panel Member, Research Initiatives Program, Alberta Cancer Board |
| 11/2002 | 11/2006 | Member, CIHR, Institute of Genetics Bioinformatics Priority and Planning Committee |
| 07/2003 | 07/2006 | Member, CIHR, Genomics Grants Committee |
| 06/2004 | 06/2006 | Member, BC Cancer Agency, Tumour Tissue Repository Governing Board |
| 08/2004 | 05/2006 | Lead Faculty Instructor, Annual Canadian Bioinformatics Workshops (CBW) |
| 06/2002 | 05/2006 | Member, University of British Columbia, Medical Genetics Graduate Program Advisory Committee |
| 02/2002 | 05/2006 | Core Faculty Member, Canadian Bioinformatics Workshops (CBW) |
| 01/2000 | 05/2006 | Instructor Lecturer, Annual Canadian Bioinformatics Workshops (CBW) |
| 01/2004 | 01/2006 | Member, Genome BC, Scientific Advisory Committee |
| 11/2005 | 11/2005 | Participant & Speaker, Wellcome Trust & EBI, Cis-Regulation Workshop |
| 10/2005 | 10/2005 | Participant & Speaker, International cGRASP Workshop |
| 05/2005 | 05/2005 | Member, Genome BC, BC Proteomics Network Research Committee |
| 05/2004 | 05/2005 | Member, OHRI, International Regulome Consortium |

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|---|---|---|
| 04/2005 | 04/2005 | Panelist, Genome BC, Technology Development Panel, Genomics Forum 2005 |
| 03/2005 | 03/2005 | Participant & Speaker, Genome Canada (ICI) & University of British Columbia, Joint Workshop on Wine Genomics |
| 03/2004 | 03/2005 | Member, BCNET, Committee for Development of HPC in BC |
| 06/2004 | 01/2005 | Member, National Consultation on Access to Scientific Research Data (NCASRD), Task Force |
| 05/2004 | 05/2004 | Participant, BC Cancer Agency, Roundtable with Prime Minister Martin |
| 10/2002 | 05/2004 | Member, BC Cancer Agency, Tumour Tissue Repository Development Committee |
| 06/1999 | 05/2004 | Member, Simon Fraser Univeristy Alumni Association, Board of Directors |
| 02/2004 | 02/2004 | Reviewer, International Conference on Intelligent Systems for Molecular Biology (ISMB) |
| 10/2003 | 01/2004 | Search Committee Member, Simon Fraser University, Vice President Research |
| 12/2003 | 12/2003 | Participant, CIHR, First Annual Workshop of CIHR Training Programs |
| 12/2003 | 12/2003 | Invited Speaker, CIHR, Institute Advisory Board Meeting |
| 12/2003 | 12/2003 | Participant, Genome Canada, Modelling and Computational Biology Workshop |
| 02/2002 | 12/2003 | Member, BC Cancer Research Centre, Patent Committee |
| 11/2003 | 11/2003 | Panelist, BCNET/NewMIC, Breakfast Panel Discussion |
| 10/2003 | 11/2003 | Member, Canadian Foundation for Innovation (CFI), Multidisciplinary Advisory Committee |
| 10/2003 | 10/2003 | Speaker, Genome BC, Public Forums “Who’s Got Their Hands On My Genes?” |
| 09/2003 | 09/2003 | Roundtable on Genetic Information and Privacy, Industry Canada |
| 03/2003 | 03/2003 | Invited Speaker, Simon Fraser University, Dean’s Science Reception |
| 03/2003 | 03/2003 | Session Chair, Cold Spring Habour Laboratory, Genome Informatics, CSHL, NY |
| 02/2003 | 02/2003 | Session Chair, Advances in Genome Biology & Technology Conference, Automation in DNA Mapping and Sequencing, Marco Island, Florida, USA |
| 02/2003 | 02/2003 | Participant, CIHR, Gene Environment Initiative |
| 12/2001 | 01/2003 | Member, CIHR, Institute of Genetics Career Transition Awards Peer Review Committee |
| 12/2002 | 12/2002 | New Frontiers: Italian/Canadian Genomic Population Genetics and Bioinformatic Collaborations Conference |
| 11/2002 | 11/2002 | Panel Participant, BCNET/NewMIC, Breakfast Panel Discussion |
| 2000 | 2000 | NIH/NHGRI sub-committee for computational and analytical issues for the sequencing of the mouse genome |
| 2001 | 2001 | Joint workshop on bioinformatics, CIHR (Genetics) & Genome Canada |
| 2001 | 2001 | Search Committee Member, Simon Fraser University, Vice President Research |
| 2001 | 2002 | Tumour Tissue Repository Steering Committee, BC Cancer Agency |

## EDITORIAL RESPONSIBILITIES:

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|---|---|
| 02/2014- Present | Editor, *CSH Molecular Case Studies* |
| 2004 - Present | Member, Editorial Board, *Genome Research* |
| 1999 – Present | Reviewer, *Bioinformatics* |
| 1999 – Present | Reviewer, *Genome Research* |

## PUBLIC OUTREACH/SERVICE:

| | |
|---|---|
| 08 Mar 2024 | Zoom interview with Mariella Bodemeier Loayza Careaga of The Scientist Magazine re. ChIP Seq. |
| 21 Feb 2018 | Phone interview w/Karina Dill, 10xgenomics. https://community.10xgenomics.com/t5/10x-Blog/Reference-Quality-genome-assemblies-for-conservation-biology/ba-p/805 |
| 03 Jan 2018 | Phone interview w/Beatrice Riche, www.whalesonline.org (GREMM) . http://baleinesendirect.org/genome/ |

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|---|---|
| 11 Dec 2017 | On camera interview w/Linda Aylesworth, Global TV Re: Beluga and Otter Genomes. https://globalnews.ca/video/3910868/researchers-mapping-beluga-whale-genome-for-the-first-time |
| 29 Sept 2017 | On camera interview w/Laura Tretheway, Vancouver Aquarium Re: Beluga Sequencing . https://ocean.org/stories/beluga-genome/#cover |
| 17 Jan 2017 | Picchoine Lecture Series, Halifax Public Library, Halifax, Nova Scotia. January 17, 2017. "Genome sequencing for the improvement of cancer diagnosis and treatment", talk and panel discussion. |
| 02 Oct 2015 | Phone interview w/Jackie Amsden. **Simon Fraser University's 50 Inspiring Alumni**. https://www.sfu.ca/dean-gradstudies/blog/year/2015/09/StevenJones-MBB.html |
| 29 Jun 2015 | Phone interview w/Pamela Feyerman of the Vancouver Sun re: Can a computer select the best cancer treatment? https://shar.es/1txxAN; https://shar.es/1tyARs |
| 15 June 2015 | Live telephone interview w/Pamela McCall of CFAX Radio, Victoria re: Genomics Network. https://soundcloud.com/pamela-mccall-cfax/june-15-10am?in=pamela-mccall-cfax/sets/pamela-mccall&utm_source=soundcloud&utm_campaign=share&utm_medium=email |
| 28 May 2015 | Telephone interview w/Ivan Semeniuk of The Globe and Mail re: CFI CGen Project. Published on Saturday May 30th Globe and Mail Page A13.<br>PDF<br>Genes, isotopes & oil spills.pdf |
| 07 May 2015 | Telephone interview w/Jackie Amsden, Graduate Student Engagement Office, SFU re "Department of Molecular Biology and Biochemistry nomination as their most inspiring graduate student over the past 50 years." |
| 02 Mar 2015 | Telephone interview w/Micaela Evans of "The Peak" Newpaper at SFU re: Researchers map genes to better treat cancer. http://temporary-the-peak.ca/researchers-map-genes-to-better-treat-cancer/ |
| 20 Feb 2015 | Telephone interview w/Tereza Verenca of "Burnaby Now" Newspaper re: Massive scientific road map. http://www.burnabynow.com/news/sfu-researcher-and-co-reveal-massive-scientific-road-map-1.1770029 |
| 01 Nov 2014 | Telephone interview w/Pamela Fayerman of The Vancouver Sun re: Mystery Revealed. https://shar.es/1txxVx |
| 14 Jul 2014 | Telephone interview w/Amanda Smith of "The Peak" Newspaper at SFU re: SFU Scientists recognized as "World's Most Influential Scientific Minds" by Thomson Reuters. . http://www.the-peak.ca/2014/07/sfu-scientists-recognized-as-worlds-most-influential-scientific-minds/ |
| 04 Jul 2014 | Mentioned by Ivan Semeniuk of The Globe & Mail re: Examining Canada's Scientific Footprint. Read this on The Globe and Mail |

## CONTRIBUTIONS TO THE TRAINING OF HIGHLY QUALIFIED PERSONNEL:

**PhD Graduate Students: 4 current students, 20 over career**
**MD and PhD/MD Graduate Students: 0 current students, 3 over career**
**MSc Graduate Students: 3 current, 16 over career**

| **Name** | **Mo/Year** | **Mo/ Year** | **Degree** | **Current Position** |
|---|---|---|---|---|
| Riya Saju<br>**Title:** RapidOmics 2.0 project, title TBC<br>(Co-supervisor with Jan Friedman) | 09/2023 | Present | MSc, UBC (Bioinformatics) | Graduate Student |

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|---|---|---|---|---|
| Andrew Galbraith<br>**Title:** Genome-Wide Detection of DNA Hydroxymethylation in Various Cancer Types Using Nanopore Sequencing | 09/2022 | Present | MSc, UBC (Bioinformatics) | Graduate Student |
| Faeze Keshavarz Rahaghi<br>**Title**: Using machine learning to identify active and druggable pathways in metastatic cancers through reference-free pathway analysis | 09/2020 | Present | PhD, UBC (Bioinformatics) | Graduate Student |
| Sarah Dada<br>**Title**: Integration of genomic and phenomic data for precision diagnosis and treatment within Autism Spectrum Disorder | 09/2020 | Present | PhD, UBC (Bioinformatics) | Graduate Student |
| Caralyn Reisle<br>**Title**: Automatic Text Summarization of Genomic Findings for a Targeted Audience using Machine Learning | 09/2020 | Present | PhD, UBC (Bioinformatics) | Graduate Student |
| Yerin Kim<br>**Title:** Nanopore-based native RNA sequencing of human transcriptomes reveals the complexity of mRNA modifications and crosstalk between RNA regulatory features (Co-supervisor with Ly Vu) | 01/2022 | 04/2024 | MSc, UBC (Bioinformatics) | Graduate Student |
| Glenn Chang<br>**Title**: Allele specific expression in human cancer | 01/2022 | 12/2023 | MSc, UBC (Bioinformatics) | Graduate Student |
| Zheming (Jeremy) Fan<br>**Title:** Structural Variant Calling and Resolution from Long Reads Sequencing Data | 09/2020 | 01/2024 | MSc, UBC (Bioinformatics) | Graduate Student |
| Tyler Kolisnik<br>**Title:** A Machine Learning Approach to Deciphering Novel Genomic and Microbial Features in Colorectal Cancer<br>(Co-supervisor with Olin Silander) | 09/2020 | 10/2022 | PhD, Massey University NZ | Graduate Student |
| Vahid Akbari<br>**Title:** Detecting DNA Methylation Using Nanopore Sequencing: From Genome-Wide Analysis to Haplotype-Resolved and Parent-of-Origin Phasing | 07/2019 | 12/2023 | PhD, UBC (Medical Genetics) | Graduate Student |
| Michael Disyak<br>**Title**: A Hierarchical Neural Network Approach to Pan-Cancer Classification | 09/2019 | 02/2021 | MSc, UBC | Graduate Student |
| Luka Culibrk<br>**Title:** Copy number variation in metastatic cancer: methods and analysis of somatic copy number variation in advanced human cancers | 09/2017 | 04/2024 | PhD, UBC (Bioinformatics) | Graduate Student |
| Jasleen Grewal<br>**Title:** Developing machine learning methods for using transcriptomic data to discriminate between tumour types | 08/2015 | 01/2021 | PhD, UBC | Post Doctoral Fellow Genome Sciences Centre |

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|---|---|---|---|---|
| Jenny Yang<br>**Title**: Machine-learning and image analysis in general tumour identification and prediction of therapeutically informative genomic events from cancer biopsies | 05/2019 | 09/2020 | MSc, UBC | Bioinformatics, Fusion Genomics |
| Emre Erhan<br>**Title:** An integrative machine learning approach for predicting metastatic cancer patient response to cancer therapies | 08/2018 | 08/2020 | MSc, UBC | Software Engineer, 10x Genomics |
| Harwood Kwan<br>**Title:** Investigating the non-coding mutational landscape and treatment associated mutations of treated metastatic cancers. | 05/2018 | 03/2020 | MSc, UBC | Research Programmer, Genome Sciences Centre |
| My Linh Thibodeau (Medical Resident)<br>**Title**: Whole genome and whole transcriptome genomic profiling of a metastatic eccrine porocarcinoma | 07/2016 | 10/2019 | MD, UBC | Staff Physician, Dept Pediatrics, Sick Kids |
| Kevin Fan<br>**Title:** Tumour-immune landscape and response to checkpoint inhibitors in diverse metastatic cancers | 04/2018 | 05/2019 | MD/PhD, UBC | Medical Student, UBC |
| Jake Lever<br>**Title:** Building and Inferring Knowledge Bases Using Biomedical Text Mining | 05/2014 | 09/2018 | PhD, UBC | Lecturer at University of Glasgow, UK |
| Eric Zhao<br>**Title:** Searching for targettable mutation signatures in human cancer | 08/2013 | 06/2018 | MD/PhD, UBC | Radiation Oncology Postgraduate resident, U of T |
| Celia Siu<br>**Title:** Characterization of the normal reference thyroid epigenome | 08/2015 | 02/2017 | MSc, UBC | Data Engineer, Visier, Inc, Vancouver |
| Santina Lin<br>**Title:** Identifying Relevant Biomedical Papers with Latent Semantic Analysis | 08/2015 | 02/2017 | MSc, UBC | Software Engineer, Microsoft, Bellevue, WA |
| Daryanaz Dargahi<br>**Title:** Development of Therapeutic Approaches to Human Breast Cancer Using Mouse Models | 09/2011 | 11/2016 | PhD, SFU | Associate Scientist in Bioinformatics, Zymeworks Inc, Vancouver |
| Shing Zhan<br>**Title:** Ultradeep population-level sequencing of mutant Caenorhaditis elegans | 09/2011 | 03/2016 | PhD, UBC | Lead Bioinformatics Scientist, Biodiversity Research Centre, UBC |
| Katayoon Kasaian<br>**Title:** Genomics of Thyroid Cancer | 09/2009 | 09/2015 | PhD, UBC | Post Doctoral Fellow, The Ontario Institute for Cancer, Toronto |
| Anthony Fejes<br>**Title:** The development and application of algorithms for interpreting next-generation Solexa sequencing data: creation of a genome-wide breast cancer mutation map. | 10/2006 | 03/2012 | PhD, UBC | Co-Founder & CEO, HTuO Biosciences, Vancouver, BC |

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|---|---|---|---|---|
| Yvonne Li<br>**Title:** Drug-target interaction maps for computational drug repositioning discovery | 01/2006 | 11/2011 | PhD, UBC | Post Doctoral Fellow, Dana Farber Cancer Institute |
| Denil Wickrama<br>**Title:** ChIP-seq analysis of SATB1, a metastatic chromatin remodeller | 09/2008 | 02/2011 | MSc | Unknown |
| Adam Hall<br>**Title:** Custom Hardware for Solexa/Illumina DNA Short-Read Sequence Alignment | 09/2008 | 11/2010 | MSc, UBC | Uknown |
| Elizabeth Chun<br>**Title:** Toward personalized immunotherapy: identifying tumour-specific factors that dictate the response of spontaneous mammary cancers to different T-cell therapies | 08/2007 | 08/2010 | MSc, UBC | PhD Graduate Student, Marra Lab, BC Cancer |
| Heesun Shin, co-supervised w. David Baillie<br>**Title:** Transcriptome analysis for C. elegans based on expressed sequence tags (ESTs) | 09/2004 | 06/2010 | PhD, SFU | Product Manager, Thermo Fisher Scientific, San Francisco |
| Ben (Binhua) Liang, co-supervised w. Frank Plummer<br>**Title**: Evolution of Human Immunodeficiency Virus Type-1 Envelope Gene | 09/2005 | 02/2010 | PhD, U of Manitoba | Senior Biologist and Head of Viral Bioinformatics, National Microbiology Laboratory, Public Health Agency of Canada |
| Monica Sleumer<br>**Title:** The search for novel regulatory elements in C.elegans | 09/2003 | 07/2009 | PhD, UBC | Senior Research Scientist, Novo Nordisk, Beijing, China |
| Obi Griffith<br>**Title:** Identification of gene regulatory changes involved in cancer progression by gene expression studies and bioinformatic analyses | 09/2003 | 04/2008 | PhD, UBC | Assistant Professor of Medicine, Division of Oncology , Assistant Director, McDonnell Genome Institute Washington University School of Medicine |
| Adrian Quayle<br>**Title:** Application of biological networks to cancer therapy | 01/2005 | 10/2006 | PhD, UBC | Unknown |
| Stephen Montgomery<br>**Title:** Computational Identification of Genetic Variation in Gene Regulatory Networks | 09/2002 | 09/2006 | PhD, UBC | Assistant Professor & Director of Genome Informatics, Dept. Pathology, Stanford University, California |
| Erin Pleasance<br>**Title:** Identification & analysis of programmed cell death genes in Drisophila Melanogaster and human cancer using bioinformatic analysis of gene expression**.** | 05/2000 | 12/2005 | PhD, UBC | Staff Scientist, Genome Sciences Centre |

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|---|---|---|---|---|
| Angelique Schnerch, co-supervised w. M. Marra<br>**Title:** Global gene expression profiling in human embryonic stem cells | 09/2001 | 12/2005 | MSc, UBC | Unknown |
| Michael Thorne<br>**Title:** Transcriptional regulation & C. elegans in silico | 07/1999 | 09/2001 | MSc, UBC | Unknown |

**Post-doctoral Fellows: 0 Current Post Doc, 19 over career**

| **Area** | **Name** | **Mos/Years** | **Mos/Years** | **Current Position** |
|---|---|---|---|---|
| Genomics and epigenomics, Hereditary cancer, Rare disorders | Vahid Akbari | 01/2024 | Present | Postdoctoral Fellow |
| Developing subtype-level cancer classifiers using multi-omics data | Jasleen Grewal | 01/2021 | 04/2022 | Senior Applied Scientist, NVIDIA |
| Defining the landscape of genetic and epigenetic variation in cancer predisposition syndromes using nanopore long-read sequencing | Katherine Dixon | 12/2020 | 09/2023 | Postdoctoral Fellow, BC Children's and Women's |
| Integrated transcriptomic technologies to improve upon RNA expression | Jean-Michel Garant | 07/2019 | 12/2020 | Research Associate, Genome Sciences Centre |
| Oxford Nanopore Sequencing for Cancer Diagnosis | Kieran O'Neill | 10/2018 | 03/2020 | Research Associate, Genome Sciences Centre |
| Preclinical studies of small molecule modulators for KMT2D mutant lymphoma | Sreeja Leelakumari | 02/2013 | 01/2019 | Research Associate, Genome Sciences Centre |
| Bioinformatics | Jahanshah Ashkani | 01/2017 | 05/2019 | Research Associate, Genome Sciences Centre |
| Integration of the CIViC knowledgebase into the Personalized OncoGenomics program | Cameron Grisdale | 05/2017 | 05/2019 | Research Associate, Genome Sciences Centre |
| Bioinformatics | Pinaki Bose | 09/2013 | 07/2015 | Director, Tumour Biology and Translational Research, Ohlson Research Initiative Arnie Charbonneau Cancer Institute Departments of Biochemistry & Molecular Biology and Surgery University of Calgary |

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|---|---|---|---|---|
| Bioinformatics | Yaoqing Shen | 01/2012 | 05/2014 | Staff Scientist, Genome Sciences Centre |
| Bioinformatics | Alexander Yakovenko | 09/2009 | 01/2014 | Data Solutions Developer at CONCURED Vancouver |
| Bioinformatics | Yvonne Li | 12/2011 | 08/2013 | Post Doctoral Fellow, Dana Farber Cancer Institute |
| Bioinformatics | Cydney Nielsen | 09/2008 | 06/2013 | Research Associate, Department of Pathology, University of British Columbia |
| Bioinformatics | Athanasios Zovoilis | 08/2011 | 07/2012 | Canada Research Chair in RNA Bioinformatics and Genomics<br>Dept. of Chemistry and Biochemistry<br>Dept. of Neuroscience<br>University of Lethbridge |
| Bioinformatics | Obi Griffith | 04/2008 | 03/2010 | Assistant Professor of Medicine, Division of Oncology Assistant Director, McDonnell Genome Institute Washington University School of Medicine |
| Bioinformatics | Nawar Malhis | 09/2007 | 03/2009 | Research Associate, Michael Smith Labs, University of British Columbia |
| Bioinformatics | Peter Ruzanov | 11/2001 | 11/2006 | Scientific Associate at Ontario Institute for Cancer Research |
| Bioinformatics | Erin Pleasance | 01/2006 | 04/2006 | Staff Scientist, Genome Sciences Centre |
| Pathogenomics | Artem Tcherkassov | 04/2001 | 01/2003 | Senior Research Scientist, Vancouver Prostate Centre Professor, Dept. of Urologic Sciences, University of British Columbia; Adjunct Professor, Computer Science, Simon Fraser University |

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|---|---|---|---|---|
| Bioinformatics | Hans Greberg | 03/2000 | 12/2000 | Informatics Scientist, AstraZeneca, Sweden |

**Computational Biologists: 0 Current Computational Biologist**

| Area | Name | Mos/Years | Mos/Years |
|---|---|---|---|
| Bioinformatics - CP | Sitanshu Gakkhar | 09/2012 | 10/2022 |

**Research Programmers: 1 Current Research Programmer**

| Area | Name | Mos/Years | Mos/Years |
|---|---|---|---|
| Bioinformatics /Jones Lab – RP | Javier Castillo-Arnemann | 02/2022 | Present |
| Bioinformatics /Jones Lab - RP | Courtney Gosselin | 05/2021 | 01/2022 |
| Bioinformatics /Jones Lab - RP | Jimmy Li | 05/2018 | 05/2022 |
| Bioinformatics /Jones Lab - DO | Amir Muhammadzadeh | 11/2018 | 12/2019 |
| Bioinformatics /Jones Lab - RP | Adam Lipski | 04/2018 | 10/2019 |
| Bioinformatics /Jones Lab - RP | Neelam Memon | 01/2017 | 01/2018 |

**Team Lead, Purchasing: 0**
**Head, Knowledge Translation: 0**
**Systems Manager/ Research Projects Manager: 1**

| Area | Name | Mos/Years | Mos/Years |
|---|---|---|---|
| Team Lead, Purchasing | George Yang | 01/2022 | 07/2022 |
| Head, Knowledge Translation | Kevin Sauve | 01/2022 | 06/2022 |
| Systems Manager/ Research Projects Manager | Brendan O'Huiginn | 2021 | Present |

**Research Associates: 1 Current; 15 Research Associates over Career**

| Area | Name | Mos/Years | Mos/Years |
|---|---|---|---|
| Bioinformatics | David Mulder | 11/2023 | Present |
| Bioinformatics | Solenne Correard | 10/2022 | 12/2023 |
| Bioinformatics | Samantha Jones | 08/2021 | 08/2022 |
| Bioinformatics /Clinical Informatics | Chandra Lebovitz | 05/2021 | 09/2022 |
| Bioinformatics | Rohan Abraham | 04/2021 | 05/2023 |
| Bioinformatics | Jean-Michel Garant | 12/2020 | 10/2022 |
| Bioinformatics /Clinical Informatics | Sreeja Leelakumari | 01/2019 | 01/2022 |
| Bioinformatics /Clinical Informatics | Jahanshah Ashkani | 05/2019 | 09/2021 |
| Bioinformatics /Clinical Informatics | Zoltan Bozoky | 09/2017 | 05/2020 |
| Bioinformatics /Clinical Informatics | Yvonne (Yuk Yin) Lai | 01/2016 | 01/2017 |
| Bioinformatics /Clinical Informatics | Martin Jones | 05/2014 | 07/2016 |
| Bioinformatics /Clinical Informatics | Yaoqing Shen | 05/2014 | 07/2016 |
| Bioinformatics /Clinical Informatics | Erin Pleasance | 02/2010 | 07/2016 |
| Bioinformatics /Clinical Informatics | Alexander Yakovenko | 01/2014 | 12/2015 |
| Bioinformatics /Clinical Informatics | Brad Davis | 11/2012 | 03/2015 |

**Staff Scientists: 9 Current Research Scientist, 15 over career**

| Area | Name | Mos/Years | Mos/Years |
|---|---|---|---|
| Bioinformatics | Samantha Jones | 08/2022 | Present |
| Bioinformatics /Clinical Informatics | Sreeja Leelakumari | 01/2022 | Present |
| Bioinformatics | Kieran O'Neill | 05/2020 | Present |
| Sequencing (Group Leader) | Richard Moore | 2019 | 05/2023 |
| Bioinformatics /Clinical Informatics | Laura Williamson | 04/2018 | 05/2023 |

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|---|---|---|---|
| Bioinformatic Databases (Group Leader) | Eric Chuah | 2018 | Present |
| Bioinformatic Analysis (Group Leader) | Karen Mungall | 2018 | Present |
| Group Leader-Clinical Genetics | Yaoqing Shen | 07/2016 | Present |
| Bioinformatics /Clinical Informatics | Erin Pleasance | 07/2016 | Present |
| Bioinformatics | Misha Belinky | 03/2005 | Present |
| Bioinformatics | Jianghong An | 06/2005 | Present |
| Bioinformatics | Gordon Robertson | 10/2002 | 11/2021 |
| Bioinformatics | Yussanne Ma | 01/2013 | 06/2018 |
| Bioinformatics /Clinical Informatics | Martin Jones | 07/2016 | 04/2018 |
| Bioinformatics | Inanc Birol | 01/2008 | 01/2013 |

**Mentor for CIHR Bioinformatic Training Program Students**

| Name | Mo/Year | MosYear | Degree | Supervisor |
|---|---|---|---|---|
| Rashedul Islam | 09/2014 | 11/2021 | PhD | Martin Hirst |
| Shaun Jackman | 09/2012 | 06/2019 | PhD | Inanc Birol, GSC |
| Tyler Funnell | 09/2014 | 08/2018 | PhD | Sohrab Shah, BCCRC |
| Raunak Shrestha | 09/2011 | 07/2018 | PhD | Colin Collins, Prostate Centre, VGH |
| Rodrigo Goya | 09/2009 | 11/2017 | PhD | Marco Marra |
| Michael Gottlieb | 09/2014 | 12/2016 | MSc | Aly Karsan, GSC |
| Bhav Khaira | 09/2009 | 09/2016 | PhD | Fiona Brinkman, SFU |
| Dean Attali | 09/2013 | 04/2016 | MSc | Jenny Bryan, UBC |
| Michael Peabody | 09/2010 | 04/2016 | PhD | Fiona Brinkman, MBB, SFU |
| Casper Shyr | 09/2010 | 04/2016 | PhD | Wyeth Wasserman, CMMT, UBC |
| Emilia Lim | 09/2010 | 03/2016 | PhD | Marco Marra, GSC, BCCA |
| Sohrab Saheli | 09/2013 | 12/2015 | MSc | Sohrab Shah & Alex Bouchard, BCCRC & UBC |
| Andrew Roth | 09/2009 | 11/2015 | PhD | Sohrab Shah, BCCA |
| Andrew McPherson | 09/2009 | 07/2015 | PhD | David Huntsman |
| Calvin Lefebvre | 09/2011 | 05/2015 | MSc | Sohrab Shah, BCCRC, BCCA |
| Sarah Perez | 09/2012 | 05/2015 | MSc | Steve Hallam, UBC |
| Tyler Funnel | 09/2011 | 12/2014 | MSc | Sohrab Shah, BCCRC, BCCA |
| Gavin Ha | 09/2009 | 06/2014 | PhD | Sam Aparicio |
| Ian Wood | 09/2011 | 06/2014 | MSc | Irmtraud Meyer, CS, UBC |
| Jake Lever | 09/2012 | 05/2014 | MSc | Steven Jones, GSC |
| Carolyn Ch'ng | 09/2011 | 08/2013 | MSc | Paul Pavlidis, CHiBi |
| Peichen Xin | 09/2010 | 04/2013 | MSc | Robert Hancock, UBC |
| Luisa Chan | 09/2010 | 01/2013 | MSc | Fiona Brinkman – MBB, SFU |
| Patrick Tan | 09/2010 | 11/2012 | MSc | Paul Pavlidis, CHiBi, UBC |
| Nima Aghaeepour | 09/2009 | 11/2012 | PhD | Ryan Brinkman |
| Raymond Lim | 09/2009 | 08/2011 | MSc | Paul Pavlidis |
| Mark Okada | 09/2009 | 02/2011 | MSc | Martin Ester, SFU |
| Bora Uyar | 09/2009 | 12/2010 | MSc | Cenk Sahinalp, SFU |
| Kendric Wang | 09/2009 | 03/2012 | MSc | Colin Collins, Prostate Centre, UBC & Cenk Sahinalp, CS, SFU |
| Fong Chan | 09/2009 | 12/2011 | MSc | Randy Gascoyne, BCCA |
| AnaMaria Crisan | 09/2009 | 09/2010 | MSc | Sam Aparicio |

**Other Student Involvement**

| Status | Name | Mos/Years | Mos/Years | Degree | University |
|---|---|---|---|---|---|

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|---|---|---|---|---|---|
| Rotation Student | Ruby Liao | 11/2023 | 12/2023 | MSc | UBC |
| Student Volunteer | Andy Hsu | 10/2023 | Present | MD | UBC |
| Internship | Mahima Sanyal | 07/2022 | 08/2022 | PhD | Ohio University |
| Student Volunteer | Daniel Shirvani | 11/2021 | 12/2021 | BSc | UBC |
| GSAT Rotation | Glenn Chang | 10/2021 | 11/2021 | MSc | UBC |
| Student Volunteer | Kevin An | 05/2021 | 07/2021 | BSc | UBC |
| Student Volunteer | Jenny Yang | 01/2019 | 05/2019 | B.A.Sc | UBC |
| Honours Thesis | Tariq Vira | 09/2018 | 04/2019 | BSc | UBC |
| Directed Studies | Reva Shenwai | 09/2018 | 12/2018 | BSc | UBC |
| Co-op Student | Samantha Feng | 04/2018 | 08/2018 | BSc | BCIT |
| Go Global Internship Student | Mihir Jain | 05/2018 | 07/2018 | B.Tech | UBC |
| Directed Studies | Jenny Yang | 09/2017 | 05/2018 | B.A.Sc | UBC |
| Co-op Student | Keyu Zhuang | 09/2017 | 04/2018 | BSc | UVic |
| Co-op Student | Andrew Ponomarov | 09/2017 | 12/2017 | Associate in Science | Langara |
| GSAT Rotation | Zheng Dong | 09/2017 | 10/2017 | MSc | UBC |
| Summer Student | Hillary Pearson | 05/2017 | 07/2017 | BSc | UBC |
| Co-op Student | Jenny Yang | 05/2017 | 09/2017 | B.A.Sc | UBC |
| Co-op Student | Yin (Ian) Peng | 01/2017 | 08/2017 | BSc | UVIC |
| Summer Student | Jenny Yang | 07/2016 | 08/2016 | BSc | UBC |
| Co-op Student | Emily Kamma | 05/2016 | 12/2016 | BSc | BCIT |
| Co-op Student | Evan Ben-Oliel | 05/2015 | 12/2015 | BSc | UVic |
| Co-op Student | Fan (Helena) Xu | 01/2015 | 04/2015 | BSc | UBC |
| Co-op Student | Chon-Wai (Jeremy) Chan | 09/2014 | 04/2015 | BSc | UBC |
| Co-op Student | Boyang (Tom) Jin | 09/2014 | 12/2014 | BSc | UBC |
| Co-op Student | Tara Rashnavadi | 05/2014 | 12/2014 | MSc | UBC |
| Honors Thesis Student | Alice Liang | 09/2013 | 08/2014 | MSc | UBC |
| Co-op Student | Jenny Phan | 01/2014 | 08/2014 | BSc | UVic |
| Co-op Student | Patrick Hopkins | 04/2013 | 12/2013 | BSc | UBC |
| Co-op Student | Maia Smith | 09/2013 | 12/2013 | BSc | SFU |
| Co-op Student | Patrick Hopkins | 04/2013 | 12/2013 | BSc | UBC |
| Student Researcher | Hamid Younesy | 02/2013 | 12/2013 | PhD | SFU |
| Co-op Student | Jasleen Grewal | 01/2013 | 08/2013 | BSc | UBC |
| Co-op Student | Albert Badiong | 09/2012 | 04/2013 | BSc | SFU |
| Student Researcher | Pierre Cheung | 05/2011 | 06/2012 | BSc | UBC |
| Student Researcher | Lisa Miao | 01/2011 | 04/2011 | BSc | UBC |
| Directed Studies | Adam McLeod | 05/2009 | 09/2009 | BSc | SFU |
| Co-op Student | Yu Liu | 02/2008 | 05/2008 | BSc | |
| Directed Studies Student | Lydia Xu | 01/2008 | 05/2008 | BSc | UBC |
| Co-op Student | Katayoon Kasaian | 09/2007 | 12/2007 | BSc | UBC |
| Co-op Student | Bridget Bernier | 01/2007 | 08/2007 | BSc | |
| Co-op Student | Bryan Chu | 05/2006 | 08/2006 | BSc | |
| Co-op Student | Yuliya Prychyna | 09/2005 | 12/2005 | BSc | |
| Co-op Student | Xin (Maggie) Zhang | 01/2005 | 12/2005 | BSc | |
| Co-op Student | Elbert Chang | 05/2004 | 01/2005 | BSc | |
| Co-op Student | Yan Jia Pan | 09/2004 | 12/2004 | BSc | |
| Co-op Student | Wen Jia Pan | 05/2004 | 08/2004 | BSc | |
| Co-op Student | Jun Guan | 05/2004 | 08/2004 | BSc | |
| Co-op Student | William Chow | 01/2004 | 04/2004 | BSc | |

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|---|---|---|---|---|---|
| CIHR Rotation Student | Debra Fulton | 01/2004 | 04/2004 | MSc | UBC |
| Co-op Student | Wendy Yuen | 05/2004 | 08/2004 | BSc | |
| Co-op Student | Eddy Tsang | 05/2004 | 08/2004 | BSc | |
| Co-op Student | Yvonne Li | 01/2004 | 08/2004 | BSc | UBC |
| Directed Studies | Adrian Quayle | 10/2003 | 12/2004 | NA | UBC |
| Co-op Student | James Kennedy | 09/2003 | 04/2004 | BSc | |
| Co-op Student | Jeremy Ung | 09/2003 | 12/2003 | BSc | |
| Co-op Student | Eddy Tsang | 09/2003 | 12/2003 | BSc | |
| CIHR Rotation Student | Byron Kuo | 09/2003 | 12/2003 | MSc | UBC |
| CIHR Rotation Student | Keith Boroevich | 05/2003 | 08/2003 | MSc | UBC |
| Co-op Student | Aliya Hasham | 05/2003 | 08/2003 | BSc | |
| Co-op Student | Wendy Yuen | 05/2002 | 09/2002 | BSc | |
| Co-op Student | Dean Cheng | 01/2002 | 05/2002 | BSc | |
| Co-op Student | Michael Mao | 09/2001 | 12/2001 | BSc | |
| Directed Studies | Peter Lypkie | 05/2001 | 08/2001 | BSc | |
| Co-op Student | Christopher Liew | 04/2001 | 12/2001 | BSc | |
| Co-op Student | Heather Mosbrucker | 01/2001 | 04/2001 | BSc | |
| Co-op Student | Ivan Wan | 01/2000 | 08/2000 | BSc | |
| Co-op Student | Edward Dere | 08/2000 | 12/2000 | BSc | |
| Co-op Student | Thomas Fogg | 04/1999 | 07/1999 | BSc | |
| Co-op Student | David Tsang | 01/1999 | 04/1999 | BSc | |

## STUDENT ADVISORY COMMITTEE INVOLVEMENT:

| Date | End | Student | Supervisor | Program |
|---|---|---|---|---|
| 05/23 | Present | Anthony Oppedisano | Philip Hieter | PhD Medical Genetics Program, UBC |
| 04/23 | Present | Lilian Cordova | Kasmintan Schrader | MSc Medical Genetics Program, UBC |
| 07/22 | Present | Cathy Yan | Marco Marra | MSc Genome Science & Technology Program, UBC |
| 07/22 | Present | Shanwei (David) Tong | William Hsiao/Xiaonan Lu | MSc. Bioinformatics Program, UBC |
| 06/22 | Present | Signe MacLennan | Marco Marra | MSc Medical Genetics Program, UBC |
| 12/21 | Present | Andrew Sherrard | Jan Friedman | PhD, Genome Science & Technology Program, UBC |
| 06/21 | Present | Kyle Jenkins | Inanc Birol/Jan Friedman | MSc. Medical Genetics Program, UBC |
| 2019 | Present | Yuka Takemon | Marco Marra | PhD. Genome Science & Technology Program |
| 2019 | Present | Justin White | Peter Stirling | PhD. Medical Genetics Program, UBC |
| 2015 | Present | Prasath Pararajalingam | Ryan Morin | PhD. Molecular Biology & Biochemistry,SFU |
| 07/21 | 04/2023 | Ivan Gill | William Hsiao | MSc. Bioinformatics Program, UBC |
| 06/21 | 04/2023 | Pouya Ahmadvand | Ali Bashashati | MSc. Bioinformatics Program, UBC |
| 2019 | 2021 | Nicole Zhang | Wyett Wasserman/Sara Mostafavi | MSc. Bioinformatics Program UBC |
| 2019 | 2021 | Jordan Sicherman | Paul Pavlidis | MSc. Bioinformatics Program, UBC |
| 2019 | 2020 | Figali Taho | Inanc Birol | MSc. Bioinformatics Program, UBC |
| 2018 | 2022 | Venus Lau | Fiona Brinkman | PhD, Molecular Biology & Biochemistry,SFU |
| 2018 | 2022 | Kristina Gagalova | Inanc Birol | PhD. Bioinformatics Program, UBC |

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|---|---|---|---|---|
| 2015 | 2017 | Emma Hitchcock | Bill Gibson | MSc. Medical Genetics Program, UBC |
| 2015 | 2021 | Veronique LeBlanc | Marco Marra | MSc. Genome Science & Technology Program |
| 2012 | 12/2020 | Elizabeth Chun | Marco Marra | PhD. Bioinformatics Program |
| 2018 | 03/2018 | Annie Cavalla | Marco Marra | MSc. Bioinformatics Program, UBC |
| 2009 | 12/2017 | Rodrigo Goya | Marco Marra/ Imtraud Meyer | PhD. Bioinformatics Program |
| 2015 | 04/2017 | Alborz Maxloomian | Sohrab Shah | PhD. Bioinformatics Program, UBC |
| 2012 | 01/2017 | Ana Cohen | Bill Gibson | PhD. Medical Genetics Program, UBC |
| 2011 | 03/2016 | Daniel Lai | Imtraud Meyer | PhD. Bioinformatics Program |
| 2013 | 11/2015 | Andrew Roth | Sohrab Shah | PhD Bioinformatics Program, UBC |
| 2014 | 08/2015 | Emily Hindalong | Sohrab Shah | MSc. Bioinformatics Program, UBC |
| 2012 | 05/2015 | Annie Tam | Ann Rose | MSc. Medical Genetics Program, UBC |
| 2010 | 09/2014 | Mauro Castellarin | Rob Holt | PhD. Molecular Biology & Biochemistry |
| 2009 | 12/2013 | Lorraine Brown (Yu) | Fiona Brinkman | MSc. Molecular Biology & Biochemistry |
| 2011 | 09/2012 | Xin Ren | Art Cherkasov | MSc. Experimental Medicine |
| 2008 | 2012 | Alex Chang | Aly Karsan | PhD. Experimental Medicine |
| 2005 | 2012 | Warren Cheung | Wyeth Wasserman | MSc, Genetics Program |
| 2009 | 2011 | Raymond Lim | Paul Pavlidis | MSc. Bioinformatics Program |
| 2008 | 2011 | Ryan Morin | Marco Marra | PhD. Bioinformatics Program |
| 2002 | NA. | Christopher Walsh | Frederic Pio | MSc, Molecular Biology & Biochemistry |
| 2005 | 2010 | Malachi Griffith | Marco Marra | PhD. Medical Genetics |
| 2004 | 2010 | Sorana Morrissy | Marco Marra | PhD, Medical Genetics |
| 2003 | 2010 | Carri-Lyn Mead | Rob Holt/Gregg Morin | PhD. Medical Genetics |
| 2008 | 2009 | Tang Lee | Randy Gascoyne | MSc. Bioinformatics Program |
| 2008 | 2009 | Kaida Ning | Raphael Gottardo | MSc. Bioinformatics Program |
| 2003 | 2009 | James Taylor | Philip Hieter | PhD, Genetics Program |
| 2004 | 2008 | Chris Fjell | Artem Cherkasov | PhD, Experimental Medicine |
| 2003 | 2008 | Gang Wang | Marianne Sadar | MSc, Pathology & Laboratory Medicine |
| 2002 | 2008 | Shannan Ho Sui | David Baillie | MSc, Molecular Biology & Biochemistry |
| 2001 | 2008 | Ian Bosdet | Marco Marra | PhD, Medical Genetics |
| 2002 | 2007 | Maja Tarailo | Ann Rose | PhD, Medical Genetics |
| 2001 | 2006 | Steven Quayle | Marianne Sadar | PhD, Pathology and Laboratory Medicine |
| 2001 | 2006 | Kristen Tangen | Jim Kronstad | PhD, Microbiology and Immunology |
| 2001 | 2006 | Louie van der Lagemaat | Dixie Mager | PhD, Genetics Program |
| 2005 | 2005 | Michael Hsing | Artem Cherkasov | MSc, Genetics Program |
| 2002 | 2005 | Keith Boroevich | David Baillie | MSc, Molecular Biology & Biochemistry |
| 2002 | 2005 | Byron Kuo | Elizabeth Simpson | MSc, Genetics Program |
| 2001 | 2005 | Natalie Blaszczyk | Marianne Sadar | PhD, Pathology and Laboratory Medicine |
| 2001 | 2005 | Iris Cheung | Peter Lansdorp | PhD, Medical Genetics |

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|---|---|---|---|---|
| 2002 | 2004 | Fred Peng | David Baillie | MSc, Molecular Biology & Biochemistry |
| 2002 | 2004 | Perseus Missirlis | Philip Hieter | MSc, Genetics Program |
| 2002 | 2003 | Andrew Kwon | Holger Hoos/Raymond Ng | MSc, Computer Science |
| 2002 | 2003 | Elaine Chan | Frederic Pio | MSc, Molecular Biology & Biochemistry |
| 2001 | 2003 | Bernard Lee | Jan Friedman | MSc, Medical Genetics |
| 2001 | 2002 | Nancy Price | Ann Rose | MSc, Genetics Program |

## EXAMINER FOR PHD/MSC THESES:

| Date | Student | Program | University |
|---|---|---|---|
| 09/2023 | Vallijah Subasri | PhD, Medical Biophysicss | University of Toronto **(External Examiner)** |
| 06/2022 | Burak Ogan Mancarci | MSc, Bioinformatics | University of British Columbia **(Chair)** |
| 03/2022 | Elizabeth Stephens | PhD, Medical Genetics | University of British Columbia **(University Examiner)** |
| 09/2021 | Mona Siu | PhD, Medical Genetics | University of British Columbia **(Comprehensive Exam Chair)** |
| 07/2021 | Romulo Segovia | PhD, Botany | University of British Columbia **(Non-Supervisory Committee Examiner)** |
| 05/2021 | Nicole Knoetze | PhD, Bioinformatics | University of British Columbia **(Comprehensive Exam Chair)** |
| 08/2020 | Michale Vermeulen | MSc, Medical Genetics | University of British Columbia **(University Examiner)** |
| 08/2020 | Alexander Morin | PhD , Bioinformatics | University of British Columbia **(Comprehensive Exam Chair)** |
| 10/2019 | Allison Tai | MSc, Bioinformatics | University of British Columbia **(Chair)** |
| 11/2017 | Chen Yang | PhD, Bioinformatics | University of British Columbia **(Comprehensive Exam Chair)** |
| 10/2017 | Rachelle Farkas | MSc, Bioinformatics | University of British Columbia **(Chair)** |
| 09/2017 | Rashedul Islam | PhD, Bioinformatics | University of British Columbia **(Comprehensive Exam Chair)** |
| 08/2017 | Shams Bhuiyan | PhD, Bioinformatics | University of British Columbia **(Comprehensive Exam Chair)** |
| 05/2017 | Hamid Mohamadi | PhD, Bioinformatics | University of British Columbia **(University Examiner)** |
| 04/2017 | Erdi Kucuk | MSc, Bioinformatics | University of British Columbia **(Chair)** |
| 03/2017 | Beryl Zhuang | MSc, Bioinformatics | University of British Columbia **(Chair)** |
| 01/2017 | Allen Zhang | MD/PhD, Bioinformatics | University of British Columbia **(Comprehensive Exam University Examiner)** |
| 12/2016 | Mike Gottlieb | MSc, Bioinformatics | University of British Columbia **(Chair)** |
| 08/2016 | Maia Smith | MSc, Bioinformatics | University of British Columbia **(Chair)** |
| 05/2016 | Jiarui Ding | PhD, Computer Sciences | University of British Columbia **(University Examiner)** |
| 04/2016 | Nik Fortelny | PhD. Biochemistry & Molecular Biology | University of British Columbia **(University Examiner)** |
| 04/2016 | Jessica Pilsworth | MSc, Bioinformatics | University of British Columbia **(Chair)** |
| 03/2016 | Lauren Chong | MSc, Bioinformatics | University of British Columbia **(Chair)** |
| 10/2015 | Raunak Shrestha | PhD, Bioinformatics | University of British Columbia **(Chair)** |
| 08/2015 | Jing Yun Alice Zhu | MSc, Bioinformatics | University of British Columbia **(Chair)** |
| 07/2015 | Shaun Jackman | PhD, Bioinformatics | University of British Columbia **(Qualifying Exam Chair)** |

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|---|---|---|---|
| 06/2015 | Varune Rohan Ramnarine | PhD, Bioinformatics | University of British Columbia **(Qualifying Exam Chair)** |
| 05/2015 | Sarah Perez | MSc, Bioinformatics | University of British Columbia **(Chair)** |
| 04/2015 | Fong Chun Chan | PhD, Bioinformatics | University of British Columbia **(Qulifying Exam Chair)** |
| 04/2015 | Ryan Huff | MSc. Bioinformatics | University of British Columbi **(Chair)** |
| 04/2015 | Javad Safaei | PhD, Computer Science | University of British Columbia |
| 12/2014 | Tyler Funnell | MSc, Bioinformatics | University of British Columbi **(Chair)** |
| 11/2014 | Raewyn Billings | MSc, Medical Genetics | University of British Columbia **(University Examiner)** |
| 10/2014 | Pier-Luc Clermont | PhD, Interdiciplinary Oncology Program | Univeristy of British Columbia **(Comprehensive Exam Committee)** |
| 06/2014 | Marjan Farahbod | PhD, Bioinformatics | University of British Columbia **(Chair)** |
| 11/2013 | Niels Hanson | PhD, Bioinformatics | University of British Columbia **(Qualifying Exam Chair)** |
| 08/2013 | Carolyn Ch'ng | MSc, Bioinformatics | University of British Columbia **(Chair)** |
| 05/2013 | Huifang Li | MSc, Bioinformatics | University of British Columbia **(Chair)** |
| 04/2013 | Evan Gatev | PhD, Bioinformatics | University of British Columbia **(Qualifying Exam Chair)** |
| 03/2013 | Emilia Lim | PhD, Bioinformatics | University of British Columbia **(Comprehensive Exam Chair)** |
| 11/2012 | Patrick Tang | MSc, Bioinformatics | University of British Columbia **(Chair)** |
| 09/2012 | Jeff Proctor | MSc, Bioinformatics | University of British Columbia **(Chair)** |
| 06/2012 | Melanie Courtot | PhD, Bioinformatics | University of British Columbia **(Comprehensive Exam Chair)** |
| 03/2012 | Kendric Wang | MSc, Bioinformatics | University of British Columbia **(Chair)** |
| 12/2011 | Gerben Duns | PhD | University of Groningen |
| 02/2011 | Ben VanderValk | MSc, Bioinformatics | University of British Columbia **(Chair)** |
| 02/2011 | Jeff Chu | PhD, Molecular Biology and Biochemistry | Simon Fraser University |
| 12/2010 | Kieran O'Niell | PhD, Bioinformatics | University of British Columbia **(Comprehensive Exam Chair)** |
| 09/2010 | Varun Ramraj | MSc, Bioinformatics | University of British Columbia **(Chair)** |
| 09/2010 | Anamaria Crisan | MSc, Bioinformatics | University of British Columbia **(Chair)** |
| 09/2010 | Paul Krzyzanowski | PhD, Cellular and Molecular Medicine | University of Ottawa |
| 08/2010 | Soroush Samadien | PhD, Bioinformatics | University of British Columbia **(Comprehensive Exam Chair)** |
| 02/2010 | Adrian Cortes | MSc, Bioinformatics | University of British Columbia **(Chair)** |
| 12/2009 | Vaneet Lotay | MSc, Bioinformatics | University of British Columbia **(Chair)** |
| 08/2009 | Daniel Horspool | MSc, Bioinformatics | University of British Columbia **(Chair)** |
| 07/2009 | Samuel Chang | PhD | University of British Columbia |
| 12/2008 | Leon French | PhD, Bioinformatics | University of British Columbia **(Comprehensive Exam Chair)** |
| 08/2008 | Xiaohoui Chen | MSc, Bioinformatics | University of British Columbia **(Chair)** |
| 06/2008 | Michael Hsing | PhD, Bioinformatics | University of British Columbia **(Comprehensive Exam Chair)** |
| 10/2007 | Ryan Morin | MSc, Bioinformatics | University of British Columbia **(Chair)** |
| 09/2007 | Siddhartha Srivastava | MSc, Bioinformatics | University of British Columbia **(Chair)** |
| 07/2007 | William Hsiao | PhD, Molecular Biology and Biochemistry | Simon Fraser University |
| 04/2007 | Jessica Lee | MSc, Bioinformatics | University of British Columbia **(Chair)** |

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|---|---|---|---|
| 09/2006 | Sanja Rogic | PhD, Computer Science | University of British Columbia |
| 12/2005 | Ben Good | PhD, Bioinformatics | University of British Columbia<br>**(Comprehensive Exam Chair)** |
| 02/2002 | Junaid Gamieldien | PhD, Bioinformatics | SANBI, University of the Western Cape |

## TRAINEE AWARDS, SCHOLARSHIPS & FELLOWSHIPS:

| **Trainee** | **Award Name** | **Awarding Agency** | **$ Amount** | **Year (s)** |
|---|---|---|---|---|
| Vahid Akbari | Lloyd Skarsgard 2023 Research Excellence Prize - 2nd Place (CGS M) | BC Cancer Foundation | $750 | 2023 |
| Faeze Keshavarz-Rahaghi | GSC Graduate Student Travel Scholarship | John Bosdet Memorial Fund | $1,500 | 2023 |
| Andrew Galbraith | Canada Graduate Scholarship-Master’s (CGS M) | Canadian Institutes of Health Research | $17,500 | 2023 |
| Faeze Keshavarz-Rahaghi | Canada graduate scholarship - doctoral award | Canadian Institutes of Health Research | $105,000 | 2022-2025 |
| Caralyn Reisle | Canada graduate scholarship - doctoral award | Canadian Institutes of Health Research | $105,000 | 2022-2025 |
| Sarah Dada | BC Cancer Rising Stars Award | BC Cancer Foundation | $50,000 | 2022-2024 |
| Caralyn Reisle | Killam Doctoral Scholarship | University of British Columbia | $4000 | 2022-2024 |
| Luka Culibrk | Medical Genetics Doctoral Fellowship | University of British Columbia | $36,400 | 2022-2024 |
| Katherine Dixon | Research Trainee Award | Michael Smith Foundation for Health Research | $103,125 | 2021 - 2023 |
| Caralyn Reisle | Cordula and Gunter Paetzold Fellowship | University of British Columbia | $12,000 | 2021 - 2022 |
| Faeze Keshavarz-Rahaghi | GSC Graduate Student Travel Scholarship | John Bosdet Memorial Fund | $215 USD | 2021 |
| Caralyn Reisle | GSC Graduate Student Travel Scholarship | John Bosdet Memorial Fund | $185 USD | 2021 |
| Caralyn Reisle | Post Secondary Scholarship | Invermere Health Auxiliary Society | $1500 | 2020 |
| Faeze He | Four Year Doctoral Fellowship (Y4F) | University of British Columbia | $72,800 | 2020 - 2024 |
| Vahid Akbari | Four Year Doctoral Fellowship (Y4F) | University of British Columbia | $72,800 | 2020 - 2024 |
| Jasleen Grewal | Travel Award to ISMB/ECCB “Bayesian modelling as an unsupervised approach to infer biological patterns in cancers and normal tissues” | ISCB Travel Fellowship Award | $1200 USD | 2019 |
| Jasleen Grewal | Travel Award to ISMB/ECCB “Bayesian | CIHR ICS Travel Award | $1500 | 2019 |

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| | modelling as an unsupervised approach to infer biological patterns in cancers and normal tissues” | | | |
| Jasleen Grewal | Women's early career accelerator award, GPU Technology Conference 2019 | Nvidia | $1200 USD | 2019 |
| Luka Culibrk | Canada graduate scholarship “ Genome-wide discovery and analysis of copy number variation in metastatic cancer” | CIHR Doctoral Award | $105,000 | 2019 - 2022 |
| Eric Zhao | Canadian Medical Hall of Fame (CMHF) Award | Canadian Medical Hall of Fame | $5000 | 2018 |
| Jahanshah Ashkani | Travel Award to Summit for Cancer Immunotherapy (Summit4CI) | BioCanRx | $1100 | 2018 |
| Jasleen Grewal | Travel Award to American Society of Human Genetics (ASHG) | Canadian Cancer Society Research Institute | $1750 | 2018 |
| Jasleen Grewal | GSC Graduate Student Travel Scholarship | John Bosdet Memorial Fund | $1250 | 2018 |
| Luka Culibrk | Genome BC Genomics Forum "Research Exchange 2018". | Genome BC | 1st Place Poster Prize $500 | 2018 |
| Eric Zhao | Travel Award to American Society of Clinical Oncology (ASCO) | Canadian Cancer Society Research Institute | $1070 | 2018 |
| Eric Zhao | Lloyd Skarsgard Award 1st place (tied) | BC Cancer Foundation | $1000 | 2018 |
| Jake Lever | Translation Cancer Genomics Trainee Collaboration and Travel Award | University of British Columbia | $860 | 2018 |
| Harwood Kwan | Canada graduate scholarship “Biochemical Analysis of Mutant Alpha1 Antitrypsin in Family with History of Intracranial Aneurysm” | CIHR Master’s Award | $17,500 | 2018 - 2019 |
| Jasleen Grewal | Translation Cancer Genomics Trainee Collaboration and Travel Award | University of British Columbia | $2,500 | 2017 |
| Jasleen Grewal | GSC Graduate Student Travel Scholarship | John Bosdet Memorial Fund | $1,000 | 2017 |
| Eric Zhao | Young Investigator Forum | Canadian Society for Clinical Investigation and the Clinician Investigator Trainee Association of Canada | $50 Poster Prize | 2017 |

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| Kieran O'Neill | Fellowship Program "Determining the Mechanis of Myelodysplastic Syndrome Progression and Resistance to Azacytidine Therapy using Single-cell DNA Methylation Sequencing" | CIHR Doctoral Award | $135,000 | 2017 - 2020 |
| My Linh Thibodeau | Clinical Investigator Fellowship Award | Royal College of Physicians and Surgeons Canada. | $142,000 | 2017 - 2019 |
| Jake Lever | Bioinformatics (BIG) Research Retreat "A fast and easy to use framework for automatic biological knowledge base construction" | University of British Columbia | 3rd Place Poster Prize | 2017 |
| Jake Lever | Genome BC 13th Annual Genomics Forum 2017 "A fast and easy to use framework for automatic biological knowledge base construction" | Genome British Columbia | 2nd Place Poster Prize | 2017 |
| Jake Lever | BC Cancer Agency Research Day 2017 "A fast and easy to use framework for automatic biological knowledge base construction" | BC Cancer Agency | 1st Place Poster Prize | 2017 |
| Jenny Yang | Nature Physics Poster Competition " Identifying Functional Clusters of Genes from Energy Landscapes in Autoencoders for Personalized Therapy in Medicine " | International Conference of Physics Students, Turin, Italy | Best Poster Contribution Award - 3rd Place and travel bursary of €220 | 2017 |
| Celia Siu | Outstanding Presentation Prize "Bioinforamatic characterization of the normal thyroid reference epigenome" | F1000 Research at ISMB Regulatory Genonics Special Interest Group (RegGenSIG) 2016 | Outstanding Presentation Prize | 2016 |
| Celia Siu | Travel Award to present "Bioinformatic characterization of the normal thyroid reference epigenome" | CEEHRC | $1000 | 2016 |
| Jasleen Grewal | 5th Annual Terry Fox Node Research Day "Using machine learning to identify site of origin of metastatic tumours" | The Terry Fox Research Institute | Best Poster Prize $200 | 2016 |

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| Jasleen Grewal | Four Year Doctoral Fellowship (Y4F) | University of British Columbia | $72,800 | 2015 - 2019 |
| Eric Zhao | Doctoral Research Award (Networks, signatures, and personalized medicine: a whole genome approach to cancer therapy) | CIHR Vanier Award | $150,000 | 2015 - 2018 |
| Jake Lever | Doctoral Research Award (Personalised treatment of glioblastoma using machine-learning driven network analysis of drug sensitivity data) | CIHR Vanier Award | $150,000 | 2014 - 2017 |
| Daryanaz Dargahi | Bioinformatic Identification of Optimal Targets and Therapeutic Antibody Development in Oncology | MITACS | $90,000 | 2013 - 2016 |
| Katayoon Kasaian | Doctoral Research Award (Whole Genome and Transcriptome Analysis of Thyroid Cancers) | CIHR | $105,000 | 2013 - 2016 |
| Shing Zhan | Doctoral Research Award (Identification of drivers of metastasis in Ewing sarcoma using next-generation sequencing technologies) | CIHR | $105,000 | 2013 - 2016 |
| Sreeja Leelakumari | Travel Awards - Institute Community Support | CIHR | $1000 | 2015 |
| Sreeja Leelakumari | Knowledge Fund | John Jambor | $500 | 2015 |
| Daryanaz Dargahi | Graduate Fellowship (Development of Therapeutic Approaches to Human Breast Cancer Using Mouse Models) | Simon Fraser University | $6,250 | 2013 |
| Katayoon Kasaian | Post Doctoral Travel Scholarship (12th International Symposium on Mutation in the Genome) | John Bosdet Memorial Fund | $2,601 | 2013 |
| Cydney Nielsen | Postdoctoral Fellowship Research award | MSFHR | $27,333 | 2011 -2013 |
| Shing Zhan | Univeristy Graduate Fellowship (Genome-wide identification of essential genes in Caenorhabditis elegans in a single whole genome sequencing experiment) | University of British Columbia | $87,900 | 2011 - 2015 |
| Athanasios Zovoilis | Post Doctoral Fellowship | EMBO | $51,701 | 2011 - 2012 |
| Cydney Nielsen | Fellowship Trainee Award | CIHR | $135,000 | 2010 -2013 |
| Katayoon | Master’s Trainee Award | CIHR | $17,500 | 2010 -2011 |

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| Kasaian | | | | |
| Anthony Fejes | Graduate Student Travel Fund | UBC | $400 | 2010 |
| Cydney Nielsen | GSC Postdoctoral Travel Scholarship | John Bosdet Memorial Fund | $2,500 | 2010 |
| Elizabeth Chun | Bioinformatics Genetic Retreat Travel Award | CIHR Bioinformatics Training Program | $500 | 2010 |
| Katayoon Kasaian | Celebrate Research Week Interdisciplinary Poster Competition | UBC | $200 | 2010 |
| Katayoon Kasaian | BCCA/MSFHR Incentive Training Award | MSFHR/BC Cancer Agency | $10,000 | 2009 -2010 |
| Anthony Fejes | CIHR National Poster Competition, | CIHR<br>*Winnipeg, Canada* | Silver Award of Excellence ($250) | 2009 |
| Katayoon Kasaian | MSc. Graduate Entrance Scholarship | UBC | $2,200 | 2009 |
| Anthony Fejes | Senior Graduate Studentship | MSFHR | $75,000 | 2008 -2011 |
| Elizabeth Chun | GSC Graduate Student Travel Scholarship | John Bosdet Memorial Fund | $700 | 2008 |
| Binhua Liang | Canadian Graduate Scholarship (CGS) | Canadian Institute of Health Research (CIHR) | $105,000.00 | 2007–2010 |
| Binhua Liang | Keystone Symposia<br>*Mar 25 - Mar 30, 2007, Whistler, Canada* | Keystone Symposia: HIV Vaccines: Progress and Prospects. | $1000 US Poster Award | 2007 |
| Obi Griffith | Lloyd Skarsgard Research Excellence Award | BC Cancer Agency | - | 2007 |
| Yvonne Li | GSC Graduate Student Travel Scholarchip | John Bosdet Memorial Fund | $2,125 | 2007 |
| Yvonne Li | Canada Graduate Scholarships Doctoral Award (D3) | NSERC | $105,000 | 2006 -2009 |
| Ben Binhua Liang | CIHR-IG for Short-term Research | CIHR Institute for Genetics | $3,280 | 2006 -2007 |
| Obi Griffith | Senior Trainee Award (Bonus Award) | MSFHR | $14,000 | 2006 - 2008 |
| Binhua Liang | XVI International AIDS Conference: *August 13-18, 2006, Toronto,Canada* | XVI International AIDS Conference | $1000 Cdn Poster Award | 2006 |
| Stephen Montgomery | Lloyd Skarsgard Research Excellence Award | BC Cancer Agency | - | 2006 |
| Yvonne Li | The Sixth Canadian Computational Chemistry Conference. | Taylor & Francis Books CRC Press Award for Excellence in Computational Chemistry | Best Poster | 2006 |
| Yvonne Li | Genomics Forum Research Exchange | Genome BC | Best Student Poster Presentation | 2006 |
| Monica Sleumer | Senior Graduate Award | MSFHR | $67,500 | 2005 - 2008 |
| Obi Griffith | Canada Graduate Scholarship (CGS) Doctoral | CIHR | $105,000 | 2005 - 2008 |

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| | Award | | | |
| Stephen Montgomery | Post Graduate Scholarship-Doctoral | NSERC | $63,000 | 2005 - 2008 |
| Binhua Liang | International Centre for Infectious (ICID) Disease Retreat: *October 1-3, 2005, Winnipeg, Canada* | International Centre for Infectious (ICID) Disease Retreat. | $100 Cdn<br>Poster Award | 2005 |
| Binhua Liang | International Symposium on Recent Advances in Molecular, Clinical and Social Medicine. *Dec3-5, 2005, Shantou, China* | International Symposium on Recent Advances in Molecular, Clinical and Social Medicine. | $1000 Chinese Yen<br>Poster Award | 2005 |
| Erin Pleasance | Genomics Forum Research Exchange | Genome BC | Best Student Poster Presentation | 2005 |
| Yvonne Li | UBC Genetics Graduate Retreat | UBC | Best Student Poster Presentation<br>$350 travel Prize | 2005 |
| Yvonne Li | Bioinformatics Training Program Stipend | CIHR/MSFHR | $36,000 | 2004 -2006 |
| Stephen Montgomery | Senior Graduate Award | MSFHR | $28,500 | 2004 - 2007 |
| Erin Pleasance | Doctoral Research Award | CIHR | $70,000 | 2004 - 2006 |
| Ben Binhua Liang | CIHR-IG for Short-term Research | CIHR Institute for Genetics | $5,080 | 2004 - 2005 |
| Obi Griffith | GSC Graduate Student Travel Scholarship | John Bosdet Memorial Fund | $670 | 2004 |
| Obi Griffith | Summer Research Award | Albert B. & Mary Steiner | $650 | 2004 |
| Obi Griffith | CIHR Canadian Student Health Research Forum: *Winnipeg, Canada* | CIHR Canadian Student Health Research Forum, | Silver Award of Excellence ($250) | 2004 |
| Stephen Montgomery | BCNET Coolest Applications Contest | BCNET | Best overall Application | 2004 |
| Obi Griffith | PhD Tuition Fee Award | UBC | $12,660 | 2003 -2006 |
| Obi Griffith | Trainee Award (top-up, bonus award, travel allowance) | MSFHR | $24,400 | 2003 - 2005 |
| Obi Griffith | PGS-A Award | NSERC | $34,600 | 2003 - 2005 |
| Erin Pleasance | Steiner Summer Research Award | UBC | $1150 | 2003 - 2004 |
| Obi Griffith | Graduate Entrance Scholarship | UBC | $4,000 | 2003 |
| Erin Pleasance | Salary Award | MSFHR | $38,960 | 2002 - 2006 |
| Erin Pleasance | Honorary Killam Predoctoral Travel Award | UBC | $1500 | 2002 - 2004 |

## CONTRIBUTIONS TO THE TRAINING OF HIGHLY QUALIFIED PERSONNEL (HQP):

Further significant contributions have been in the field of helping to establish bioinformatics training within Canada, including my involvement as founding director of the CIHR/MSFHR Bioinformatics Training

Program for Health Research and as a founding Chair of the UBC Bioinformatics Graduate Program. I have also previously served for several years a core faculty member of the Canadian Bioinformatics Workshop Series. In recognition of my contributions to bioinformatics training I have been a recipient of the UBC Medical Genetics teaching award and also in 2012 was a recipient of a prestigious UBC Killam Teaching Prize. I have developed Bioinformatic and Genomic Courses, including Problem Based Learning in Bioinformatics and Genomic Analysis. I have trained numerous PhD student and Post-doctoral fellows students who are themselves now faculty members at institutions such as Stanford and Washington University.

## ACTIVITIES AND CONTRIBUTIONS:

My bioinformatics group at Canada's Michael Smith Genome Sciences Centre is using data from genomic analyses of human cancers to help understand the molecular genetic events that underly the disease. We are involved in a number cancer sequencing studies, including genomic studies of acute myeloid leukaemia (AML), breast cancer, lymphomas and thyroid cancer. We have developed computational analytic approaches to the analysis of RNA-seq data as well as genomic analysis of tumours. In 2010, my group was the first to publish the genome of an adenocarcinoma of the tongue as well as the first to demonstrate clinical utility of complete genomic sequencing in cancer.

I have also been involved in using next-generation DNA sequencing techniques to study protein-DNA interactions. My group was one of the first groups to report on the utility of ChIP-seq approaches using the STAT1 transcription factor as a model and also one of the first to develop computational software tools for the analysis of ChIP-seq data. I have used this approach to further study epigenomics and have numerous publications in the study of histone modifications in both human and mouse.

My group also is also involved in developing a number of genomic related tools and approaches, involving the development of DNA assembly techniques and alignment algorithms. In 2009 we were the first to publish the sequence of a fungal genome, using a hybrid assembly approach, combining data from Sanger, 454 and illumina sequencing approaches.

I worked at the Sanger Centre, Cambridge, UK, 1994-1998. During this time I was responsible for the computational analysis of the 45MB of *Caenorhabditis elegans* sequence generated at the Sanger Centre as part of the *C. elegans* Genome Project [Science (1998) 282:2012-2018]. This project resulted in the derivation of the first complete genome of a multi-cellular organism. This involved the implementation of database schemas, database accessibility, utilizing genefinding algorithms and other software tools to distinguish genomic features, as well as the annotation and submission of sequence entries to the public sequence repositories. During this time I also provided the bioinformatic resources required for the *Brugia Malayi* EST project at the Sanger Centre as part of the Filarial Genome Network.

Further contributions include my involvement as the founding director of the CIHR/MSFHR Bioinformatics Training Program as well as being a core faculty member of the Canadian Bioinformatics Workshop up until May 2006.

## MOST SIGNIFICANT CONTRIBUTIONS:

1. **Genome Analysis:** I have been involved in numerous genomic projects. Most notably the computational analysis of the *C. elegans* genome, whilst at the Sanger Institute (PMID 9851916). This project resulted in the derivation of the first complete genomic sequence of a multi-cellular organism. I also carried out the first genomic analysis on the Sea Squirt *Ciona intestinalis, Drosophila melanogaster* and the white spruce (PMID 23698863). I continue to implement and develop genome sequencing methodology and more recently sequenced the genomes

of the beluga whale (PMID 29232881) and the sea otter (PMID 29232880). I have also developed methods to determine the parent-of-origin of human alleles using imprinting information without the requirement for parental samples (PMID: 36777186).

2. **Cancer Genomics:** I have been involved in a number of cancer sequencing studies, including the first genome of a breast cancer (PMID 19812674). I also published the first study to demonstrate the utility of whole genome sequencing of a human cancer to inform clinical decision making (PMID 20696054). I have been involved the bioinformatics processing and analysis of several thousand miRNA libraries deriving from human tumours as part of the Cancer Genome Atlas project. Other contributions involve the sequencing of the first parathyroid cancer genome (PMID 23616356) as well as the first ghost cell odontogenic cancer. I also helped to develop the CIRCOS genome viewer, which is used widely in the field of cancer genomics (PMID 19541911).

3. **Genome and Transcriptome assembly:** My group has invested significant research resources into the analysis of genomic and transcriptomic data derived from next-generation DNA sequencing devices. For example, the group has developed novel approaches for both the alignment of the sequence reads to the reference genome (PMID 18974170), as well as approaches for the identification of sequence variants (PMID 20190250). I have developed an ensemble approach for the identification of structural rearrangements from DNA sequence and assembly data (PMID 30016509).

4. **Protein-DNA interactions.** I have been involved in the application of next-generation DNA sequencing for other uses including the identification of DNA-protein interactions and represented one of the first groups to develop the ChIP-seq approach (PMID 17558387) as well as the software to allow the determination of ChIP-enriched regions (PMID 18599518.). My work has also contributed to the identification of epigenomic changes involving both histone modifications and also DNA methylation (PMID 33618748).

5. **Disease sequencing** I am also the co-discoverer of the causative gene for Weaver syndrome, which was found to be due to *de-novo* mutations in the key epigenomic modifying enzyme EZH2 (PMID 22177091). I was part of the team that sequenced the SARS coronavirus, specifically responsible for the sequence assembly and the bioinformatic analysis. The resulting Science (PMID 12730501) paper describing this has been cited more than 2,892 times (as of February 2023).

## GRANTS AND AWARDS APPLIED FOR:

| Granting Agency | Subject | Years | Amount | Principal Investigator | Co-Investigator |
|---|---|---|---|---|---|
| TFRI | MOHCCN Pathfinder Phase II | 05/2023 to 10/2024 | Total CAD $218,868 | S Jones | M Marra |

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| NIH | Accelerating the expert-crowdsourcing of cancer variant interpretation in CIViC | 04/2024 to 03/2029 | Total CAD $499,610 | O Griffith | S Jones,<br>J Laskin |
| NIH | Early assessment of malignant progression of oral premalignant mucosal lesions | 12/2023 to 11/2028 | Total CAD $1,350,000 | DT Wong | C Poh,<br>S Jones,<br>C MacAulay |
| CRS | Investigating high-penetrant hereditary factors in Rwandan women with breast cancer | 09/2024 to 08/2026 | Total CAD $130,000 | S Jones | K Schrader<br>ML Thibodeau |
| CIHR | The Canadian Bioinformatics Computational Biology and Health Data Sciences Training and Community Platform (CANBCBHDS) Training Program | 09/2024 to 03/2030 | Total CAD $8,866,661<br>GSC CAD: $242,565 | M Brazas (NPI),<br>G Bourque,<br>W Hsiao,<br>N Hughes,<br>J Hussin,<br>J Kong,<br>S Pai,<br>M Sukhai,<br>W Wasserman,<br>D Wishart | S Jones |
| NIH | Early Detection of Malignant Progression of Oral Pre-malignant Lesions (OPL) | 09/01/2024 to 08/31/2029 | Total USD $2,351,645<br>GSC USD: $1,346,260 | | S Jones<br>C Poh<br>C MacAulay |

**GRANTS HELD:**

In order of start date (oldest first, most recent at end).

| Granting Agency | Subject | Years | Amount | Principal Investigator | Co-Investigators |
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| BCCF | Personalized OncoGenomics | 07/2012 to 03/2025 | Total CAD $40,700,000 | J Laskin,<br>M Marra | S Jones,<br>K Glemon,<br>H Lim |
| CIHR | Early detection of cancer in high-risk patients through profiling of circulating tumour DNA | 07/2018 to 03/2025 | Total CAD $1,977,525 | T Pugh (NPI),<br>R Kim,<br>A Pollet | S Jones,<br>K Schrader,<br>A Karsan,<br>R Khokha |
| TFRI | The Enhanced Pancreatic Cancer Profiling for Individualized Care project | 07/2017 to 06/2025 | Total CAD $4,085,288 | D Renouf,<br>D Schaeffer,<br>S Gallinger,<br>G Zogopoulos,<br>O Bathe | S Jones,<br>M Marra,<br>G Morin,<br>J Knox,<br>S Fischer,<br>C O'Callaghan,<br>M Moore |
| CIHR | Canadian Epigenetics, Environment and Health Research Consortium Network Phase II | 07/2019 to 06/2024 | Total CAD $1,108,161 | M Hirst (NPI),<br>G Bourque | S Jones,<br>C Arrowsmith,<br>J Davie,<br>S Bilodeau,<br>J Dillworth,<br>C Brown,<br>S Kimmins,<br>M Gallo |
| TFRI | Marathon of Hope Cancer Centres Network (MOHCCN) | 06/2020 to 03/2024 | Total CAD $13,056,160 | M Marra,<br>D Renouf | S Jones,<br>C Steidl |
| CFI | CGEn – A National Platform for Genome Sequencing and Analysis<br>*(Innovation Fund)* | 04/2022 to 03/2026 | Total CAD $28,655,584 | S Scherer (NPI),<br>S Jones,<br>M Lathorp | M Marra,<br>G Bourque,<br>L Armstrong,<br>N Jabado,<br>I Ragoussis,<br>L Strug |
| Genome Canada | The Canadian Biogenome Project | 10/2021 to 09/2025 | Total CAD $6,294,530 | S Jones (NPI),<br>M Murray | S Scherer,<br>P Herbert,<br>I Ragoussis,<br>M Engstrom,<br>K Howe,<br>P Pulsifer,<br>A Chabot |
| CIHR | Discovery of HPV-associated genomic alterations in cervical cancer | 07/2022 to 03/2027 | Total CAD $420,750 | M Marra | S Jones |

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| Genome Canada | Parent-of-Origin-Aware genomics analysis | 10/2022 to 08/2025 | Total CAD $6,040,300 | K Schrader,<br>S Jones,<br>P Lansdorp | S Yip,<br>S Sun,<br>A Virani,<br>D Regier |
| CIHR | Parent-of-Origin-Aware Genomic Analysis in Hereditary Cancer | 04/2023 to 03/2026 | Total CAD $1,115,000 | K Schrader (NPI),<br>S Jones (NPI),<br>P Lansdorp | L Lefebvre,<br>D Regier,<br>S Sun,<br>A Virani,<br>S Yip |
| CIHR | Evaluating the utility of long-read genome sequencing for uncovering causal genetic variation and epigenetic signatures of rare disease | 04/2023 to 03/2027 | Total CAD $1,070,000 | S Jones (NPI), | C Boerkoel,<br>W Gibson,<br>R Weksberg |
| CFI | CGEn-Canada's national facility for genome sequencing and analysis<br>*(Major Science Initiatives Fund)* | 04/2023 to 03/2029 | Total CAD $14,864,120 | N Aziz (NPI),<br>S Scherer,<br>M Lathrop,<br>S Jones | |
| Genome Canada | CGEn - national facility for genome sequencing and analysis<br>*(Technology Development)* | 04/2023 to 03/2026 | Total CAD $1,333,333 | S Scherer (NPI),<br>L Strug,<br>S Jones,<br>I Ragoussis, | |
| Genome BC | Genome BC Marathon of Hope Cancer Centre program (MOH002) | 04/2022 to 03/2024 | Total CAD $2,000,000 | M Marra,<br>D Renouf | S Jones |
| CIHR | Pan-Canadian Human Genome Library | 09/2023 to 08/2028 | Total CAD $529,205 | G Bourque (NPI),<br>C Bherer,<br>M Brazas,<br>M Brudno,<br>N Caron,<br>M Courtot,<br>V Ferretti,<br>Y Joly,<br>S Jones,<br>J Lerner-Ellis,<br>I Stedman,<br>L Stein,<br>W Wasserman,<br>M Zawati | |

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| Genome Canada | RapidOmics 2.0: Long-read Genome Sequencing for Urgent Genetic Disease Diagnosis | 10/2023 to 09/2026 | Total CAD: $3,583,291 | J Friedman<br>C Ivany | A Elliott<br>W Gibson<br>S Jones<br>L Lynd |
| CFI | CGEn – Canada's national platform for genome sequencing and analysis<br>*(Innovation Fund)* | 01/2024 to 12/2028 | Total CAD $18,496,520<br>GSC amount: $5,942,140 | S Scherer (NPI),<br>M Lathrop,<br>S Jones | N Jabado,<br>G Bourque,<br>M Marra,<br>K Schrader,<br>L Strug,<br>P Subbarao,<br>I Ragoussis |

**PAST GRANTS:**

In order of end date (most recent first, oldest at end)

| **Granting Agency** | **Subject** | **Years** | **Amount** | **Principal Investigator** | **Co-Investigators** |
|---|---|---|---|---|---|
| CIHR | Characterization of the integrative epigenetic and epitranscriptomic landscape of acute myeloid leukemias | 01/2021 to 12/2023 | Total CAD $300,000 | L Vu | S Jones |
| UBC | Use of Long Read Whole Genome Sequencing to Drive Community-Based Patient-Oriented Care for Autism Spectrum Disorder | 05/2022 to 06/2023 | Total CAD $49,285 | A Richardson (NPI) | S Lewis,<br>S Jones |
| TFRI | MOHCCN Pathfinder | 11/2021 to 04/2023 | Total CAD $155,610 | S Jones (NPI) | |
| NIH | Standardized and Genome-Wide Clinical Interpretation of Complex Genotypes for Cancer | 04/2019 to 03/2024 | Total US $3,690,154 | O Griffith | S Jones,<br>J Laskin |
| TFRI | The Terry Fox Precision Oncology For Young peopLE | 04/2016 to 03/2023 | Total CAD $5,000,000 | D Malkin | S Jones,<br>M Marra,<br>G Morin |
| Genome Canada | BC Cancer Agency Genome Sciences Centre Genomics Technology Platform | 04/2017 to 03/2023 | Total CAD $9,641,002 | M Marra (NPI),<br>S Jones,<br>M Hirst,<br>C Nislow | |
| CFI | Canada's Genomics Enterprise (CGEn-MSI): A national genomic tools network for transforming life science research | 04/2017 to 03/2023 | Total CAD $44,317,600 | S Scherer (NPI),<br>S Jones,<br>M Lathorp | |

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| Genome Canada | Tackling Childhood Brain Cancer at the root to improve survival and quality of life | 04/2018 to 03/2023 | Total CAD $12,997,400 | J Nada,<br>M Jacek,<br>M Taylor | S Jones & 17 others |
| CIHR | Centre for Epigenome Mapping Technologies | 02/2017 to 01/2023 | Total CAD $4,534,483 | M Hirst (NPI),<br>S Jones,<br>M Marra | S Aparicio,<br>C Eaves,<br>P Lavoie,<br>D Renouf,<br>K Schultz |
| Genome Canada | CanCOGeN HostSeq program | 07/2020 to 12/2022 | Total CAD $20,000,000 | S Scherer | S Jones,<br>M Lathrop |
| Pacific Northwest Prostate Cancer SPORE | Signatures of genomic instability in prostate cancer circulating tumor DNA | 12/2020 to 11/2022 | Total US $50,000 | S Jones,<br>A Wyatt | |
| Genome BC | Genome BC Marathon of Hope Cancer Centre program | 10/2021 to 09/2022 | Total CAD $1,000,000 | M Marra,<br>D Renouf | S Jones |
| BCCF | Hereditary male breast cancer: characterization of known and novel familial predispositions using short and long reads sequencing technologies | 03/2020 to 09/2022 | Total CAD $74,891 | S Jones,<br>K Schrader | ML Thibodeau,<br>S Sun,<br>A Karsan,<br>S Yip,<br>J Laskin,<br>M Marra |
| NIH | Integrative miRNA data analysis for clinical cancer genomics | 09/2016 to 08/2022 | Total US $1,974,969 | S Jones,<br>T Knijnenburg | I Shmulevich,<br>Y Ma,<br>G Robertson,<br>S Reynolds |
| UBC | Dermatology Point-of-Care Intelligent Imaging Network-Digital Pathology | 08/2019 to 06/2022 | Total CAD $423,074 | S Jones,<br>M Marra,<br>S Yip | Key personnel:<br>R Coope |
| NSERC | Training Program In High-Dimensional Bioinformatics (HBD) | 04/2015 to 03/2022 | Total CAD $1,650,000 | P Pavlidis | S Jones,<br>R Morin,<br>F Brinkman,<br>J Bryan,<br>N Chen,<br>R Ng,<br>W Wasserman |
| CIHR | Canadian Epigenetics, Environment and Health Research Consortium Network | 07/2015 to 03/2022 | Total CAD $2,000,000 | M Hirst,<br>S Jones,<br>C Arrowsmith,<br>G Bourque,<br>L Foster,<br>T Pastinen | 12 co-applicants |

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| Genome Canada | Spruce-Up: Advanced spruce genomics for productive and resilient forests | 10/2016 to 03/2022 | Total CAD $10, 417,350 | J Bohlmann, J Bousquet | S Jones, I Birol, M Hirst, J Cook, N Gelinas |
| CANARIE | ClinDIG, a distributed system for clinical and genomics data | 04/2020 to 03/2022 | Total CAD $691,967 | M Brudno (NPI), G Bourque | S Jones |
| CIHR | Identification of Genetic Factors for Familial Lymphoid Cancers | 10/2013 to 03/2022 | Total CAD $799,698 | A. Brooks-Wilson | S Jones, M Marra, J Connors, H Lynch, S Slager, K Offit |
| CIHR | Modulators of epigenomic processes - a novel approach to cancer therapy | 07/2015 to 01/2022 | Total CAD $560,420 | S Jones | K Humphries |
| CCSRI | Long read DNA methylation sequencing for early detection of pancreatic adenocarcinoma | 01/2021 to 01/2022 | Total CAD $150,000 | S Jones, M Marra | P Bhatti, D Renouf, D Schaeffer |
| CFI | Preparing for the Next Wave: Technology to Detect and Analyze SARS-CoV-2 | 11/2020 to 09/2021 | Total CAD $401,238 | M Marra (NPI), S Jones, M Hirst, N Prystajecky | |
| CFI | Canadian Distributed cyber-Infrastructure for Genomics | 04/2016 to 09/2021 | Total CAD $3,920,000 | M Brudno (NPI), S Jones & 9 others | |
| Genome Canada | Enhancing Production In Coho: Culture, Community, Catch (EPIC4) | 10/2015 to 03/2021 | Total CAD $3,796,906 | W Davidson, L Bernatchez | S Jones |
| TFRI | The Terry Fox New Frontiers Program Project Grant in Discovery and Therapeutic Development of Antibody-Based Targets in Oncology | 07/2015 to 09/2020 | Total CAD $2,250,000 | Steven Jones | J Babcook, F Benard, G Morin, KS Lin, P Schaffer, T Hudlicky |
| Canarie | CanDIG National Genomic Data Service:CHORD | 10/2018 to 03/2020 | Total CAD $380,500 | G Bourque (NPI), M Brudno | S Jones |
| Genome BC | Personalized OncoGenomics 3.0 | 10/2016 to 03/2020 | Total CAD $2,000,000 | Marco Marra, Janessa Laskin | Steve Jones, Dean Regier |

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| TFRI | Terry Fox Canadian Comprehensive Cancer Centre Netwofrk Pilot (TF4CN Pilot) | 04/2017 to 03/2020 | Total CAD $2,000,000 | Francios Benard, Bradley Wouters | S Jones, M Marra, T Pugh, B Nelson, P Ohashi, D Jaffray, A Berlin |
| CFI | Canada's Genomics Enterprise (CGEn): A national genomic tools network for transforming life science research | 04/2015 to 03/2020 | Total CAD $58,435,136 | Steven Jones (NPI)<br>S Scherer, M Lathorp, G Bourque, M Brudno, R Holt, A Karsan, M Marra , H Ragoussis, M Taylor | |
| BCKDF | Canada's Genomics Enterprise (CGEn): A national infrastructure genomic tools for a transformative impact on biomedical and other life science research | 04/2015 to 03/2020 | Total CAD $8,364,268<br><br>Included in above CFI | Steven Jones | |
| CHIR | Centre for Epigenome Mapping Technologies | 01/2012 to 03/2019 | Total CAD $5,161,843 | Marco Marra, Steven Jones, Martin Hirst | Aparicio, Samuel; Cynader, Max; Eaves, Connie; Gascoyne, Randy; |
| NIH | Princess Margaret Phase 1 Consortium (PMP1C) | 04/2014 to 02/2019 | Total US $1,756,985 | L Siu, D, Sullivan, S Hotte, K Chi | S Jones, M Marra, S Aparicio & 8 others |
| TFRI | Modeling and Therapeutic Targeting of the Clinical and Genetic Diversity of Glioblastoma.<br>**245-TFRI-1247** | 07/2012 to 06/2018 | Total CAD $8,178,787 | Greg Cairncross | M Marra, S Jones, S Weiss, S Robbins, D Kaplan, D Mason |
| OpenMinTeD | Simplifying text mining of the PubMed and PubMed Central resources for up-to-date results | 02/2018 to 04/2018 | Total Euro €6,900 | Steven Jones | Jake Lever |
| Genome Canada | Personalized Treatment of Lymphoid Cancer: British Columbia as Model Province. | 04/2013 to 03/2018 | Total CAD $10,232,800 | J. Connors, M. Marra, R. Gascoyne | |
| CIHR | Epigenetic Modifications Regulating Hepatocellular Carcinoma and Hepatocyte Differentiation<br>**13-CIHR-1341** | 04/2013 to 03/2018 | Total CAD $1,200,000 | Pamela Hoodless | Steve Jones, Stephen Duncan, Isabella Tai |

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| CIHR | An Epigenomic Data Coordination Centre for Canada | 01/2012 to 03/2018 | Total CAD $1,478,992 | Steven Jones | Birol, Inanc; Lorincz, Matthew; Nielsen, Cydney; Hirst, Martin Milosavljevic, Aleksandar; Wang, Ting; Karimi, Mohammad |
| CFI | Genomics approaches to personalizing cancer diagnosis and treatment | 04/2014 to 12/2017 | Total CAD $14,140,000 | Marra M, Jones S, Holt R, Karsan A, Aparicio S, Huntsman, D, Gelmon, K, Laskin J, Rogers P, Toyota B. | |
| Genomics Innovation Network (GIN) | Methods and Technology Development at the Sequencing Platform at the BC Cancer Agency Genome Sciences Centre | 10/2015 to 09/2017 | Total CAD $2,000,000 | R Holt, M Marra | S Jones, I Birol, C Hansen, R Coope, A Mungall, R Morin, R Roscoe. |
| NIH | HIV tumour molecular characterization project<br>**31-NIH-1002** | 07/2011 to 05/2017 | Total US $12,670,280 | Marco Marra | Steven Jones, Martin Hirst |
| CIHR | Bioinformatics training for Health Research<br>**13-CIHR-800** | 09/2009 to 03/2017 | Total CDN amount $1,950,000 | Fiona Brinkman, Steven Jones | David Baillie, Jenny Bryan, Jack Chen, Anne Condon, Marco Marra, Paul Pavlidis, Cenk Sahinalp Wyeth |
| CCSRI | Modulators of FBXL2 to induce degradation of oncogenes – an innovative therapeutic approach<br>**256-CCSRI-1510** | 02/2014 to 01/2017 | Total CAD $195,240 | Steven Jones | Keith Humphries, Robert Young |
| Genome BC | Molecular and physiological characteristics of early ripening events in grapevine | 07/2014 to 12/2016 | Total CAD $200,000 | Simone Castellarin | Steve Jones, Gregory Gambetta |
| Genome Canada | Next Generation Bioinformatics for Clinical Genomics: using de novo assembly in personalized medicine | 10/2013 to 09/2016 | Total CAD $750,000 | Steven Jones, Inanc Birol, Aly Karsan | |

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| TFRI | The Terry Fox New Frontiers Program Project in Molecular Correlates of Treatment Failure in Lymphoid Cancers | 07/2013 to 06/2016 | Total CAD $3,885,626 | R Gascoyne, J Connors, M Marra, S Jones, S Shah, C Steidl | Ryan Morin |
| BC Cancer Foundation | Next Generation Bioinformatics for Clinical Genomics: using de novo assembly in personalized medicine | 07/2015 to 06/2016 | Total CAD $250,000 | Inanc Birol, Aly Karsan, Steven Jones | |
| NIH | Cancer transcriptome characterization using massively parallel DNA sequencing | 08/2009 to 06/2016 | Total US $10,876,220 | Marco Marra | Allen Delaney, Martin Hirst, Rob Holt, Steven Jones, Richard Moore, Ryan Morin, Robyn Roscoe, YJ Zhao |
| CFI | Ultra-high-throughput DNA Sequencing Platform for Large Scale Genome Analysis | 01/2010 to 03/2016 | Total CAD $10,065,940 | Marco Marra | Steven Jones Sam Aparicio, David Baillie, Joerg Bohlmann, Rob Brunham, Jan Friedman, Phil Hieter, Rob Holt, David Huntsman |
| BCKDF | Ultra-high-throughput DNA Sequencing Platform for Large Scale Genome Analysis | 02/2010 to 03/2016 | Total CAD $10,065,940 | Marco Marra | Steven Jones, Sam Aparicio, David Baillie, Joerg Bohlmann, Rob Brunham, Jan Friedman, Phil Hieter, Rob Holt, David Huntsman |
| CIHR | CIHR Team in Investigating Autophagy Proteins as Molecular Targets for Cancer Treatment | 12/2009 to 03/2016 | Total CAD $1,414,650 | Marcel Bally, Karen Gelmon, Julian Lum, Robert Young<br>S Gorski (nominated PI) | Helene Cote, Keith Humphries, Jiaoyan Jiang, Steven Jones.<br>Collaborators:<br>A Edwards, DL Forrest, C Lopez-Otin, Marco Marra, RI Nabi, B Nelson, P Watson, S Wiseman |
| Genome Canada | Genome Canada Science & Technology Innovation Centre | 01/2013 to 09/2015 | Total CAD $8,983,109 | Marco Marra, Steven Jones, Rob Holt | |

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| CHIR | Identifying Cytoprotective Responses Triggered Following Initial Exposure to Targeted Therapy: Defining Improved Treatment Strategies for Patients with HER-2 Positive Breast Cancer.<br>**13-CIHR-967** | 10/2010 to 09/2015 | Total CAD amount $774,155 | Marcel Bally | Steven Jones, Karen Gelmon |
| CIHR | Toward personalized immunotherapy: identifying tumour-specific factors that dictate the response of spontaneous mammary cancers to T cells | 10/2010 to 09/2015 | Total CAD amount: $671,932 | Brad Nelson | Allen Delaney, Steven Jones, Peter Watson |
| Genome BC | Bioinformatic Identification of Optimal Targets and Therapeutic Antibody Development in Oncology (SOF5) | 07/2013 to 03/2015 | Total CAD amount $196,846 | Steven Jones, John Babcook | Jianghong An |
| CIHR | CIHR Team Chromatin marks in normal and malignant stem cells | 10/2008 to 03/2015 | Total CAD amount $2,497,744 | Peter Lansdorp | Martin Hirst, Keith Humphries, Steve Jones, Louis Lefebvre, Matthew Lorincz |
| Genome BC | Stratifying and Targeting Pediatric Medulloblastoma Through Genomics | 07/2011 to 03/2015 | Totol CAD amount $9,856,814 | Marco Marra, Michael Taylor, David Malkin | Steven Jones, et al (12 others) |
| Genome Canada | SMarTForest: Spruce Marker Technologies for Sustainable Forestry | 07/2011 to 06/2014 | Total CAD amount $9,900,000 | J MacKay, J Bohlmann | K Ritland, J Bousquet, J Cooke, N Gelinas, S Jones, A Yanchuk, N Isabel, J Beaulieu, G |
| NIH-SAIC-Frederick | Sequencing for Discovery of Candidate Mutations in Lymphoma Transcriptomes | 07/2008 to 06/2014 | Total US Amount $14,213,780 | Marco Marra | Steven Jones, Joe Connor, Randy Gascoyne, Martin Hirst, Doug Horsman |

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| NIH | Integrated Epigenetic Maps of Human Embryonic and Adult Cells | 08/2008 to 06/2014 | Total US amount $14,630,140 | Joseph Costello, Marco Marra | Steven Jones, Martin Hirst, Robyn Roscoe<br>Alvarez-Buylla, Arturo<br>Farnham, Peggy<br>Fisher, Susan<br>Haussler, David<br>Kent, James<br>McManus, Michael<br>Tlsty, Thea<br>Wang, Ting<br>Weiss, Arthur<br>Balmain, Allan<br>De Jong, Pieter<br>Gray, Joe<br>Karpen, Gary<br>Kwok, Pui-Yan<br>Panning, Barbara<br>Pinkel, Dan<br>Segal, Mark |
| Genome Canda | Genomics-Based Forest Health Diagnostics and Monitoring | 04/2011 to 04/2014 | Total CAD amount $4,179,683 | Richard Hamelin | Steven Jones, Kermit Ritland, Andre Marziali, Jeremy Kent, Phillippe Tanguay, Adrian Uzunovic |
| Genome BC | Genomics applied to the management of high-risk AML/myelodysplastic syndromes | 07/2011 to 03/2014 | Total CAD amount $3,113,494 | Aly Karsan, Marco Marra | Steven Jones, Donna Hogge, Keith Humphries, Stuart Peacock, Peter Chow-White, Andrew Feenberg |
| Genome BC | Sequencing and comparative genome mapping of Chardonnay grapevine clones | 11/2011 to 02/2014 | Total CAD amount $224,988 | Hennie Van Vuuren, Isak Pretorius | J Bohlmann, A Borneman, P Chambers, M Herderich, D Johnson, S Jones, S Schmidt. |
| CCSRI | The Genomic Characterization of Thyroid Cancers | 07/2010 to 06/2013 | Total CAD amount $408,520 | Steven Jones | Sam Wiseman |
| NCIC | Biology of Cancer: Insights from Genomic Analyses of Lymphoid Neoplasms | 07/2008 to 06/2013 | Total CAD amount $6,284,994 | Joseph Connors, Randy Gascoyne, Doug Horsman, Marco Marra | Steven Jones |
| MSFHR **Senior Scholar Award** | Bioinformatic approaches for the interpretation of cancer genomes | 07/2008 to 06/2013 | Total CAD amount $500,000 | Steven Jones | Collaborators:Angie Brook-Wilson, Pamela Hoodless, Isabella Tai |
| Genome Canada | Genomics Innovation Centre at the BC Cancer Agency | 04/2011 to 03/2013 | Total CAD amount $7,189,816 | Marco Marra, Steven Jones, Rob Holt | |

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| Genome Canada | Genomics-Enhanced Forecasting Tools to Secure Canada's Near-Term Lignocellulosic Feedstock Supply for Bioenergy using the Mountain Pine Beetle-Pinus supp. System | 04/2010 to 03/2013 | Total CAD amount $7,795,145 | Joerg Bohlmann, Janice Cooke | Steven Jones, Brian Aukema, Colette Breuil, David Coltman, Nadir Erbilgin, Maya Evenden, Richard Hamelin, Dezene Huber, Chris Keeling, Brent Murray,Feliz |
| Genome Canada | The Canadian Pediatric Cancer Genome Consortium: Translating next-generation sequencing technologies into improved therapies for high-risk childhood cancer. | 07/2011 to 03/2013 | Total CAD amount $2,827,359 | P Sorenson, C Fernandez, C Hawkins, A Huang, N Jabado, D Malkin, D Sinnett, M Taylor | S Jones, M Marra, A Monpetit, K Schultz, C Strahlendorf, G Bourque, S Yip. |
| Genome Canada<br>(FORGE) | Canadian Pediatric Genetic Disorders Sequencing (CPGDS) Consortium | 04/2011 to 03/2013 | Total CAD amount $2,874,956 | Kym Boycott | Steven Jones, Jan Friedman, Jacques Michaud |
| CIHR | CIHR Team in Genomic, Imaging and Modeling Approaches to Advance Population-Based Colorectal Cancer Screening<br>**13-CIHR-501** | 10/2007 to 03/2013 | Total CAD amount $2,384,996 | A. Coldman, M. Elwood, C. MacAulay, S. Peacock., I. Tai, H. Zeng | Collaborators:<br>S. Jones, M. Marra, et al |
| NCIC | The identification of mutation specific inhibitors through whole genome re-sequencing of breast cancer cell-lines<br>**28-NCIC-27** | 07/2007 to 06/2012 | Total CAD amount $605,066 | Steven Jones | Jianghong An |
| CIHR | Improving computational inference of single nucleotide variants from next generation sequencing of cancer genomes | 10/2010 to 09/2011 | Total CAD amount $100,000 | Sam Aparicio | Steven Jones, Ann Condon, David Huntsman, Kevin P Murphy,Sohrab P. Shah |
| NIH | A Comprehensive Catalog of Human DnaseI Hypersensitive Sites | 09/2007 to 08/2011 | Total US amount $443,064 | John Stammatoyannopolous | Steven Jones, Marco Marra |
| Genome Canada | Genome BC Genomics Platforms at BC Cancer Agency Genome Sciences Centre | 01/2009 to 03/2011 | Total CAD amount: $6,471,892 | Marco Marra, Steven Jones, Rob Holt | Inanc Birol, Jacquie Schein, Allen Delaney, Martin Hirst, Richard Moore |
| CIHR | 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<br>**13-CIHR-685** | 07/2008 to 06/2011 | Total CAD amount $477,534 | Marcel Bally | Sam Aparicio, Steven Jones, Janessa Laskin, Marco Marra |

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| CIHR | Toward personalized immunotherapy: Identifying tumour-specific factors that dictate the response of spontaneous mammary cancers to different T cell therapies | 04/2007 to 09/2010 | Total CAD amount: $379,347 | Brad Nelson | Allen Delaney, Steven Jones, Peter Watson |
| Genome BC | Short Sequencing Assembly and Finishing of Large Genomes. | 10/2009 to 09/2010 | Total CAD $95,000 | Inanc Birol, Steven Jones | |
| Heart & Stroke Foundation of Canada | Dissecting Gene Regulatory Networks in Cardiac Cushion Development | 07/2007 to 07/2010 | Total CAD amount: $376,416 | Aly Karsan | Pamela Hoodless, Marco Marra<br>Steven Jones |
| Genome Canada | Production-Scale Deployment of Next-Generation Sequencing Instruments | 01/2008 to 03/2010 | Total CAD amount $1,912,521 | Rob Holt, Steven Jones,<br>Marco Marra | Martin Hirst |
| Genome Canada | Towards Single Cell Genomic Analysis | 04/2008 to 03/2010 | Total CAD amount $1,824,278 | Carl Hansen, Marco Marra | Sam Aparicio, Martin Hirst, Steven Jones |
| SFU CTEF<br>Community Trust Endowment Fund | Bioinformatics for Combating Infectious Diseases: Novel methods for drug and target identification and evaluation | 04/2007 to 03/2012<br>Funding completed 2010 | Total CAD amount $350,000 | Fiona Brinkman, Cenk Sahinalp | Steven Jones, Peter Unrau, Jack Chen, David Baillie, Martin Ester, Jian Pei, Eldon Emberly, Carl Lowenberger, Peter Wilson, Art Cherkasov |
| Genome Canada | Dissecting Gene Expression Networks in Mammalian Organogenesis | 01/2006 to 06/2010 | Total CAD amount:<br>$7,770,032 | Pamela Hoodless, Marco Marra | Aly Karsan, Cheryl Helgason, Steven Jones, Sidney Katz, Ed Levy |
| NIH | Genomic and proteomic analysis of androgen independent prostate cancer<br>Grant # 1 R01 CA105304-01 | 04/2004 to 02/2010 | Total USD amount:<br>$1,078,854 | Marianne Sadar | Marco Marra, Steven Jones, Yuzhou Wang, Robert Holt, Katie Meehan |
| Genome BC | Development of Efficient Algorithms and Technologies for Structural Variation Detection by Single Molecule Sequencing<br>**19-GBC-750** | 01/2009 to 12/2009 | Total CAD amount $68,000 | Inanc Birol, Cenk Sahinalp | Steven Jones |
| Genome BC | The Mountain Pine Beetle Epidemic | 01/2008 to 12/2009 | Total CAD amount $4,063,524 | Joerg Bohlmann, Janice Cooke | Robert Holt, Steven Jones, Marco Marra, et al |
| Genome Canada | High Resolution Analysis of Follicular Lymphoma genomes | 01/2006 to 12/2009 | Total CAD amount: $9,341,856 | Marco Marra, Joseph Connors, Randy Gascoyne | Doug Horsman, Martin Krzywinski, Jacquie Schein, Robert Holt, Steven Jones, Carlo Marra |

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| Genome Canada | Pleiades Promoter Project | 01/2006 to 12/2009 | Total CAD amount: $10,118,120 | Elizabeth Simpson | Dan Goldowitz, Steven Jones, Rob Holt, Wyeth Wasserman, |
| Genome Canada | Genome BC Large Scale, High Throughput Genomics Platforms at BCCA-GSC<br>(Competition III Platform) | 01/2006 to 12/2008 | Total CAD amount: $8,907,686 | Marco Marra, Steven Jones, Rob Holt | Asim Siddiqui, Agnes Baross, Martin Hirst, Inanc Birol, Martin Krzywinski, Allen Delaney, Francis Ouellette, Jacquie |
| NIH/NCI | Optical Systems for In Vivo Molecular Imaging of Cancer | 09/2004 to 08/2009 | Total USD amount: $8,583,213 | Rebecca Rae Richards-Kortum | Michael Descour, Calum MacAulay, Konstantin Sokolov, Steven Jones, Mladen Korbelik, Brian Korgel, Stephen Lam, Wan Lam, Peter Lansdorp, Mia Markey, Marco Marra, Renata Pasqualini, Miriam Rsin, Krishnendu Roy, William |
| NIH | Mechanisms of HOX Protein Mediated Transformation<br># 1R01CA116570-01A1 | 08/2006 to 06/~~2011~~<br>08/2009 | Total USD amount: $1,361,525 | Jay Hess | Steven Jones, Gordon Robertson, Ali Shilatifard |
| CIHR | Bioinformatics training for health research<br>Training Program<br>Grant# STP-53919 | 03/2002 to 08/2009 | Total CAD amount: $2,020,821 | Steven Jones | David Baillie, Phil Heiter, Marco Marra, Fiona Brinkman, Jenny Bryan, Anne Condon, Arvind |
| MSFHR | Cancer, the Environment and Occupation (CEO): the program of the Cancer Control Research Unit at the BCCA<br>**56-MSFHR-155** | 07/2004 to 03/2009 | Total CAD amount: $724,311 | Rick Gallagher | A. Brooks-Wilson, M. Marra, S. Jones, J. Spinelli, N. Le, C. Bajdik et al |
| CIHR | Characterization of regulatory regions, modules and elements in mammalian genomes. | 07/2007 to 06/2008 | Total CAD amount $100,000 | Steve Jones | Marco Marra, Pamela Hoodless |
| NCIC | Biology of Cancer: Follicular Lymphoma as a Model of Cancer Progression | 07/2005 to 06/2008 | Total CAD amount: $3,540,067 | Joseph Connors | Co-Applicants:<br>Marco Marra, Randy Gascoyne, Doug Horsman<br>Collaborators:<br>Jacquie Schien, Steven Jones, |
| CIHR | Genomics, Genetics & Gerontology (G3): A multidisciplinary team for the study of healthy aging<br>Grant #:116074 | 04/2003 to 03/2008 | Total CAD amount: $1,159,844 | Marco Marra and Angela Brooks-Wilson | Steven Jones, Nhu Le, Joseph Connors, Graydon Meneilly |

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| Prostate Cancer Research Foundati-on of Canada | Structure Based Drug Discovery against Novel Binding Pockets of Androgen Receptors | 03/2006 to 02/2008 | Total CAD amount: $60,000 | Steven Jones | Marianne Sadar, Jianghong An |
| Genome Canada | Bioinformatics Platform (Applied Genomics and Proteomics) | 01/2005 to 12/2007 | Total CAD Amount: $367,367 | Steven Jones | |
| Genome Spain / Genome Canada | A Genomic Approach to the identification of the genetic and environmental components underlying Berry quality in Grapevine (GRAPEgen) | 11/2004 to 10/2007 | Total CAD amount: $3,134,481 | Steven Lund, Jose Miguel Martinez-Zapatar | Joerg Bohlmann, Steve Jones |
| MSFHR | Supplemental Training Program Award (CIHR: Bioinformatics training for health research) | 03/2002 to 02/2007 | Total CAD amount: $300,000 | Steven Jones | |
| Genome Canada | Bovine Genome Project: Full Insert cDNA Sequencing Plan | 08/2004 to 07/2007 | Total CAD amount: $6,595,723 | Marco Marra, R.Holt, S.Jones, Stephen Moore | |
| Genome Canada | Genomic Tools for Diagnosis & Evaluation of Mental Retardation | 04/2004 to 09/2007 | Total CAD Amount: $5,558,741 | Jan Friedman & Marco Marra | Jacquie Schein, Steven Jones, Sylvie Langlois, Patrice Eydoux, Bartha Knoppers, Donna Albertson, Wan Lam, Dan Pinkel, Evica Rajcan-Separovic, Carlo Marra, Rob Holt |
| NIH / NHGRI | Improvements in BAC fingerprinting and end sequencing Grant# U01 HG002743-01 | 04/2003 to 11/2006 | Total USD amount: $4,316,678 | Marco Marra | Stephane Flibotte, Dan Fuhrmann, Steven Jones, Martin Krzywinski, Andre Marziali, |
| NIH | Large Scale Genome Sequencing / Validation and improvement of Whole Genome Assemblies Grant # 1 U54 HG03079-01 | 11/2003 to 10/2006 | Total USD amount: $274,603 | Richard Wilson | Steven Jones |
| Genome Canada / Genome BC | Bioinformatics Platform – Competition I & II & Other | 10/2001 to 03/2005 | Total CAD amount: $8,795,055 | Steven Jones | |
| Genome Canada / Genome BC | Cancer Genomics – Competition I | 10/2001 to 03/2005 | Total CAD amount: 16,740,911 | Victor Ling, Marco Marra, Connie Eaves | Steven Jones, Stephen Lam, Wan Lam, Calum MacAulay, Miriam Rosin, Juergen Vielkind |
| Genome Canada / Genome BC | A quantitative and comprehensive atlas of gene expression in mouse development – Competition II | 07/2002 to 03/2006 | INCLUDED IN BIOINFORMATICS PLATFORM Total CAD amount: $13,195,524 | Marco Marra and Pamela Hoodless | Robert Strausberg, Elizabeth Simpson, Cheryl Helgason, Gregory Riggins, Steven Jones |

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| Genome Canada / Genome BC | Bioinformatics of mammalian gene expression (BoMGE) – Competition II | 07/2002 to 03/2006 | Total CAD amount: $6,134,386 | Steven Jones | Marco Marra |
| BCKDF | Matching funds: Bioinformatics of Mammalian Gene Expression (Genome Canada: BoMGE) | 10/2005 – 03/2006 | Total CAD amount: $411,848 | Steven Jones | |
| Genome Canada / Genome BC | Expression profiles of cells and tissues in *C. elegans* – Competition II | 07/2002 to 03/2006 | INCLUDED IN BIOINFORMATICS PLATFORM: Total CAD amount: $3,000,000 | David Baillie | Steven Jones, Marco Marra, Francis Ouellette, Don Moerman, Claes Wahlestedt, Erik Sonnhammer, |
| MSFHR | Institutional Infrastructure Proposal for Health Research for the BCCA | 06/2003 to 03/2006 | Total CAD amount: $2,198,039 | 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 Lansforp, W Linden, C MacAulay, D Mager, M Marra, L Mayer, M McBride, N Murray, B Nelson, S O'Reilly, P Olive, I Olivotto, M Rosin, T Ruth, M Sadar, C Smith, J Spinelli |
| CIHR | Development of a mass spectrometry-based method of full-length sequencing of proteins | 03/2003 to 02/2006 | Total CAD amount: $283,386 | Juergen Kast | Steven Jones |
| Genome Canada | Functional Pathogenomics of Mucosal Immunity | 07/2002 to 03/2005 | Total CAD amount $13,465,710 | Lorne Babiuk<br>Robert Hancock | Mitchell Abrahamsen, Fiona Brinkman, Brett Finlay, Philip Gribel, Steven Jones, Andy Potter |
| Genome Canada / Genome BC | Comparative and functional genomics of the human pathogen *Cryptococcus neoformans* – Competition II | 07/2002 to 03/2005 | INCLUDED IN BIOINFORMATICS PLATFORM | Jim Kronstad | Robert Bruhham, Marco Marra, Steven Jones, Colleen Nelson |

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| Alfred P. Sloan Foundation | Supplemental Training Program Award (CIHR: Bioinformatics training for health research) | 10/2003 to 12/2004 | Total CAD amount: $87,990 | Steven Jones | |
| CIHR | SARS: A scientific collaborative to support public health response through vaccination | 08/2003 to 08/2004 | Total CAD amount: $500,000 | 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, Michael Drebot |
| Canadian Cancer Etiology Research Network | Identifying groups of genetically-related cancers<br>Grant #03-03-04 | 05/2003 to 04/2004 | Total CAD amount: $20,228 | Chris Bajdik | Angela Brooks-Wilson, Steven Jones |
| Alberta Science & Research Authority (ASRA) | Bovine Genome Project | 03/2001 to 03/2004 | Total CAD amount: $500,000 | Steve Moore | Marco Marra, Steven Jones, Bernie Benkel |
| NIH | Full length cDNA sequencing<br>Sub-contract #:20XS180 | 08/2000 to 02/2004 | Total USD amount: $4,067,426 | Marco Marra | Steven Jones |
| Genome Canada / Genome Quebec | Functional genomics of regulation in forest trees | 01/2003 to 12/2003 | Total CAD amount: $424,900 | John McKay | Steven Jones |
| NSERC | Genome and Transcriptome analysis of the human pathogen *Cryptococcus neoformans*<br>Grant #: 228249-99 | 02/2000 to 01/2003 | Total CAD amount: $616,337 | Jim Kronstad | Marco Marra, Steven Jones |
| Peter Wall Institute for Advanced Studies | Pathogenomics – An innovative approach to the study of infectious diseases | 08/1999 to 07/2002 | Total CAD amount: $500,000 | Ann Rose | Steven Jones, Francis Ouellette, Bob Hancock, David Baillie, Sarah Otto, Brett Finlay |
| 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 CAD amount: $69,850 | Guus Bakkaren | Steven Jones, Marco Marra, Guanggan Hu |

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| CFI | CGDN and UBC Bioinformatics Infrastructure (CUBI) | 04/2001 to 03/2002 | Total CAD amount: 1,568,410 | Francis Ouellette | Steven Jones |
| CFI | Team Leaders for a Genome Sequence Centre | 04/2000 to 03/2002 | Total CAD amount: $700,000 | Victor Ling | Steven Jones, Marco Marra |

## PATENTS TOTAL 31

**Issued:**

1. **PCT International patent application # ePCT Version 4.11.007 MT/FOP 20230501/1.1 (pending)** entitled: “A method and apparatus for parent-of-origin disease allele detection for the diagnosis and management of genetic diseases.” Inventors: Vahid Akbari, Vincent C. T. Hanlon, Kieran O’Neill, Kasmintan A. Schrader, Peter M. Lansdorp and **Steven J.M. Jones. Submitted:** May 10, 2023

2. **US Patent (Filing date: May 11, 2022)** entitled: “A method and apparatus for parent-of-origin disease allele detection for the diagnosis and management of genetic diseases.” Inventors: Vahid Akbari, Vincent C. T. Hanlon, Kieran O’Neill, Kasmintan A. Schrader, Peter M. Lansdorp and **Steven J.M. Jones**. **Application** # 63/340,712: **Submitted:** May 11, 2022

3. **US Patent (Filing date: March 10, 2021)** entitled: “Immunotherapy agents targeting brachyury and methods of using same.” Inventors: Robert Holt, Laura Williamson, Craig Rive, Daniela Di Francesco, Emma Titmuss, **Steven J.M. Jones,** Janessa Laskin, Shahrad Rassekh, Rebecca Deyell, Marco Marra.. **Steven J.M. Jones**. **Application** # 63/200,483: **Submitted:** March 10, 2021

4. **US Patent (issued April 4, 2017)** entitled: “TNNT1 Mini-Promoters.” Inventors: Simpson Elizabeth M, Wasserman Wyeth W, Holt Robert A, **Jones Steven J**, Goldowitz Daniel, Portales-Casamar Elodie, D’Souza Cletus, Chopra Vikramjit, de Leeuw Charles. Publication #:20150343020 **Publication Date**:Dec 3, 2015

5. **US Patent 9,552,457 (issued January 24, 2017)** entitled "Reprogramming Effector Protein Interactions to Correct Epigenetic Defects in Cancer". Inventors: **Steven Jones,** Oleksandr Yakovenko, Silvia Thoene, Jianghong An and Pierre Yulmin CHEUNG. **Publication #:** 20150154345 **Publication Date**: June 4, 2015

6. **US Patent 9,546,357 (issued January 17, 2017)** entitled: “UGT8 Mini-Promoters.” Inventors: Simpson Elizabeth M, Wasserman Wyeth W, Holt Robert A, **Jones Steven J**, Goldowitz Daniel, Portales-Casamar Elodie, D’Souza Cletus, Chopra Vikramjit, de Leeuw Charles. **Publication #:** 20150259691 **Publication Date:** Sept 17, 2015

7. **US Patent 9,006,413 (issued April 14, 2015)** entitled “PCP2 Mini-Promoter”. Inventors: Simpson Elizabeth M, Wasserman Wyeth W, Holt Robert A, **Jones Steven J**, Goldowitz Daniel, Portales-Casamar Elodie, D’Souza Cletus, Chopra Vikramjit, de Leeuw Charles. **Publication #:** 20140141517 **Publication Date**: May 22, 2014

8. **US Patent 8,895,715 (issued November 25, 2014)** entitled “S100B mini-promoters”. Inventors: Simpson E, Wasserman W, Holt RA, **Jones SJM**, Goldowitz D, Portales-Casamar E, D’Souza C, Chopra V. **Publication #:** 20090280568 **Publication Date**: November 12, 2009

9. **US Patent 8,742,156 (issued June 3, 2014)** entitled "Anti-Viral Carbamimidothioic Acid Esters". Inventors: **Jones Steven J**; Lau Allan Sik-Yin; An Jianghong; Law Hing-Yee; Lee Chun-Wai Davy. **Publication #:** 20130143961 **Publication Date**: June 6, 2013

10. **US Patent 8,673,884 (issued March 18, 2014)** entitled "Anti-Influenza Compounds" Inventors: **JONES Steven J**; LAU Allan Sik-Yin; AN Jianghong; LAW Hing Yee; LEE Chun Wai Davy; POON Lit Man. **Publication #:** 20110009369 **Publication Date**: January 13, 2011

11. **US Patent 8,629,261 (issued January 14, 2014)** entitled "Olig1 mini-promoters". Inventors: Simpson E, Wasserman W, Holt RA, **Jones SJM**, Goldowitz D, Portales-Casamar E, D'Souza C, Chopra V. **Publication #:** 20100081201 **Publication Date**: April 1, 2010
12. **US Patent 8,598,331 (issued December 3, 2013)** Title "CLDN5 Mini-Promoters". Inventors: Simpson Elizabeth M, Wasserman Wyeth W, Holt Robert A, **Jones Steven J**, Goldowitz Daniel, Portales-Casamar Elodie, D'Souza Cletus, Chopra Vikramjit. **Publication #:** 20110097803 **Publication Date**: April 28, 2011

13. **US Patent 8,383,803 (issued February 26, 2013)** entitled "PITX3 expression promoters**".** Inventors: Simpson Elizabeth M, Wasserman Wyeth W, Holt Robert A, **Jones Steven J**, Goldowitz Daniel, Portales-Casamar Elodie, D'Souza Cletus, Chopra Vikramjit. **Publication #:** 20100129903 **Publication Date**: May 27, 2010.

14. **US Patent 8,383,800 (issued February 26, 2013) entitled** "MK167 Mini-Promoters". Inventors: Simpson Elizabeth M, Wasserman Wyeth W, Holt Robert A, **Jones Steven J**, Goldowitz Daniel, Portales-Casamar Elodie, D'Souza Cletus, Chopra Vikramjit. **Publication #:** 20110136235 **Publication Date**: June 9, 2011.

15. **US Patent 7,897,744 (issued March 1, 2011)** entitled "SARS virus nucleotide and amino acid sequences and uses thereof". Inventors: Plummer; Frank, Feldmann; Heinz, Jones; Steven , Li; Yan, Bastien; Nathalie, Brunham; Robert Conrad, Brooks-Wilson; Angela, Holt; Robert, Upton; Christopher, Roper; Rachel, Astell; Caroline, **Jones; Steven**. **Publication #:** 20070258999 **Publication Date**: November 8, 2007

16. **US Patent 7,648,827 (issued January 19, 2010)** entitled "Use of eukaryotic genes affecting cell cycle control or cell cycle progression for diagnosis and treatment of proliferative diseases". Inventors: Echeverri; Christophe, Hyman; Anthony, Gonczy; Pierre, Sonnichsen; Birte, **Jones; Steven** , Walsh; Andrew, Koski; Liisa.

17. **US Patent 7,479,369 (issued January 20, 2009)** entitled "Use of eukaryotic genes affecting spindle formation or microtubule function during cell division for diagnosis and treatment of proliferative diseases" Inventors: Echeverri; Christophe, Hyman; Anthony, Gonczy; Pierre, Sonnichsen; Birte, **Jones; Steven** , Walsh; Andrew, Koski; Liisa. **Publication #:** 20070093438 **Publication Date**: April 26, 2007

18. **US Patent 7,368,248 (issued May 6, 2008)** entitled "Eukaryotic cell division genes and their use in diagnosis and treatment of proliferative diseases" Inventors: Echeverri; Christophe, Goenczy; Pierre, Hyman; Anthony, **Jones; Steven ,** Oegema; Karen , Kirkham; Matthew.

**Pending:**

19. **US Provisional patent application # 61/988,778 (pending)** filed May 5, 2014 entitled: "SLC6A4 Mini-Promoters." Inventors: Simpson Elizabeth M, Wasserman Wyeth W, Holt Robert A, **Jones Steven J**, Goldowitz Daniel, Portales-Casamar Elodie, D'Souza Cletus, de Leeuw Charles. **Publication #:** 20150315609 **Publication Date:** November 5, 2015

20. **United States Patent Application No. 14/252,624 (pending)** filed April 14, 2014 entitled: "Cholecystokinin B Receptor (CCKBR) Mini-Promoters." Inventors: Simpson Elizabeth M, Wasserman Wyeth W, Holt Robert A, **Jones Steven J**, Goldowitz Daniel, Portales-Casamar Elodie, D'Souza Cletus, Chopra Vikramjit, de Leeuw Charles. **Publication #:** 20140315987 **Publication Date**: October 23, 2014. **Publication #:** 20140256800 **Publication Date**: September 11, 2014

21. **United States Patent Application No. 14/195,290 (pending)** filed March 3, 2014 entitled "Fev Mini-Promoters". Inventors: Simpson Elizabeth M, Wasserman Wyeth W, Holt Robert A, **Jones Steven J**, Goldowitz Daniel, Portales-Casamar Elodie, D'Souza Cletus, Chopra Vikramjit, de Leeuw Charles. **Publication #**: 20140256800 **Publication Date:** September 11, 2014.

22. **US Provisional patent application # 61/879,047 (pending)** filed September 17, 2013 entitled "GPR88 Mini-Promoters". Inventors: Simpson Elizabeth M, Wasserman Wyeth W, Holt Robert A, **Jones Steven J**, Goldowitz Daniel, Portales-Casamar Elodie, D'Souza Cletus, Chopra Vikramjit, de Leeuw Charles. **Publication #:** 20150166636 **Publication Date:** Jne 18, 2015.

23. **US Provisional patent application # 61761940 (pending)** filed February 7, 2013 entitled "Compositions and Methods for Treatment of Prostate Cancer". Inventors: **Steven Jones**, Jianghong An, Marianne Sadar, Nasrin (Rina) Mawji and Amina Zoubeidi

24. **US Provisional patent application # 61/756,876 (pending)** filed January 25, 2013 entitled "DXC Mini-Promoters". Inventors: Simpson Elizabeth M, Wasserman Wyeth W, Holt Robert A, **Jones Steven J**, Goldowitz Daniel, Portales-Casamar Elodie, D'Souza Cletus, Chopra Vikramjit, de Leeuw Charles

25. **PCT International patent application # PCT/CA2012/050902 (pending)** filed on December 14, 2012 entitled "Mutations Indicative of Weaver Syndrome". Inventors: GIBSON, William T.; **JONES, Steven J. M.**

26. **PCT International patent application # PCT/CA2012/050767 (pending)** filed on October 26, 2012 entitled "Epigenetic Regulators and Uses Thereof". Inventors: Mungall, Andrew; Cheung, Pierre Yulmin, **Jones, Steven J.M.**, Yakovenko, Oleksandr, Thoene, Silvia.

27. **Canadian patent application # 2713848 (pending)** filed on February 4, 2009 entitled "Anti-Influenza Compounds" Inventors: **JONES, Steven, J**.; LAU, Allan, Sik-Yin; AN, Jianghong; LAW, Hing, Yee; LEE, Chun, Wai, Davy; POON, Lit, Man.

28. **European patent # EP1682573A2 (pending)** filed September 15, 2004 entitled "Use of eukaryotic genes affecting cell cycle control or cell cycle progression for diagnosis and treatment of proliferative diseases". Inventors: Echeverri; Christophe, Hyman; Anthony, Gonczy; Pierre, Sonnichsen; Birte, **Jones; Steven** , Walsh; Andrew, Koski; Liisa.

29. **European patent # EP1682663A2 (pending)** filed September 15, 2004 entitled "Use of eukaryotic genes affecting spindle formation or microtubule function during cell division for diagnosis and treatment of proliferative diseases". Inventors: Echeverri; Christophe, Hyman; Anthony, Gonczy; Pierre, Sonnichsen; Birte, **Jones; Steven** , Walsh; Andrew, Koski; Liisa.

30. **Canadian patent application #2523875 (pending)** filed on April 28, 2004 entitled "SARS virus nucleotide and amino acid sequences and uses thereof". Inventors: Plummer; Frank, Feldmann; Heinz, Jones; Steven , Li; Yan, Bastien; Nathalie, Brunham; Robert Conrad, Brooks-Wilson; Angela, Holt; Robert, Upton; Christopher, Roper; Rachel, Astell; Caroline, **Jones; Steven**.

31. **European patent # EP1334123B1 (pending)** filed September 11, 2001 entitled "Eukaryotic cell division genes and their use in diagnosis and treatment of proliferative diseases" Inventors: Echeverri; Christophe, Goenczy; Pierre, Hyman; Anthony, **Jones; Steven** , Oegema; Karen , Kirkham; Matthew. **Publication #:** 2002224838 **Publication Date**: April 11, 2002.

## BOOK CHAPTERS AND REVIEW ARTICLES: TOTAL 16

1. Akbari, V, **Jones, SJM** (2022). Phasing DNA Methylation. In: Peters, B.A., Drmanac, R. (eds) **Haplotyping**. Methods in Molecular Biology, vol 2590, pp 219-235. Humana, New York, NY.

2. Kasaian K, Li YY, **Jones SJM** (2013). Bioinformatics for Cancer Genomics. In Dellaire G & Berman JN & Arceci RJ (Eds.), *Cancer Genomics: From Bench to Personalized Medicine* (pp 134-152). San Diego, CA: Academic Press.

3. Li YY, **Jones SJ**. Drug repositioning for personalized medicine. **Genome Med**. 2012 Mar 30;4(3):27. PMID: 22494857.

4. Kasaian K, **Jones SJ**. A new frontier in personalized cancer therapy: mapping molecular changes. **Future Oncol**. 2011 Jul;7(7):873-94. Review.

5. Montgomery SB, Kasaian K, **Jones SJ**, Griffith OL. Annotating the regulatory genome. Methods Mol Biol. 2010. 674: p. 313-49. Review.

6. Griffith Ol, Melck A, **Jones SJM**, Wiseman SM. Thyroid Cancer: Identification of Gene Expression Markers for Diagnosis. **Methods of Cancer Diagnosis, Therapy and Prognosis.** Hyat MA, editor, Springer Publishing Company, New York, NY. 7(3):353-377, DOI: 10.1007/978-90-481-3186-0_24. Published: January 3, 2010.

7. Hoffman BG, **Jones SJM**. Genome-wide identification of DNA-protein interactions using Chromatin Immunoprecipitatio coupled with flow cell Sequencing. **Journal of Endocrinology.** 2009 Jan: 201,1-13.

8. Fejes AP, **Jones SJM**. Chapter contribution to "Next generation genome sequencing – toward personalized medicine" **Wiley-VCH.** Ed. Janitz. 978-3-527-32090-5**.** Published Oct. 2008.

9. Griffith OL, Chiu CG, Gown AM, **Jones SJ**, Wiseman SM. Biomarker panel diagnosis of thyroid cancer: a critical review. Expert Rev Anticancer Ther. 2008 Sep;8(9):1399-413.

10. Holt RA, **Jones SJM**. The new paradigm of flow cell sequencing. **Genome Research.** Invited review article. 2008 Jun;18(6):839-46

11. **Jones SJM.** "Prediction of Genomic Functional Elements." **Annual Review of Genomics and Human Genetics**: Vol 7**.** 2006;7:315-38.

12. Pleasance ED, **Jones SJM**. "Evaluation of SAGE tags for transcriptome study". **SAGE Technologies: Current Technologies and Applications**.Ed San Ming Wang. Norwich, UK: Horizon Bioscience, 2005.

13. Siddiqui A, **Jones S**. "Contig Mapping and Analysis." **Encyclopedia of Genetics, Genomics, Proteomics and Bioinformatics**. Ed. A Kuspa. Chichester, UK: John Wiley & Sons, Ltd, 2004.

14. Astell CR, Holt RA, **Jones SJM**, Marra MA. "Genome Organization and Structural Aspects of the SARS-related Virus." **Birkhauser Advances in Infectious Diseases**: Vol I. Eds A. Schmidt, M.H. Wolff, S.H.E. Kaufman. Basel, CHE: Birkhauser, 2004. 101-128pp.

15. Bird D, Opperman CH, **Jones SJM**, Baillie DL. "The *Caenorhabditis elegans* genome: A guide in the post genomics age." **Annual Review of Phytopathology**: Vol 37. Palo Alto, CA, 1999. 247-265pp.

16. **Jones SJM,** Hodgson D. "Internet resources for invertebrates." **Internet for the Molecular Biologist.** Eds S.R. Swindell, R.R. Miller, G.S.A. Myers. Norwich, UK: Horizon Scientific Press, 1996.

## PEER REVIEWED PUBLICATIONS: TOTAL 551

**Google Scholar: [https://goo.gl/QxjJ34](https://goo.gl/QxjJ34) h-index = 153; Citations = 196,342 (As of Mar 2024)**

1. 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.

2. Warren RL, Abraham R, Calingo M, Garant J-M, **Jones SJM**, Birol I, CGEn HostSeq Initiative. Establishing association between HLA-C*04:01 and severe COVID-19. **HLA**. 2024 Jan;103(1):e15355. doi: 10.1111/tan.15355. PMID: 38273454

3. Lo T, Coombe L, Gagalova KK, Marr A, Warren RL, Kirk H, Pandoh P, Zhao Y, Moore RA, Mungall AJ, Ritland C, Pavy N, **Jones SJM**, Bohlmann J, Bousquet J, Birol I, Thomson A. Assembly and annotation of the black spruce genome provide insights on spruce phylogeny and evolution of stress response. **G3 (Bethesda)**. 2023 Dec 29;14(1):jkad247. PMID: 37875130

4. Elbert A, Dixon K, Shen Y, Hamilton S, Boerkoel CF, **Jones SJ**, Kanungo AK. Mitofusin 2 Variant Presenting With a Phenotype of Multiple System Atrophy of Cerebellar Subtype. **Neurol Genet**. 2023 Dec 7;10(1):e200114. doi: 10.1212/NXG.0000000000200114 PMID: 38170145

5. Omairi HK, Grisdale CJ, Meode M, Bohm AK, Black S, Adam NJ, Chapman CP, Maroilley T, Kelly JJ, Tarailo-Graovac M, **Jones SJM**, Blough MD, Cairncross JG. Mitogen-Induced Defective Mitosis Transforms Neural Progenitor Cells. **Neuro Oncol**. 2023 Oct 3;25(10):1763-1774. PMID: 37186014

6. COVID-19 Host Genetics Initiative. A second update on mapping the human genetic architecture of COVID-19. **Nature**. 2023 Sep;621(7977):E7-E26. doi: 10.1038/s41586-023-06355-3. PMID: 37674002

7. 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. PMID: 37558751

8. 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

9. Chang G, Jones S, Leelakumari S, Ashkani J, Culibrk L, O'Neill K, Tse K, Cheng D, Chuah E, McDonald H, Kirk H, Pandoh P, Pari S, Angelini V, Kyle C, Bertorelle G, Zhao Y, Mungall A, Moore R, Vilaça S, **Jones S**. The genome sequence of the Loggerhead sea turtle, Caretta caretta Linnaeus 1758 **F1000Res**. 2023 Jun 27;12:336. doi: 10.12688/f1000research.131283.2. eCollection 2023.PMID: 37455852

10. Li Z, Jiao X, Robertson AG, Di Sante G, Ashton AW, DiRocco A, Wang M, Zhao J, Addya S, Wang C, McCue PA, South AP, Cordon-Cardo C, Liu R, Patel K, Hamid R, Parmar J, DuHadaway JB, **Jones SJM**, Casimiro MC, Schultz N, Kossenkov A, Phoon LY, Chen H, Lan L, Sun Y, Iczkowski KA, Rui H, Pestell RG. The DACH1 gene is frequently deleted in prostate cancer, restrains prostatic intraepithelial neoplasia, decreases DNA damage repair, and predicts therapy responses. **Oncogene**. 2023 Jun;42(22):1857-1873. PMID: 37095257

11. Nikolic A, Maule F, Bobyn A, Ellestad K, Paik S, Marhon SA, Mehdipour P, Lun X, Chen HM, Mallard C, Hay AJ, Johnston MJ, Gafuik CJ, Zemp FJ, Shen Y, Ninkovic N, Osz K, Labit E, Berger ND, Brownsey DK, Kelly JJ, Biernaskie J, Dirks PB, Derksen DJ, **Jones SJM,** Senger DL, Chan JA, Mahoney DJ, De Carvalho DD, Gallo M. macroH2A2 antagonizes epigenetic programs of stemness in glioblastoma. **Nat Commun**. 2023 May 27;14(1):3062. PMID: 37244935

12. Dixon K, Shen Y, O'Neill K, Mungall KL, Chan S, Bilobram S, Zhang W, Bezeau M, Sharma A, Fok A, Mungall AJ, Moore R, Bosdet I, Thibodeau ML, Sun S, Yip S, Schrader KA, **Jones SJM**. Defining the heterogeneity of unbalanced structural variation underlying breast cancer susceptibility by nanopore genome sequencing. **Eur J Hum Genet**. 2023 May;31(5):602-606. PMID: 36797466

13. Yoo S, Garg E, Elliott LT, Hung RJ, Halevy AR, Brooks JD, Bull SB, Gagnon F, Greenwood C, Lawless JF, Paterson AD, Sun L, Zawati MH, Lerner-Ellis J, Abraham R, Birol I, Bourque G, Garant JM, Gosselin C, Li J, Whitney J, Thiruvahindrapuram B, Herbrick JA, Lorenti M, Reuter MS, Adeoye OO, Liu S, Allen U, Bernier FP, Biggs CM, Cheung AM, Cowan J, Herridge M, Maslove DM, Modi BP, Mooser V, Morris SK, Ostrowski M, Parekh RS, Pfeffer G, Suchowersky O, Taher J, Upton J, Warren RL, Yeung R, Aziz N, Turvey SE, Knoppers BM, Lathrop M, **Jones S**, Scherer SW, Strug LJ. HostSeq: a Canadian whole genome sequencing and clinical data resource. **BMC Genom Data**. 2023 May 2;24(1):26. PMID: 37131148

14. Arora R, Haynes L, Kumar M, McNeil R, Ashkani J, Nakoneshny SC, Matthews TW, Chandarana S, Hart RD, **Jones SJM**, Dort JC, Itani D, Chanda A, Bose P. NCBP2 and TFRC are novel prognostic biomarkers in oral squamous cell carcinoma. **Cancer Gene Ther**. 2023 May;30(5):752-765. PMID: 36635327

15. Rondeau EB, Christensen KA, Minkley DR, Leong JS, Chan MTT, Despins CA, Mueller A, Sakhrani D, Biagi CA, Rougemont Q, Normandeau E, **Jones SJM**, Devlin RH, Withler RE, Beacham TD, Naish KA, Yáñez JM, Neira R, Bernatchez L, Davidson WS, Koop BF. Population-size history inferences from the coho salmon (Oncorhynchus kisutch) genome. **G3 (Bethesda)**. 2023 Apr 11;13(4):jkad033. PMID: 36759939

16. Tsang ES, Csizmok V, Williamson LM, Pleasance E, Topham JT, Karasinska JM, 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. PMID: 36964191

17. 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, Marra MA. Immune Activation following Irbesartan Treatment in a Colorectal Cancer Patient: A Case Study. **Int J Mol Sci**. 2023 Mar 20;24(6):5869. PMID: 36982943

18. Ritch EJ, Herberts C, Warner EW, Ng SWS, Kwan EM, Bacon JVW, Bernales CQ, Schönlau E, Fonseca NM, Giri VN, Maurice-Dror C, Vandekerkhove G, **Jones SJM**, Chi KN, Wyatt AW. A generalizable machine learning framework for classifying DNA repair defects using ctDNA exomes. **NPJ Precis Oncol**. 2023 Mar 13;7(1):27. PMID: 36914848

19. Krysiak K, Danos AM, Saliba J, McMichael JF, Coffman AC, Kiwala S, Barnell EK, Sheta L, Grisdale CJ, Kujan L, Pema S, Lever J, Ridd S, Spies NC, Andric V, Chiorean A, Rieke DT, Clark KA, Reisle C, Venigalla AC, Evans M, Jani P, Takahashi H, Suda A, Horak P, Ritter DI, Zhou X, Ainscough BJ, Delong S, Kesserwan C, Lamping M, Shen H, Marr AR, Hoang MH, Singhal K, Khanfar M, Li BV, Lin WH, Terraf P, Corson LB, Salama Y, Campbell KM, Farncombe KM, Ji J, Zhao X, Xu X, Kanagal-Shamanna R, King I, Cotto KC, Skidmore ZL, Walker JR, Zhang J, Milosavljevic A, Patel RY, Giles RH, Kim RH, Schriml LM, Mardis ER, **Jones SJM**, Raca G, Rao S, Madhavan S, Wagner AH, Griffith M, Griffith OL.

CIViCdb 2022: evolution of an open-access cancer variant interpretation knowledgebase. **Nucleic Acids Res**. 2023 Jan 6;51(D1):D1230-D1241. PMID: 36373660

20. Akbari V, **Jones SJM**. Phasing DNA Methylation. **Methods Mol Biol**. 2023;2590:219-235. PMID: 36335502

21. Akbari V, Hanlon CT, O'Neill K, Lefebvre L, Schrader KA, Lansdorp PM, **Jones SJM.** Parent-of-origin detection and chromosome-scale haplotyping using long-read DNA methylation sequencing and Strand-seq. **Cell Genom**. 2022 Dec 21;3(1):100233. PMID: 36777186

22. Farahani H, Boschman J, Farnell D, Darbandsari A, Zhang A, Ahmadvand P, **Jones SJM**, Huntsman D, Köbel M, Gilks CB, Singh N, Bashashati A. Deep learning-based histotype diagnosis of ovarian carcinoma whole-slide pathology images. **Mod Pathol**. 2022 Dec;35(12):1983-1990. PMID: 36065012

23. Topham JT, Tsang ES, Karasinska JM, Metcalfe A, Ali H, Kalloger SE, Csizmok V, Williamson LM, Titmuss E, Nielsen K, Negri GL, Spencer Miko SE, Jang GH, Denroche RE, Wong HL, O'Kane GM, Moore RA, Mungall AJ, Loree JM, Notta F, Wilson JM, Bathe OF, Tang PA, Goodwin R, Morin GB, Knox JJ, Gallinger S, Laskin J, Marra MA, **Jones SJM**, Schaeffer DF, Renouf DJ. Integrative analysis of KRAS wildtype metastatic pancreatic ductal adenocarcinoma reveals mutation and expression-based similarities to cholangiocarcinoma. **Nat Commun**. 2022 Oct 8;13(1):5941. PMID: 36209277

24. 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. PMID: 34843087

25. Titmuss E, Corbett RD, Davidson S, Abbasi S, Williamson LM, Pleasance ED, Shlien A, Renouf DJ, **Jones SJM**, Laskin J, Marra MA. TMBur: a distributable tumor mutation burden approach for whole genome sequencing. **BMC Med Genomics**. 2022 Sep 7;15(1):190. PMID: 36071521

26. 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 Y, 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. **Ann Oncol**. 2022 Sep;33(9):939-949. PMID: 35691590

27. 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. PMID: 36131014

28. Gagalova KK, Warren RL, Coombe L, Wong J, Nip KM, Yuen MMS, Whitehill JGA, Celedon JM, Ritland C, Taylor GA, Cheng D, Plettner P, Hammond SA, Mohamadi H, Zhao Y, Moore RA, Mungall AJ, Boyle B, Laroche J, Cottrell J, Mackay JJ, Lamothe M, Gérardi S, Isabel N, Pavy N, **Jones SJM**, Bohlmann J, Bousquet J, Birol I. Spruce giga-genomes: structurally similar yet distinctive with differentially expanding gene families and rapidly evolving genes. **Plant J**. 2022 Sep;111(5):1469-1485. PMID: 35789009

29. 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 Y, Holmes DT, Romney MG, **Jones SJM**, Marra MA. Automated Library Construction and Analysis for High-Throughput Nanopore Sequencing of SARS-CoV-2. **J Appl Lab Med**. 2022 Sep 1;7(5):1025-1036. PMID: 35723286

30. Keshavarz-Rahaghi F, Pleasance E, Kolisnik T, **Jones SJM**. A p53 transcriptional signature in primary and metastatic cancers derived using machine learning. **Front Genet**. 2022 Aug 29;13:987238. PMID: 36134028

31. Yu IS, Wee K, Williamson L, Titmuss E, An J, Naderi-Azad S, Metcalf C, Yip S, Horst B, **Jones SJM**, 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. PMID: 35726793

32. Akbari V, Garant JM, 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 Jul 5;11:e77898. PMID: 35787786

33. 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. PMID: 35257510

34. Krysiak K, Danos AM, Kiwala S, McMichael JF, Coffman AC, Barnell EK, Sheta L, Saliba J, Grisdale CJ, Kujan L, Pema S, Lever J, Spies NC, Chiorean A, Rieke DT, Clark KA, Jani P, Takahashi H, Horak P, Ritter DI, Zhou X, Ainscough BJ, Delong S, Lamping M, Marr AR, Li BV, Lin WH, Terraf P, Salama Y, Campbell KM, Farncombe KM, Ji J, Zhao X, Xu X, Kanagal-Shamanna R, Cotto KC, Skidmore ZL, Walker JR, Zhang J, Milosavljevic A, Patel RY, Giles RH, Kim RH, Schriml LM, Mardis ER, **Jones SJM**, Raca G, Rao S, Madhavan S, Wagner AH, Griffith OL, Griffith M. A community approach to the cancer-variant-interpretation bottleneck. **Nat Cancer**. 2022 May;3(5):522-525. PMID: 35624339

35. Boerkoel PK, Dixon K, Fitzsimons C, Shen Y, Huynh S, Schlade-Bartusiak K, Culibrk L, Chan S, Boerkoel CF, **Jones SJM**, Chin HL. Long-read genome sequencing resolves a complex 13q structural variant associated with syndromic anophthalmia. **Am J Med Genet A**. 2022 May;188(5):1589-1594. PMID: 35122461

36. Lavoie JM, 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. PMID: 35483882

37. Gagalova KK, Whitehill JGA, Culibrk L, Lin D, Lévesque-Tremblay V, Keeling CI, Coombe L, Yuen MMS, Birol I, Bohlmann J, **Jones SJM**. The genome of the forest insect pest Pissodes strobi reveals genome expansion and evidence of a Wolbachia endosymbiont. **G3 (Bethesda)**. 2022 Apr 4;12(4):jkac038. PMID: 35171977

38. Cheng X, Liu Y, Wang J, Chen Y, Robertson AG, Zhang X, **Jones SJM**, Taubert S. cSurvival: a web resource for biomarker interactions in cancer outcomes and in cell lines. **Brief Bioinform**. 2022 Apr 2:bbac090. PMID: 35368077

39. Evans DR, Qiao Y, Trost B, Calli K, Martell S, **Jones SJM**, Scherer SW, Lewis MES. Complex Autism Spectrum Disorder with Epilepsy, Strabismus and Self-Injurious Behaviors in a Patient with a De Novo Heterozygous POLR2A Variant. **Genes (Basel).** 2022 Mar 7;13(3):470. PMID: 35328024

40. Cronin TJ, **Jones SJM**, Baeza JA. The complete mitochondrial genome of the spot prawn, *Pandalus platyceros* Brandt in von Middendorf, 1851 (Decapoda: Caridea: Pandalidae), assembled from linked-reads sequencing. Journal of Crustacean Biology. 2022 Mar 2, 42(1), 1–9.

41. Chin HL, Huynh S, Ashkani J, Castaldo M, Dixon K, Selby K, Shen Y, Wright M, Boerkoel CF, Hendson G, **Jones SJM**. An infant with congenital respiratory insufficiency and diaphragmatic paralysis: A novel BICD2 phenotype? **Am J Med Genet** A. 2022 Mar;188(3):926-930. PMID: 34825470

42. 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. PMID: 35140225

43. Boschman J, Farahani H, Darbandsari A, Ahmadvand P, Van Spankeren A, Farnell D, Levine AB, Naso JR, Churg A, **Jones SJ**, Yip S, Köbel M, Huntsman DG, Gilks CB, Bashashati A. The utility of color normalization for AI-based diagnosis of hematoxylin and eosin-stained pathology images. **J Pathol**. 2022 Jan;256(1):15-24. PMID: 34543435

44. Lewin HA, Richards S, Lieberman Aiden E, Allende ML, Archibald JM, Bálint M, Barker KB, Baumgartner B, Belov K, Bertorelle G, Blaxter ML, Cai J, Caperello ND, Carlson K, Castilla-Rubio JC, Chaw SM, Chen L, Childers AK, Coddington JA, Conde DA, Corominas M, Crandall KA, Crawford AJ, DiPalma F, Durbin R, Ebenezer TE, Edwards SV, Fedrigo O, Flicek P, Formenti G, Gibbs RA, Gilbert MTP, Goldstein MM, Graves JM, Greely HT, Grigoriev IV, Hackett KJ, Hall N, Haussler D, Helgen KM, Hogg CJ, Isobe S, Jakobsen KS, Janke A, Jarvis ED, Johnson WE, **Jones SJM**, Karlsson EK, Kersey PJ, Kim JH, Kress WJ, Kuraku S, Lawniczak MKN, Leebens-Mack JH, Li X, Lindblad-Toh K, Liu X, Lopez JV, Marques-Bonet T, Mazard S, Mazet JAK, Mazzoni CJ, Myers EW, O'Neill RJ, Paez S, Park H, Robinson GE, Roquet C, Ryder OA, Sabir JSM, Shaffer HB, Shank TM, Sherkow JS, Soltis PS, Tang B, Tedersoo L, Uliano-Silva M, Wang K, Wei X, Wetzer R, Wilson JL, Xu X, Yang H, Yoder AD, Zhang G. The Earth BioGenome Project 2020: Starting the clock. **Proc Natl Acad Sci U S A**. 2022 Jan 25;119(4):e2115635118. PMID: 35042800

45. Haile S, Nikiforuk AM, Pandoh PK, Twa DDW, Smailus DE, Nguyen J, Pleasance S, Wong A, Zhao Y, 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. PMID: 34687784

46. 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. PMID: 34931022

47. Christensen KA, Rondeau EB, Sakhrani D, Biagi CA, Johnson H, Joshi J, Flores AM, Leelakumari S, Moore R, Pandoh PK, Withler RE, Beacham TD, Leggatt RA, Tarpey CM, Seeb LW, Seeb JE, **Jones SJM**, Devlin RH, Koop BF. The pink salmon genome: Uncovering the genomic consequences of a two-year life cycle. **PLoS One**. 2021 Dec 17;16(12):e0255752. PMID: 34919547

48. 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 tumors reveal interactions with therapy. **Cell Rep**. 2021 Nov 16;37(7):110023. PMID: 34788622

49. Dursi LJ, Bozoky Z, de Borja R, Li H, Bujold D, Lipski A, Rashid SF, Sethi A, Memon N, Naidoo D, Coral-Sasso F, Wong M, Quirion PO, Lu Z, Agarwal S, Pavlov Y, Ponomarev A, Husic M, Pace K, Palmer S, Grover SA, Hakgor S, Siu LL, Malkin D, Virtanen C, Pugh TJ, Jacques PE, Joly Y, **Jones SJM,** Bourque G, Brudno M. CanDIG: Federated network across Canada for multi-omic and health data discovery and analysis. **Cell Genomics**. 2021 Nov 10;1(2):100033. PMID: 36778585

50. Rehm HL, Page AJH, Smith L, Adams JB, Alterovitz G, Babb LJ, Barkley MP, Baudis M, Beauvais MJS, Beck T, Beckmann JS, Beltran S, Bernick D, Bernier A, Bonfield JK, Boughtwood TF, Bourque G, Bowers SR, Brookes AJ, Brudno M, Brush MH, Bujold D, Burdett T, Buske OJ, Cabili MN, Cameron DL, Carroll RJ, Casas-Silva E, Chakravarty D, Chaudhari BP, Chen SH, Cherry JM, Chung J, Cline M, Clissold HL, Cook-Deegan RM, Courtot M, Cunningham F, Cupak M, Davies RM, Denisko D, Doerr MJ, Dolman LI, Dove ES, Dursi LJ, Dyke SOM, Eddy JA, Eilbeck K, Ellrott KP, Fairley S, Fakhro KA, Firth HV, Fitzsimons MS, Fiume M, Flicek P, Fore IM, Freeberg MA, Freimuth RR, Fromont LA, Fuerth J, Gaff CL, Gan W, Ghanaim EM, Glazer D, Green RC, Griffith M, Griffith OL, Grossman RL, Groza T, Auvil JMG, Guigó R, Gupta D, Haendel MA, Hamosh A, Hansen DP, Hart RK, Hartley DM, Haussler D, Hendricks-Sturrup RM, Ho CWL, Hobb AE, Hoffman MM, Hofmann OM, Holub P, Hsu JS, Hubaux JP, Hunt SE, Husami A, Jacobsen JO, Jamuar SS, Janes EL, Jeanson F, Jené A, Johns AL, Joly Y, **Jones SJM**, Kanitz A, Kato K, Keane TM, Kekesi-Lafrance K, Kelleher J, Kerry G, Khor SS, Knoppers BM, Konopko MA, Kosaki K, Kuba M, Lawson J, Leinonen R, Li S, Lin MF, Linden M, Liu X, Udara Liyanage I, Lopez J, Lucassen AM, Lukowski M, Mann AL, Marshall J, Mattioni M, Metke-Jimenez A, Middleton A, Milne RJ, Molnár-Gábor F, Mulder N, Munoz-Torres MC, Nag R, Nakagawa H, Nasir J, Navarro A, Nelson TH, Niewielska A, Nisselle A, Niu J, Nyrönen TH, O'Connor BD, Oesterle S, Ogishima S, Wang VO, Paglione LAD, Palumbo E, Parkinson HE, Philippakis AA, Pizarro AD, Prlic A, Rambla J, Rendon A, Rider RA, Robinson PN, Rodarmer KW, Rodriguez LL, Rubin AF, Rueda M, Rushton GA, Ryan RS, Saunders GI, Schuilenburg H, Schwede T, Scollen S, Senf A, Sheffield NC, Skantharajah N, Smith AV, Sofia HJ, Spalding D, Spurdle AB, Stark Z, Stein LD, Suematsu M, Tan P, Tedds JA, Thomson AA, Thorogood A, Tickle TL, Tokunaga K, Törnroos J, Torrents D, Upchurch S, Valencia A, Guimera RV, Vamathevan J, Varma S, Vears DF, Viner C, Voisin C, Wagner AH, Wallace SE, Walsh BP, Williams MS, Winkler EC, Wold BJ, Wood GM, Woolley JP, Yamasaki C, Yates AD, Yung CK, Zass LJ, Zaytseva K, Zhang J, Goodhand P, North K, Birney E. GA4GH: International policies and standards for data sharing across genomic research and healthcare. **Cell Genom**. 2021 Nov 10;1(2):100029. PMID: 35072136

51. Allen JL, **Jones SJM**, McMullin RT. Draft Genome Sequence of the Lichenized Fungus Bacidia gigantensis. **Microbiol Resour Announc**. 2021 Nov 4;10(44):e0068621. PMID: 34734769

52. Yang KC, Kalloger SE, Aird JJ, Lee MKC, 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. PMID: 34644566

53. 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. Clinical and cost outcomes following genomics-informed treatment for advanced cancers. **Cancer Med**. 2021 Aug;10(15):5131-5140. PMID: 34152087

54. Chin HL, O'Neill K, Louie K, Brown L, Schlade-Bartusiak K, Eydoux P, Rupps R, Farahani A, Boerkoel CF, **Jones SJM**. An approach to rapid characterization of DMD copy number variants for prenatal risk assessment. **Am J Med Genet A**. 2021 Aug;185(8):2541-2545. PMID: 34018669

55. Povysil G, Butler-Laporte G, Shang N, Wang C, Khan A, Alaamery M, Nakanishi T, Zhou S, Forgetta V, Eveleigh RJ, Bourgey M, Aziz N, **Jones SJ**, Knoppers B, Scherer SW, Strug LJ, Lepage P, Ragoussis J, Bourque G, Alghamdi J, Aljawini N, Albes N, Al-Afghani HM, Alghamdi B, Almutairi MS, Mahmoud ES, Abu-Safieh L, El Bardisy H, Harthi FSA, Alshareef A, Suliman BA, Alqahtani SA, Almalik A, Alrashed MM, Massadeh S, Mooser V, Lathrop M, Fawzy M, Arabi YM, Mbarek H, Saad C, Al-Muftah W, Jung J, Mangul S, Badji R, Thani AA, Ismail SI, Gharavi AG, Abedalthagafi MS, Richards JB, Goldstein DB, Kiryluk K. Rare loss-of-function variants in type I IFN immunity genes are not associated with severe COVID-19. **J Clin Invest**. 2021 Jul 15;131(14):e147834. PMID: 34043590

56. Dhaliwal J, Qiao Y, Calli K, Martell S, Race S, Chijiwa C, Glodjo A, **Jones S**, Rajcan-Separovic E, Scherer SW, Lewis S. Contribution of Multiple Inherited Variants to Autism Spectrum Disorder (ASD) in a Family with 3 Affected Siblings. **Genes (Basel).** 2021 Jul 8;12(7):1053. PMID: 34356069

57. Naso JR, Levine AB, Farahani H, Chirieac LR, Dacic S, Wright JL, Lai C, Yang HM, **Jones SJM**, Bashashati A, Yip S, Churg A. Deep-learning based classification distinguishes sarcomatoid malignant mesotheliomas from benign spindle cell mesothelial proliferations. **Mod Pathol**. 2021 Jun 10. PMID: 34112957

58. Haile S, Corbett RD, LeBlanc VG, Wei L, Pleasance S, Bilobram S, Nip KM, Brown K, Trinh E, Smith J, Trinh DL, Bala M, Chuah E, Coope RJN, Moore RA, Mungall AJ, Mungall KL, Zhao Y, Hirst M, Aparicio S, Birol I, **Jones SJM**, Marra MA. A Scalable Strand-Specific Protocol Enabling Full-Length Total RNA Sequencing From Single Cells. **Front Genet**. 2021 Jun 3;12:665888. PMID: 34149808

59. Zhang B, Kim MY, Elliot G, Zhou Y, Zhao G, Li D, Lowdon RF, Gormley M, Kapidzic M, Robinson JF, McMaster MT, 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. PMID: 33891899

60. 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 İ, 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. PMID: 33931648

61. 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. PMID: 33741928

62. Roston A, Evans D, Gill H, McKinnon M, Isidor B, Cogné B, Mwenifumbo J, van Karnebeek C, An J, **Jones SJM**, Farrer M, Demos M, Connolly M, Gibson WT; CAUSES Study; EPGEN Study. *SETD1B*-associated Neurodevelopmental Disorder. **J Med Genet**. 2021 Mar;58(3):196-204. PMID: 32546566

63. 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. PMID: 33618748

64. Britton HM, Levine AB, Shen Y, Mungall K, Serrano J, Snuderl M, Pleasance E, **Jones SJM,** Laskin J, Marra MA, Rassekh SR, 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. PMID: 33768871

65. Banville AC, Wouters MCA, Oberg AL, Goergen KM, Maurer MJ, Milne K, Ashkani J, Field E, Ghesquiere C, **Jones SJM,** Block MS, Nelson BH. Co-expression patterns of chimeric antigen receptor (CAR)-T cell target antigens in primary and recurrent ovarian cancer. **Gynecol Oncol.** 2021 Feb;160(2):520-529 PMID: 33342620

66. Naso JR, Topham JT, Karasinska JM, Lee MKC, Kalloger SE, Wong HL, Nelson J, Moore RA, Mungall AJ, **Jones SJM,** Laskin J, Marra MA, Renouf DJ, Schaeffer DF. Tumor infiltrating neutrophils and gland formation predict overall survival and molecular subgroups in pancreatic ductal adenocarcinoma. **Cancer Med.** 2021 Feb;10(3):1155-1165. PMID: 33372414

67. 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. PMID: 33237632

68. Pender A, Titmuss E, Pleasance ED, Fan KY, Pearson H, Brown SD, Grisdale CJ, Topham JT, Shen Y, Bonakdar M, Taylor G, Williamson LM, Mungall KL, Chuah E, Mungall AJ, Moore RA, Lavoie JM, Yip S, Lim H, Renouf DJ, Sun S, Holt RA, **Jones SJ**, Marra MA, 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. PMID: 33020056

69. Tsang ES, Grisdale CJ, Pleasance E, Topham JT, Mungall K, Reisle C, 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 HJ, Schaeffer DF, Renouf DJ, Yip S, Laskin J, Marra MA, **Jones SJM,** 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. PMID: 33148671

70. Tsang ES, Topham JT, Karasinska JM, Lee MK, Williamson LM, Mendis S, Denroche RE, Jang GH, Kalloger SE, Moore RA, Mungall AJ, Bathe OF, Tang PA, Notta F, Wilson JM, Laskin J, O'Kane GM, Knox JJ, Goodwin RA, Loree JM, **Jones SJ,** Marra MA, Gallinger S, 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. PMID: 32958704

71. Topham JT, Karasinska JM, Lee MK, Csizmok V, Williamson LM, Jang GH, Denroche RE, Tsang ES, Kalloger SE, Wong HL, O'Kane GM, Moore RA, Mungall AJ, Notta F, Loree JM, Wilson JM, Bathe OF, Tang PA, Goodwin RA, Knox JJ, Gallinger S, Laskin J, Marra MA, **Jones SJ,** 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. PMID: 33051307

72. Corbett RD, Eveleigh R, Whitney J, Barai N, Bourgey M, Chuah E, Johnson J, Moore RA, Moradin N, Mungall KL, Pereira S, Reuter MS, Thiruvahindrapuram B, Wintle RF, Ragoussis J, Strug LJ, Herbrick JA, Aziz N, **Jones SJM,** Lathrop M, Scherer SW, Staffa A, Mungall AJ. A Distributed Whole Genome Sequencing Benchmark Study. **Front Genet.** 2020 Dec 1;11:612515. PMID: 33335541

73. Levine AB, Peng J, Farnell D, Nursey M, Wang Y, Naso JR, Ren H, Farahani H, Chen C, Chiu D, Talhouk A, Sheffield B, Riazy M, Ip PP, Parra-Herran C, Mills A, Singh N, Tessier-Cloutier B, Salisbury T, Lee J, Salcudean T, **Jones SJM**, Huntsman DG, Gilks CB, Yip S, Bashashati A. Synthesis of diagnostic quality cancer pathology images by generative adversarial networks. **J Pathol**. 2020 Oct;252(2):178-188 PMID: 32686118

74. 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

75. Lavoie JM, Mitchell T, Lee SE, 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. PMID:31907737

76. De Boeck A, Ahn BY, D'Mello C, Lun X, Menon SV, Alshehri MM, Szulzewsky F, Shen Y, Khan L, Dang NH, Reichardt E, Goring KA, King J, Grisdale CJ, Grinshtein N, Hambardzumyan D, Reilly KM, Blough MD, Cairncross JG, Yong VW, Marra MA, **Jones SJM**, Kaplan DR, McCoy KD, 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. PMID: 33020472

77. Lo T, Coombe L, Lin D, Warren RL, Kirk H, Pandoh P, Zhao Y, Moore RA, Mungall AJ, Ritland C, Bousquet J, **Jones SJM**, Bohlmann J, Thomson A, Birol I. Complete Chloroplast Genome Sequence of a Black Spruce (Picea mariana) from Eastern Canada. **Microbiol Resour Announc**. 2020 Sep 24;9(39):e00877-20. PMID: 32972944

78. Bailey MH, Meyerson WU, Dursi LJ, Wang LB, Dong G, Liang WW, Weerasinghe A, Li S, Kelso S; MC3 Working Group; PCAWG novel somatic mutation calling methods working group, Saksena G, Ellrott K, Wendl MC, Wheeler DA, Getz G, Simpson JT, Gerstein MB, Ding L; PCAWG Consortium. (1446 Collaborators) including, **Jones SJM,** Marra M. Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. **Nat Commun**. 2020 Sep 21;11(1):4748. PMID: 32958763

79. Topham JT, Titmuss E, Pleasance ED, Williamson LM, Karasinska JM, Culibrk L, Lee MKC, 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 SJM**, 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. PMID: 32518206

80. Li CH, Prokopec SD, Sun RX, Yousif F, Schmitz N; PCAWG Tumour Subtypes and Clinical Translation, Boutros PC; PCAWG Consortium. Including **Jones SJM,** Holt R, Marra M, Hirst M**.** Sex differences in oncogenic mutational processes. **Nat Commun.** 2020 Aug 28;11(1):4330. PMID: 32859912

81. Bohm AK, DePetro JA, Binding CE, Gerber A, Chahley N, Berger ND, Ware MA, Thomas KA, Senapathi U, Bukhari S, Chen C, Chahley E, Grisdale CJ, Lawn S, Yu Y, Wong R, Shen Y, Omairi H, Mirzaei R, Alshatti N, Pederson H, Yong VW, Weiss S, Chan JA, Cimino PJ, Kelly JJ, **Jones SJM**, Holland EC, Blough MD, Cairncross JG. In Vitro Modeling of GBM Initiation using PDGF-AA and P53-Null Neural Progenitors. **Neuro Oncol**. 2020 Aug 17;22(8):1150-1161. PMID: 32296841

82. Gagliardi A, Porter VL, Zong Z, Bowlby R, Titmuss E, Namirembe C, Griner NB, Petrello H, Bowen J, Chan SK, Culibrk L, Darragh TM, Stoler MH, Wright TC, Gesuwan P, Dyer MA, Ma Y, Mungall KL, **Jones SJM**, 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 identifies human papillomavirus clade-specific epigenome and transcriptome landscapes. **Nat Genet**. 2020 Aug;52(8):800-810. PMID: 32747824

83. 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 Jul 6. doi: 10.1038/s41436-020-0880-8. Online ahead of print. PMID: 32624572

84. Jackman SD, Coombe L, Warren RL, Kirk H, Trinh E, MacLeod T, Pleasance S, Pandoh P, Zhao Y, Coope RJ, Bousquet J, Bohlmann J, **Jones SJM**, Birol I. Complete Mitochondrial Genome of a Gymnosperm, Sitka Spruce (Picea sitchensis), Indicates a Complex Physical Structure. **Genome Biol Evol**. 2020 Jul 1;12(7):1174-1179. PMID: 32449750

85. Vujin A, **Jones SJ**, Zetka M. NHJ-1 Is Required for Canonical Nonhomologous End Joining in *Caenorhabditis elegans***.** **Genetics** 2020 Jul;215(3):635-651. PMID: 32457132

86. Malhis N, Jacobson M, **Jones SJM**, Gsponer J. LIST-S2: taxonomy based sorting of deleterious missense mutations across species.**Nucleic Acids Re**s. 2020 Jul 2;48(W1):W154-W161. PMID: 32352516

87. 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: 317084

88. 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. PMID: 32151517

89. 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. PMID: 32677466

90. 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 May 29;4(5). PMID: 3313482

91. 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;1(4):452-468. PMID: 35121966

92. ICGC/TCGA Pan-Cancer Analysis of Whole Genomes Consortium. (1341 Collaborators) including **Jones SJM.** Pan-cancer analysis of whole genomes. **Nature**. 2020 Feb;578(7793):82-93.PMID: 32025007

93. 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)PMID: 31871216

94. 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 Feb;52(2):231-240. PMID:31932696

95. Karasinska JM, Topham JT, Kalloger SE, Jang GH, Denroche RE, Culibrk L, Williamson LM, Wong HL, Lee MKC, O'Kane GM, Moore RA, Mungall AJ, Moore MJ, Warren C, Metcalfe A, Notta F, Knox JJ, Gallinger S, Laskin J, Marra MA, **Jones SJM**, 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.PMID: 31481506

96. Chagas VS, Groeneveld CS, Oliveira KG, Trefflich S, de Almeida RC, Ponder BAJ, Meyer KB, Jones SJM, Robertson AG, Castro MAA. RTNduals: An R/Bioconductor package for analysis of co-regulation and inference of dual regulons. **Bioinformatics**. 2019 Dec 15;35(24):5357-5358. PMID: 31250887

97. Lever J, Jones MR, Danos AM, Krysiak K, Bonakdar M, Grewal JK, Culibrk L, Griffith OL, Griffith M, **Jones SJM**. Text-mining clinically relevant cancer biomarkers for curation into the CIViC database. **Genome Med**. 2019 Dec 3;11(1):78. PMID: 31796060

98. Cyrus SS, Cohen ASA, Agbahovbe R, Avela K, Yeung KS, Chung BHY, Luk HM, Tkachenko N, Choufani S, Weksberg R, Lopez-Rangel E; C.A.U.S.E.S. Study, Brown K, Saenz MS, Svihovec S, McCandless SE, Bird LM, Garcia AG, Gambello MJ, McWalter K, Schnur RE, An J, **Jones SJM**, Bhalla SK, Pinz H, Braddock SR, Gibson WT. Rare SUZ12 variants commonly cause an overgrowth phenotype. **Am J Med Genet C Semin Med Genet.** 2019 Dec;181(4):532-547 PMID: 31736240

99. 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

100. 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) PMID:31708418

101. Warren RL, Coombe L, Mohamadi H, Zhang J, Jaquish B, Isabel N, **Jones SJM,** Bousquet J, Bohlmann J, Birol I. ntEdit: scalable genome sequence polishing. **Bioinformatics**. 2019 Nov 1;35(21):4430-4432. PMID: 31095290

102. Jackman SD, Mozgacheva T, Chen S, O'Huiginn B, Bailey L, Birol I, **Jones SJM**. ORCA: A Comprehensive Bioinformatics Container Environment for Education and Research. **Bioinformatics**. 2019 Nov 1;35(21):4448-4450. PMID: 31004474

103. Groeneveld CS, Chagas VS, **Jones SJM**, Robertson AG, Ponder BAJ, Meyer KB, Castro MAA. RTNsurvival : An R/Bioconductor package for regulatory network survival analysis. **Bioinformatics.** 2019 Nov 1;35(21):4488-4489. PMID: 30923832

104. 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

105. 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. PMID: 31471491

106. Jones MR, Williamson LM, Topham JT, Lee MKC, Goytain A, Ho J, Denroche RE, Jang G, Pleasance E, Shen Y, Karasinska JM, McGhie JP, Gill S, Lim HJ, Moore MJ, Wong HL, Ng T, Yip S, Zhang W, Sadeghi S, Reisle C, 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):4674-4681PMID: 31068372

107. 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). PMID: 31371350

108. 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). PMID: 31248052

109. Wiseman SM, Kojic LD, Kassian K, **Jones SJ**, Joshi B, Nabi IR. Expression of Gp78/Autocrine Motility Factor Receptor and Endocytosis of Autocrine Motility Factor in Human Thyroid Cancer Cells. Cureus. 2019 Jun 17;11(6):e4928. Doi: 107759/cureus.4928. PMID: 31431834

110. 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

111. Lever J, Zhao EY, Grewal J, Jones MR, **Jones SJM.** CancerMine: a literature-mined resource for drivers, oncogenes and tumor suppressors in cancer. **Nat Methods.** 2019 Jun;16(6):505-507. PMID: 31110280

112. Lin D, Coombe L, Jackman SD, Gagalova KK, Warren RL, Hammond SA, McDonald H, Kirk H, Pandoh P, Zhao Y, Moore RA, Mungall AJ, Ritland C, Doerksen T, Jaquish B, Bousquet J, **Jones SJM**, Bohlmann J, Birol I. Complete Chloroplast Genome Sequence of an Engelmann Spruce (Picea engelmannii, Genotype Se404-851) from Western Canada. **Microbiol Resour Announc**. 2019 Jun 13;8(24). PMID: 31196920

113. Lin D, Coombe L, Jackman SD, Gagalova KK, Warren RL, Hammond SA, Kirk H, Pandoh P, Zhao Y, Moore RA, Mungall AJ, Ritland C, Jaquish B, Isabel N, Bousquet J, **Jones SJM,** Bohlmann J, Birol I. Complete Chloroplast Genome Sequence of a White Spruce (Picea glauca, GenotypeWS77111) from Eastern Canada. **Microbiol Resour Announc.** 2019 Jun 6;8(23). PMID: 31171622

114. Berner D, Roesti M, Bilobram S, Chan SK, Kirk H, Pandoh P, Taylor GA, Zhao Y, **Jones SJM,** DeFaveri J. De Novo Sequencing, Assembly, and Annotation of Four Threespine Stickleback Genomes Based on Microfluidic Partitioned DNA Libraries. **Genes (Basel).** 2019 Jun 3;10(6). PMID: 31163709

115. 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). PMID: 31160355

116. Brodehl A, Rezazadeh S, Williams T, Munsie NM, Liedtke D, Oh T, Ferrier R, Shen Y, **Jones SJM**, Stiegler AL, Boggon TJ, Duff HJ, Friedman JM, Gibson WT; FORGE Canada Consortium, Childs SJ, Gerull B. Mutations in ILK, encoding integrin-linked kinase, are associated with arrhythmogenic cardiomyopathy. **Transl Res**. 2019 Jun;208:15-29. PMID: 30802431

117. Saleh A, Cheng H, Martin SE, Si H, Ormanaglu P, Carlson SG, Clavijo PE, Yang X, Das R, Cornelius S, Coupar J, Chepeha DB, Danilova L, Harris TM, Prystowsky MB, Childs G, Smith RV, Robertson G, **Jones SJ**, Cherniack AD, Kim SS, Rait A, Pirollo KF, Chang EH, Chen Z, Van Waes C. Integrated genomic and functional microRNA analysis identifies miR-30-5p as a tumor suppressor and potential therapeutic nanomedicine in head and neck cancer. **Clin Cancer Res**. 2019 May 1;25(9):2860-2873.PMID: 30723145

118. Grewal JK, Tessier-Cloutier B, Jones M, Gakkhar S, Ma Y, Moore R, Mungall AJ, Zhao Y, 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. PMID: 31026023

119. Malhis N, **Jones SJM**, Gsponer J. Improved measures for evolutionary conservation that exploit taxonomy distances. **Nat Commun.** 2019 Apr 5;10(1):1556. PMID: 30952844

120. 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). PMID: 30833417

121. 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, Leal FE, Lichtenberg TM, Ma Y, Martin JP, Martin MR, 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, Wright GW, 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

122. Levine AB, Schlosser C, Grewal J, Coope R, **Jones SJM**, Yip S. Rise of the Machines: Advances in Deep Learning for Cancer Diagnosis. **Trends Cancer**. 2019 Mar;5(3):157-169. PMID: 30898263

123. Zhao EY, Jones M, **Jones SJM**. Whole-Genome Sequencing in Cancer. **Cold Spring Harb Perspect Med**. 2019 Mar 1;9(3). PMID: 29844223

124. Reisle C, Mungall KL, Choo C, Paulino D, Bleile DW, Muhammadzadeh A, Mungall AJ, Moore RA, Shlafman I, Coope R, Pleasance S, Ma Y, **Jones SJM**. MAVIS: Merging, Annotation, Validation, and Illustration of Structural variants. **Bioinformatics**. 2019 Feb 1;35(3):515-517. PMID: 30016509

125. 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). PMID:30514790

126. Pandoh PK, Corbett RD, McDonald H, Alcaide M, Kirk H, Trinh E, Haile S, MacLeod T, Smailus D, Bilobram S, Mungall AJ, Ma Y, Moore RA, Coope R, Zhao Y, **Jones SJ**, Holt RA, Karsan A, Morin RD, Marra MA. A high-throughput protocol for isolating cell-free circulating tumor DNA from peripheral blood. **Biotechniques**. 2019 Feb;66(2):85-92. doi: 10.2144/btn-2018-0148. PMID: 30744412

127. 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. doi: 10.1093/nar/gky1142. PMID: 30418619

128. 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). PMID: 30446580

129. Cancer Genome Atlas Analysis Network (216 Collaborators) including **Jones SJM** Integrative Molecular Characterization of Malignant Pleural Mesothelioma. **Cancer Discov**. 2018 Dec;8(12):1548-1565. PMID: 30322867

130. 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

131. Roach MJ, Johnson DL, Bohlmann J, van Vuuren HJJ, **Jones SJM**, Pretorius IS, Schmidt SA, Borneman AR. Population sequencing reveals clonal diversity and ancestral inbreeding in the grapevine cultivar Chardonnay. **PLoS Genet.** 2018 Nov 20;14(11):e1007807. 2018 Nov. PMID: 30458008

132. Cancer Genome Atlas Research Network (725 Collaborators) including Ally A, Balasundaram M, Bowlby R, Brooks D, Carlsen R, Chuah E, Dhalla N, Holt R, **Jones SJM**, Marra MA, Mayo M, Moore RA, Mungall AJ, Mungall K, Robertson AG, Sadeghi S, Tam A, Tse K, Wong T. Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. **Cell Rep.** 2018 Oct 30;25(5):1304-1317.e5. PMID: 30380420

133. Jackman SD, Coombe L, Chu J, Warren RL, Vandervalk BP, Yeo S, Xue Z, Mohamadi H, Bohlmann J, **Jones SJM**, Birol I. Tigmint: correcting assembly errors using linked reads from large molecules. **BMC Bioinformatics**. 2018 Oct 26;19(1):393. PMID: 30367597

134. Cancer Genome Atlas Analysis Network, (37 Collaborators) including **Jones SJM**. Corces MR, Granja JM, Shams S, Louie BH, Seoane JA, Zhou W, Silva TC, Groeneveld C, Wong CK, Cho SW, Satpathy AT, Mumbach MR, Hoadley KA, Robertson AG, Sheffield NC, Felau I, Castro MAA, Berman BP, Staudt LM, Zenklusen JC, Laird PW, Curtis C; Greenleaf WJ, Chang HY. The chromatin accessibility landscape of primary human cancers. **Science**. 2018 Oct 26;362(6413). PMID: 30361341

135. 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. PMID: 30275490

136. Cancer Genome Atlas research Network (1013 Collaborators) including Ally A, Balasundaram M, Bowlby R, Brooks D, Carlsen R, Chuah E, Dhalla N, Holt R, **Jones SJM**, Kasaian K, Lee D, Ma Y, Marra MA, Mayo M, Moore RA, Mungall AJ, Mungall K, Robertson AG, Sadeghi S, Schein JE, Sipahimalani P, Tam A, Thiessen N, Tse K, Wong T. 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

137. Wong HL, 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;2:PO.18.00057. doi: 10.1200/PO.18.00057. PMID: 32913994

138. 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

139. 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

140. Bosc D, Vezenkov L, Bortnik S, An J, Xu J, Choutka C, Hannigan AM, Kovacic S, Loo S, Clark PGK, Chen G, Guay-Ross RN, Yang K, Dragowska WH, Zhang F, Go NE, Leung A, Honson NS, Pfeifer TA, Gleave M, Bally M, **Jones SJ**, Gorski SM, Young RN. A new quinoline-based chemical probe inhibits the autophagy-related cysteine protease ATG4B. **Sci Rep.** 2018 Aug 3;8(1):11653. PMID: 30076329

141. Levine AB, Grewal JK, **Jones SJM**, and Yip S. Machine learning in pathology: A primer on techniques and applications. **Canadian Journal of Pathology.** 2018 Aug 2; Vol 10(3): 52-59.

142. Newton Y., Rassekh S. R., Deyell, R. J., Shen Y, Jones M. R., Dunham C., Yip S, Leelakumari S., Zhu J, McColl D, Swatloski T, Salama S. R, Ng T, Hendson G, Lee A. F., Ma Y, Moore R., Mungall A. J, Haussler D., Stuart J. M, Jantzen C., Laskin J, **Jones S. J. M.,** Marra M. A, & Morozova O. 2018. Comparative RNA-Sequencing Analysis Benefits a Pediatric Patient With Relapsed Cancer. **JCO Precision Oncology** (2): 1-16. PMID: 31372595

143. Cancer Genome Atlas Research Network (725 Collaborators) including **Jones SJM**. The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. **Cell Rep.** 2018 Jun 19;23(12):3698. doi: 10.1016/j.celrep.2018.06.032. PMID: 29925010

144. Cancer Genome Atlas Research Network (725 Collaborators) including **Jones SJM**. Integrated Molecular Characterization of Testicular Germ Cell Tumors. **Cell Rep.** 2018 Jun 12;23(11):3392 PMID: 29898407

145. Garzia L, Kijima N, Morrissy AS, De Antonellis P, Guerreiro-Stucklin A, Holgado BL, Wu X, Wang X, Parsons M, Zayne K, Manno A, Kuzan-Fischer C, Nor C, Donovan LK, Liu J, Qin L, Garancher A, Liu KW, Mansouri S, Luu B, Thompson YY, Ramaswamy V, Peacock J, Farooq H, Skowron P, Shih DJH, Li A, Ensan S, Robbins CS, Cybulsky M, Mitra S, Ma Y, Moore R, Mungall A, Cho YJ, Weiss WA, Chan JA, Hawkins CE, Massimino M, Jabado N, Zapotocky M, Sumerauer D, Bouffet E, Dirks P, Tabori U, Sorensen PHB, Brastianos PK, Aldape K, **Jones SJM,** Marra MA, Woodgett JR, Wechsler-Reya RJ, Fults DW, Taylor MD. A Hematogenous Route for Medulloblastoma Leptomeningeal Metastases. **Cell.** 2018 May 31;173(6):1549. PMID: 29856958

146. Lee JJY, Gottlieb MM, Lever J, **Jones SJM,** Blau N, van Karnebeek CDM, Wasserman WW. Text-based phenotypic profiles incorporating biochemical phenotypes of inborn errors of metabolism improve phenomics-based diagnosis. **J Inherit Metab Dis**. 2018 May;41(3):555-562. PMID: 29340838

147. Cancer Genome Atlas Research Network (725 Collaborators) including **Jones SJM**. An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. **Cell**. 2018 Apr 5;173(2):400-416.e11. PMID: 29625055

148. Cancer Genome Atlas Research Network (725 Collaborators) including **Jones SJM**. Comprehensive Characterization of Cancer Driver Genes and Mutations. **Cell**. 2018 Apr 5;173(2):371-385.e18. PMID: 29625053

149. Cancer Genome Atlas Research Network (725 Collaborators) including **Jones SJM**. A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. **Cell**. 2018 Apr 5;173(2):386-399.e12. PMID: 29625054

150. Cancer Genome Atlas Research Network (725 Collaborators) including **Jones SJM**. Pathogenic Germline Variants in 10,389 Adult Cancers. **Cell**. 2018 Apr 5;173(2):355-370.e14. PMID: 29625052

151. Cancer Genome Atlas Research Network (725 Collaborators) including **Jones SJM**. Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. **Cell**. 2018 Apr 5;173(2):338-354.e15. PMID: 29625051

152. Cancer Genome Atlas Research Network (725 Collaborators) including **Jones SJM**. Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. **Cell**. 2018 Apr 5;173(2):305-320.e10. PMID: 29625049

153. Cancer Genome Atlas Research Network (725 Collaborators) including **Jones SJM**. 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. PMID: 29625048

154. Cancer Genome Atlas Research Network (725 Collaborators) including **Jones SJM**. The Immune Landscape of Cancer. **Immunity.** 2018 Apr 17;48(4):812-830.e14. PMID: 29628290

155. Cancer Genome Atlas Research Network (725 Collaborators) including **Jones SJM**. Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. **Cell Rep**. 2018 Apr 3;23(1):194-212.e6. PMID: 29617660

156. Cancer Genome Atlas Research Network (725 Collaborators) including **Jones SJM**. Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. **Cell Rep.** 2018 Apr 3;23(1):213-226.e3. PMID: 29617661

157. Cancer Genome Atlas Research Network (725 Collaborators) including **Jones SJM**. Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. **Cell Rep.** 2018 Apr 3;23(1):227-238.e3. PMID: 29617662

158. Cancer Genome Atlas Research Network (725 Collaborators) including **Jones SJM**. Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. **Cell Rep**. 2018 Apr 3;23(1):239-254.e6. PMID: 29617664

159. Cancer Genome Atlas Research Network (725 Collaborators) including **Jones SJM**. Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. **Cell Rep**. 2018 Apr 3;23(1):255-269.e4. PMID: 29617665

160. Cancer Genome Atlas Research Network (725 Collaborators) including **Jones SJM**. Systematic Analysis of Splice-Site-Creating Mutations in Cancer. **Cell Rep**. 2018 Apr 3;23(1):270-281.e3. PMID: 29617666

161. Cancer Genome Atlas Research Network (725 Collaborators) including **Jones SJM**. Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. **Cell Rep**. 2018 Apr 3;23(1):282-296.e4. PMID: 29617667

162. Cancer Genome Atlas Research Network (725 Collaborators) including **Jones SJM**. 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. PMID: 29617668

163. Cancer Genome Atlas Research Network (725 Collaborators) including **Jones SJM**. Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. Cancer **Cell**. 2018 Apr 9;33(4):721-735.e8. PMID: 29622466

164. Cancer Genome Atlas Research Network (725 Collaborators) including **Jones SJM**. A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. **Cancer Cell.** 2018 Apr 9;33(4):690-705.e9. PMID: 29622464

165. Cancer Genome Atlas Research Network (725 Collaborators) including **Jones SJM**. Genomic and Functional Approaches to Understanding Cancer Aneuploidy. **Cancer Cell.** 2018 Apr 9;33(4):676-689.e3. PMID: 29622463

166. Cancer Genome Atlas Research Network (725 Collaborators) including **Jones SJM**. 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. PMID: 29622465

167. 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

168. 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

169. 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). PMID: 29438965

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

171. 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. d). PMID: 29610392

172. Cancer Genome Atlas Research Network (725 Collaborators) including **Jones SJM**. Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. **Cell Syst.** 2018 Mar 28;6(3):271-281.e7. PMID: 29596782

173. Cancer Genome Atlas Research Network (725 Collaborators) including **Jones SJM**. 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. PMID: 29596783

174. 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

175. Thibodeau ML, Bonakdar M, Zhao E, Mungall KL, Reisle C, Zhang W, Bye MH, Thiessen N, Bleile D, Mungall AJ, Ma YP, Jones MR, Renouf DJ, Lim HJ, Yip S, Ng T, Ho C, Laskin J, Marra MA, Schrader KA, **Jones SJM**. Whole genome and whole transcriptome genomic profiling of a metastatic eccrine porocarcinoma. **NPJ Precision Oncology** 2018 Mar 19,2:1(8) PMID: 29872726

176. Feau N, Beauseigle S, Bergeron MJ, Bilodeau GJ, Birol I, Cervantes-Arango S, Dhillon B, Dale AL, Herath P, **Jones SJM**, Lamarche J, Ojeda DI, Sakalidis ML, Taylor G, Tsui CKM, Uzunovic A, Yueh H, Tanguay P, Hamelin RC. Genome-Enhanced Detection and Identification (GEDI) of plant pathogens. **PeerJ.** 2018 Feb 22;6:e4392. PMID: 29492338

177. Garzia L, Kijima N, Morrissy AS, De Antonellis P, Guerreiro-Stucklin A, Holgado BL, Wu X, Wang X, Parsons M, Zayne K, Manno A, Kuzan-Fischer C, Nor C, Donovan LK, Liu J, Qin L, Garancher A, Liu KW, Mansouri S, Luu B, Thompson YY, Ramaswamy V, Peacock J, Farooq H, Skowron P, Shih DJH, Li A, Ensan S, Robbins CS, Cybulsky M, Mitra S, Ma Y, Moore R, Mungall A, Cho YJ, Weiss WA, Chan JA, Hawkins CE, Massimino M, Jabado N, Zapotocky M, Sumerauer D, Bouffet E, Dirks P, Tabori U, Sorensen PHB, Brastianos PK, Aldape K, **Jones SJM**, Marra MA, Woodgett JR, Wechsler-Reya RJ, Fults DW, Taylor MD. A Hematogenous Route for Medulloblastoma Leptomeningeal Metastases. **Cell**. 2018 Feb 22;172(5):1050-1062.e14.. PMID: 29474906

178. Lever J, Gakkhar S, Gottlieb M, Rashnavadi T, Lin S, Siu C, Smith M, Jones M, Krzywinski M, **Jones SJ**. A collaborative filtering based approach to biomedicalknowledge discovery. **Bioinformatics**. 2018 Feb 15;34(4):652-659. PMID: 29028901

179. Cancer Genome Atlas Network; 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;, 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 (141 Collaborators), including **Jones, SJM**. The Integrated Genomic Landscape of Thymic Epithelial Tumors. **Cancer Cell.** 2018 Feb 12;33(2):244-258.e10. PMID: 29438696

180. Wong HL, Yang KC, Shen Y, Zhao EY, Loree JM, Kennecke HF, Kalloger SE, Karasinska JM, Lim HJ, Mungall AJ, Feng X, Davies JM, Schrader K, Zhou C, Karsan A, **Jones SJ,** 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. PMID: 29092957

181. Velazquez-Torres G, Shoshan E, Ivan C, Huang L, Fuentes-Mattei E, Paret H, Kim SJ, Rodriguez-Aguayo C, Xie V, Brooks D, **Jones SJM**, Robertson AG, Calin G, Lopez-Berenstein G, Sood A, Bar-Eli M. A-to-I miR-378a-3p editing can prevent melanoma progression via regulation of PARVAexpression. **Nat Commun.** 2018 Jan 31;9(1):461. PMID: 29386624

182. Yakovenko O, **Jones SJM**. Modern drug design: the implication of using artificial neuronal networks and multiple molecular dynamic simulations. **J Comput Aided Mol Des**. 2018 Jan;32(1):299-311. PMID: 29134430

183. 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, Schein JE, Mungall AJ, Zhao Y, Moore RA, 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

184. **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. PMID: 29232881

185. **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). PMID: 29232880

186. Chang EY, Novoa CA, Aristizabal MJ, Coulombe Y, Segovia R, Chaturvedi R, Shen Y, Keong C, Tam AS, **Jones SJM,** Masson JY, Kobor MS, Stirling PC. RECQ-like helicases Sgs1 and BLM regulate R-loop-associated genome instability. **J Cell Biol.** 2017 Dec 4;216 (12):3991-4005. PMID: 29042409

187. 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 Y, 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

188. 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

189. Thibodeau ML, Peters CH, Townsend KN, Shen Y, Hendson G, Adam S, Selby K, Macleod PM, Gershome C, Ruben P, **Jones SJM**; FORGE Canada Consortium, Friedman JM, Gibson WT, Horvath GA. Compound heterozygous TRPV4 mutations in two siblings with a complex phenotype including severe intellectual disability and neuropathy. Am J Med Genet A. 2017 Nov;173(11):3087-3092. PMID: 28898540

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

191. TCGA Research Network. (264 Collaborators) including **SJM Jones**. Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. **Cell**. 2017 Nov 2;171(4):950-965.e28. PMID: 29100075

192. TCGA Research Network. (171 Collaborators) including 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; Weinstein JN, Kwiatkowski DJ, Lerner SP., **Jones SJM,** et al. Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. **Cell.** 2017 Oct 19;171(3):540-556.e25. PMID: 28988769

193. Mazor T, Chesnelong C, Pankov A, Jalbert LE, Hong C, Hayes J, Smirnov IV, Marshall R, Souza CF, Shen Y, Viswanath P, Noushmehr H, Ronen SM, **Jones SJM**, Marra MA, Cairncross JG, Perry A, Nelson SJ, Chang SM, Bollen AW, Molinaro AM, Bengtsson H, Olshen AB, Weiss S, Phillips JJ, Luchman HA,

Costello JF. 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

194. Hasan NA, Warren RL, Epperson LE, Malecha A, Alexander DC, Turenne CY, MacMillan D, Birol I, Pleasance S, Coope R, **Jones SJ**M, Romney MG, Ng M, Chan T, Rodrigues M, Tang P, Gardy JL, Strong M. Complete Genome Sequence of Mycobacterium chimaera SJ42, a Non out break Strain from an Immunocompromised Patient with Pulmonary Disease. Genome Announc. 2017 Sep 14;5(37). PMID: 28912319

195. Thibodeau ML, Reisle C, Zhao E, Martin LA, Alwelaie Y, Mungall KL, Ch'ng C, Thomas R, Ng T, Yip S, J Lim H, Sun S, Young SS, Karsan A, Zhao Y, Mungall AJ, Moore RA, J 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

196. Cancer Genome Atlas Research Network. (271 Collaborators) including **Jones SJM.** Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma.**Cancer Cell**. 2017 Aug 14;32(2):185-203.e13.. PMID: 28810144

197. TCGA Research Network, (170 Collaborators) including **Jones SJM**. Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. **Cancer Cell**. 2017 Aug 14;32(2):204-220.e15. PMID: 28810145

198. Jake Lever and **Steven JM Jones** "Painless Relation Extraction with Kindred". Proceedings of the BioNLP 2017 Workshop, pages 176–183, Vancouver, Canada, August 4, 2017.

199. Northcott PA, Buchhalter I, Morrissy AS, Hovestadt V, Weischenfeldt J, Ehrenberger T, Gröbner S, Segura-Wang M, Zichner T, Rudneva VA, Warnatz HJ, Sidiropoulos N, Phillips AH, Schumacher S, Kleinheinz K, Waszak SM, Erkek S, Jones DTW, Worst BC, Kool M, Zapatka M, Jäger N, Chavez L, Hutter B, Bieg M, Paramasivam N, Heinold M, Gu Z, Ishaque N, Jäger-Schmidt C, Imbusch CD, Jugold A, Hübschmann D, Risch T, Amstislavskiy V, Gonzalez FGR, Weber UD, Wolf S, Robinson GW, Zhou X, Wu G, Finkelstein D, Liu Y, Cavalli FMG, Luu B, Ramaswamy V, Wu X, Koster J, Ryzhova M, Cho YJ, Pomeroy SL, Herold-Mende C, Schuhmann M, Ebinger M, Liau LM, Mora J, McLendon RE, Jabado N, Kumabe T, Chuah E, Ma Y, Moore RA, Mungall AJ, Mungall KL, Thiessen N, Tse K, Wong T, **Jones SJM,** Witt O, Milde T, Von Deimling A, Capper D, Korshunov A, Yaspo ML, Kriwacki R, Gajjar A, Zhang J, Beroukhim R, Fraenkel E, Korbel JO, Brors B, Schlesner M, Eils R, Marra MA, Pfister SM, Taylor MD, Lichter P. The whole-genome landscape of medulloblastoma subtypes. **Nature.** 2017 Jul 19;547(7663):311-317. PMID: 28726821

200. 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 RA, Mungall AJ, Schein J, Coope RJ, Ma Y, Zhao Y, Holt RA, **Jones SJ**, Marra MA. Increasing quality, throughput and speed of sample preparation for strand-specific messenger RNA sequencing. **BMC Genomics.** 2017 Jul 5;18(1):515. PMID: 28679365

201. 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,(193 Collaborators) including **Jones SJM**. Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles**. Cell Rep.** 2017 Jun 27;19(13):2878-2880. PMID: 28658632

202. Cancer Genome Atlas Research Network. (238 Collaborators) including **Jones SJM.** Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. **Cell.** 2017 Jun 15;169(7):1327-1341.e23. PMID: 28622513

203. 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

204. 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 DW, Bala M, Hirst M, Miller D, Moore RA, Mungall AJ, Coope RJ, Ma Y, Zhao Y, Holt RA, **Jones SJ**, 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

205. 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. PMID: 28539120

206. 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

207. Wong J, Liu K, Siu C, **Jones S**, Sovka M, Wilson D, Wiseman SM. Management of PET diagnosed thyroid incidentalomas in British Columbia Canada: Critical importance of the PET report. **Am J Surg.** 2017 May;213(5):950-957. PMID: 28408111

208. Cancer Genome Atlas Research Network (146 Collaborators) Including **Jones SJ**. Integrated Molecular Characterization of Uterine Carcinosarcoma. **Cancer Cell**. 2017 Mar 13;31(3):411-423. PMID: 28292439

209. Cancer Genome Atlas Research Network. (303 Collaborators) including **Jones SJ.** Integrated genomic and molecular characterization of cervical cancer. **Nature.** 2017 Mar 16;543(7645):378-384. PMID: 28112728

210. Segovia R, Shen Y, Lujan SA, **Jones SJ**, Stirling PC. Hypermutation signature reveals a slippage and Realignment model of translesion synthesis by Rev3 polymerase in cisplatin-treated yeast. **Proc Natl Acad Sci U S A.** 2017 Mar 7;114(10):2663-2668. PMID: 28223526

211. Cancer Genome Atlas Research Network (207 Collaborators) including **Jones SJ**. Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. **Cancer Cell.** 2017 Feb 13;31(2):181-193. PMID: 28162975

212. Griffith M, Spies NC, Krysiak K, McMichael JF, Coffman AC, Danos AM, Ainscough BJ, Ramirez CA, Rieke DT, Kujan L, Barnell EK, Wagner AH, Skidmore ZL, Wollam A, Liu CJ, Jones MR, Bilski RL, Lesurf R, Feng YY, Shah NM, Bonakdar M, Trani L, Matlock M, Ramu A, Campbell KM, Spies GC,

Graubert AP, Gangavarapu K, Eldred JM, Larson DE, Walker JR, Good BM, Wu C, Su AI, Dienstmann R, Margolin AA, Tamborero D, Lopez-Bigas N, **Jones SJ**, Bose R, Spencer DH, Wartman LD, Wilson RK, Mardis ER, Griffith OL. CIViC is a community knowledgebase for expert crowdsourcing the clinical interpretation of variants in cancer. **Nat Genet.** 2017 Jan 31;49(2):170-174. PMID: 28138153

213. Lian EY, Maritan SM, Cockburn JG, Kasaian K, Crupi MJ, Hurlbut D, **Jones SJ**, Wiseman SM, Mulligan LM. Differential roles of RET isoforms in medullary and papillary thyroid carcinomas. **Endocr Relat Cancer.** 2017 Jan;24(1):53-69. PMID: 27872141

214. Cancer Genome Atlas Research Network (346 collaborators) including **Jones SJ**, Integrated genomic characterization of oesophageal carcinoma. **Nature**. 2017 Jan 12; 541(7636):169-175. PMID: 28052061

215. Sheffield BS, Tessier-Cloutier B, Li-Chang H, Shen Y, Pleasance E, Kasaian K, Li Y, **Jones SJ**, 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

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

217. Younesy H, Nielsen CB, Lorincz MC, **Jones SJ**, Karimi MM, Möller T. ChAsE: chromatin analysis and exploration tool. **Bioinformatics**. 2016 Nov 1;32(21):3324-3326. PMID: 27378294

218. International Human Epigenome Consortium (228 Collaborators) including **Jones SJ**. The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. **Cell.** 2016 Nov 17;167(5):1145-1149. PMID:27863232

219. 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: 27851968f

220. Feau N, Taylor G, Dale AL, Dhillon B, Bilodeau GJ, Birol I, **Jones SJ**, Hamelin RC. Genome sequences of six *Phytophthora* species threatening forest ecosystems. Genom Data. 2016 Oct 3;10:85-88. PMID: 27752469

221. Sheffield BS, Fulton R, Kalloger SE, Milne K, Geller G, Jones M, Jacquemont C, Zachara S, Zhao E, Pleasance E, Laskin J, **Jones SJ**, 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

222. Coombe L, Warren RL, Jackman SD, Yang C, Vandervalk BP, Moore RA, Pleasance S, Coope RJ, Bohlmann J, Holt RA, **Jones SJ**, Birol I. Assembly of the Complete Sitka Spruce Chloroplast Genome Using 10X Genomics' GemCode Sequencing Data. **PLoS One**. 2016 Sep 15;11(9):e0163059. PMID: 27632164

223. Lever, Jake, and Steven JM Jones. "VERSE: Event and Relation Extraction in the BioNLP 2016 Shared Task." ACL 2016 Aug 13, (2016): 42. Proceedings of the 4th BioNLP Shared Task Workshop, Berlin, Germany

224. 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 Jul 18. PMID: 27449082

225. Moore SE, Kasaian K, **Jones S**, Melck A, Wiseman SM. Clinical importance of bilateral disease in patients with papillary thyroid cancer. Can J Surg. 2016 Jun;59(3):213-5. doi: 10.1503/cjs.014615. PMID: 27240287

226. 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 SJ**, Marra MA, Laskin J, Lim HJ. Response to angiotensin blockade with irbesartan in a patient with metastatic colorectal cancer. **Ann Oncol**. 2016 May;27(5):801-6. PMID: 27022066

227. de Leeuw CN, Korecki AJ, Berry GE, Hickmott JW, Lam SL, Lengyell TC, Bonaguro RJ, Borretta LJ, Chopra V, Chou AY, D'Souza CA, Kaspieva O, Laprise S, McInerny SC, Portales-Casamar E, Swanson-Newman MI, Wong K, Yang GS, Zhou M,**Jones SJ**, Holt RA, Asokan A, Goldowitz D, Wasserman WW, Simpson EM. rAAV-compatible MiniPromoters for restricted expression in the brain and eye. Mol Brain. 2016 May 10;9(1):52. PMID: 27164903

228. 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.

229. Miller RR, Langille MG, Montoya V, Crisan A, Stefanovic A, Martin I, Hoang L, Patrick DM, Romney M, Tyrrell G, **Jones SJ,** Brinkman FS, Tang P. Genomic Analysis of a Serotype 5 Streptococcus pneumoniae Outbreak in British Columbia, Canada, 2005-2009. **Can J Infect Dis Med Microbiol**. 2016;2016:5381871. PMID: 27366170

230. 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

231. Lien S, Koop BF, Sandve SR, Miller JR, Kent MP, Nome T, Hvidsten TR, Leong JS, Minkley DR, Zimin A, Grammes F, Grove H, Gjuvsland A, Walenz B, Hermansen RA, von Schalburg K, Rondeau EB, Di Genova A, Samy JK, Olav Vik J, Vigeland MD, Caler L, Grimholt U, Jentoft S, Inge Våge D, de Jong P, Moen T, Baranski M, Palti Y, Smith DR, Yorke JA, Nederbragt AJ, Tooming-Klunderud A, Jakobsen KS, Jiang X, Fan D, Hu Y, Liberles DA, Vidal R, Iturra P, **Jones SJ**, Jonassen I, Maass A, Omholt SW, Davidson WS. The Atlantic salmon genome provides insights into rediploidization. **Nature**. 2016 Apr 18. PMID: 27088604

232. 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

233. 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 Mar 27. PMID:27036018

234. Davis B, Shen Y, Poon CC, Luchman HA, Stechishin OD, Pontifex CS, Wu W, Kelly JJ, Blough MD; Terry Fox Research Institute Glioblastoma Consortium. Cairncross G, Weiss S, Robbins S, Senger D, Chan J, Luchman A, Blough M, Marra M, **Jones S,** Shen Y, Bose P, Lever J, Kaplan D, Grinshtein N, Al-Awar R, Euhling D, Aman A, Singh S, Mason W, Seymour L Comparative genomic and genetic analysis of glioblastoma-derived brain tumor-initiating cells and their parent tumors. **Neuro Oncol.** 2016 Mar;18(3):350-60. PMID: 26245525

235. Chun H-Y, Lim EL, Heravi Moussavi A, Saberi S, Mungall KL, Bilenky M, Carles A, Tse K, Shlafman I, Zhu K, Qian JQ, Harvey D, He A, 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

236. 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

237. Cancer Genome Atlas Research Network. (228 collaborators including) **Jones SJ,** Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. **N Engl J Med.** 2016 Jan 14;374(2):135-45. PMID: 26536169

238. Ceccarelli M, Barthel FP, Malta TM, TCGA Research Network (162 Collaborators) including, **Jones SJ**. Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. **Cell.** 2016 Jan 28;164(3):550-63. PMID: 26824661

239. 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, 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):351-7. PMID: 26760213

240. Lesurf R, Cotto KC, Wang G, Griffith M, Kasaian K, **Jones SJ**, Montgomery SB, Griffith OL; Open Regulatory Annotation Consortium. ORegAnno 3.0: a community-driven resource for curated regulatory annotation. **Nucleic Acids Res**. 2016 Jan 4;44(D1):D126-32. PMID:26578589

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

242. Jackman SD, Warren RL, Gibb EA, Vandervalk BP, Mohamadi H, Chu J, Raymond A, Pleasance S, Coope R, Wildung MR, Ritland CE, Bousquet J, **Jones SJ,** Bohlmann J, Birol I. Organellar Genomes of White Spruce (Picea glauca): Assembly and Annotation. Genome Biol Evol. 2015 Dec 8;8(1):29-41. PMID: 26645680

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

244. Liu L, Li H, Dargahi D, Shynlova O, Slater D, **Jones SJ**, Lye SJ, Dong X. HoxA13 Regulates Phenotype Regionalization of Human Pregnant Myometrium. **J Clin Endocrinol Metab**. 2015 Dec;100(12):E1512-22. PMID: 26485220

245. Cancer Genome Atlas Research Network. (312 Collaborators including) **Jones SJ**. The Molecular Taxonomy of Primary Prostate Cancer. **Cell.** 2015 Nov 5;163(4):1011-25. PMID: 26544944

246. 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):4340-50. PMID: 26525672

247. TCGA Research Network, (126 collaborators including) **Jones SJ.** Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. **Cell.** 2015 Oct 8;163(2):506-19. PMID: 26451490

248. 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 Y, Lim H, Ma Y, Mar C, Martin M, Moore R, Mungall A, Mungall K, Pleasance E, Rassekh SR, Renouf D, Shen Y, Schein J, Schrader K, Sun S, Tinker A, Zhao E, Yip S, Marra MA. Lessons learned from the application of whole-genomeanalysis to the treatment of patients with advanced cancers. **Cold Spring Harb Mol Case Stud**. 2015 Oct;1(1):a000570. PMID: 27148575

249. 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

250. Lebovitz CB, Robertson AG, Goya R, **Jones SJ,** Morin RD, Marra MA, Gorski SM. Cross-cancer profiling of molecular alterations within the human autophagy interaction network. **Autophagy.** 2015 Sept;11(9):1668-87. PMID: 26208877

251. Younesy H, Möller T, Lorincz MC, Karimi MM, **Jones SJ**. VisRseq: R-based visual framework for analysis of sequencing data. **BMC Bioinformatics.** 2015 Aug 13;16 Suppl 11:S2. PMID: 26328469

252. Warren RL, Yang C, Vandervalk BP, Behsaz B, Lagman A, **Jones SJ,** Birol I. LINKS: Scalable, alignment-free scaffolding of draft genomes with long reads. **Gigascience**. 2015 Aug 4;4:35. PMID: 26244089

253. Choi H, Kasaian K, Melck A, Ong K, **Jones SJ,** White A, Wiseman SM. Papillary thyroid carcinoma: prognostic significance of cancer presentation. **Am J Surg**. 2015 Aug;210(2):298-301. PMID: 25997714

254. Schmouth JF, Arenillas D, Corso-Díaz 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

255. Mondal T, Subhash S, Vaid R, Enroth S, Uday S, Reinius B, Mitra S, Mohammed A, James AR, Hoberg E, Moustakas A, Gyllensten U, **Jones SJ,** Gustafsson CM, Sims AH, Westerlund F, Gorab E, Kanduri C. MEG3 long noncoding RNA regulates the TGF-β pathway genes through formation of RNA-DNA triplex structures. **Nat Commun.** 2015 Jul 24;6:7743. PMID: 26205790

256. 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 Reports**. 2015 Jul 14;5(1):1-9. PMID: 26095605

257. Warren RL, Keeling CI, Yuen MM, Raymond A, Taylor GA, Vandervalk BP, Mohamadi H, Paulino D, Chiu R, Jackman SD, Robertson G, Yang C, Hoffmann M, Weigel D, Nelson DR, Ritland C, Isabel N, Jaquish B, Yanchuk A, Bousquet J, **Jones SJ,** MacKay J, Birol I, Bohlmann J. Improved white spruce (Picea glauca) genome assemblies and annotation of large gene families of conifer terpenoid and phenolic defense metabolism. **Plant J**. 2015 Jul;83(2):189-212. PMID: 26017574

258. 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: 25631445

259. Cancer Genome Atlas Network. (352 collaborators including) **Jones, SJ.** Genomic Classification of Cutaneous Melanoma. **Cell.** 2015 Jun 18;161(7):1681-96. PMID:26091043

260. Cohen AS, Tuysuz B, Shen Y, Bhalla SK, **Jones SJ,** Gibson WT. A novel mutation in EED associated with overgrowth. **J Hum Genet**. 2015 Jun;60(6):339-42. PMID: 25787343

261. Halwani Y, Kojic LD, Chan SK, Phang TP, Masoudi H, **Jones SJ**, Nabi IR, Wiseman SM. Prognostic significance of autocrine motility factor receptor expression by colorectal cancer and lymph node metastases. **Am J Surg**. 2015 May;209(5):884-9. PMID: 25852009

262. Kasaian K, Chindris AM, 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 SJ**. MEN1 Mutations in Hürthle Cell (Oncocytic) Thyroid Carcinoma. J Clin Endocrinol Metab. 2015 Apr;100(4):E611-5. PMID: 25625803

263. 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 SJ**, Gown AM, Huntsman DG, Schaeffer DF, Churg A, Yip S, Laskin J, Marra MA. Personalized oncogenomics: clinical experience with malignant peritoneal mesothelioma using whole genome sequencing. **PLoS One**. 2015 Mar 23;10(3):e0119689. PMID: 25798586

264. Shoshan E, Mobley AK, Braeuer RR, Kamiya T, Huang L, Vasquez ME, Salameh A, Lee HJ, Kim SJ, Ivan C, Velazquez-Torres G, Nip KM, Zhu K, Brooks D, **Jones SJ**, Birol I, Mosqueda M, Wen YY, Eterovic AK, Sood AK, Hwu P, Gershenwald JE, Gordon Robertson A, Calin GA, Markel G, Fidler IJ, Bar-Eli M. Reduced adenosine-to-inosine miR-455-5p editing promotes melanoma growth and metastasis. **Nat Cell Biol**. 2015 Mar;17(3):311-21. PMID: 25686251

265. Roadmap Epigenomics Consortium (258 Collaborators including) **Jones SJ.** Integrative analysis of 111 reference human epigenomes. **Nature.** 2015 Feb 19;518(7539):317-30. PMID: 25693563

266. 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. PMID: 25690954

267. Li-Chang HH, Kasaian K, Ng Y, Lum A, Kong E, Lim H, **Jones S**, Huntsman DG, Schaeffer DF, Yip S. Retrospective review using targeted deep sequencing reveals mutational differences between gastroesophageal junction and gastric carcinomas. **BMC Cancer**. 2015 Feb 6;15:32. PMID: 25656989

268. Cancer Genome Atlas Network. (348 Collaborators including) , Ally A, Balasundaram M,Birol I, Bowlby R, Brooks D, Butterfield YS, Carlsen R, Cheng D, Chu A, Dhalla N, Guin R, Holt RA, **Jones SJ**, Lee D, Li HI, Marra MA, Mayo M, Moore RA, Mungall AJ, Robertson AG, Schein JE, Sipahimalani P, Tam A, Thiessen N, Wong T. Comprehensive genomic characterization of head and neck squamous cell carcinomas. **Nature**. 2015 Jan 29;517(7536):576-82. PMID: 25631445

269. Kulic I, Robertson G, Chang L, Baker JH, Lockwood WW, Mok W, Fuller M, Fournier M, Wong N, Chou V, Robinson MD, Chun HJ, 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

270. Dargahi D, Swayze RD, Yee L, Bergqvist PJ, Hedberg BJ, Heravi-Moussavi A, Dullaghan EM, Dercho R, An J, Babcook JS, **Jones SJ.** A pan-cancer analysis of alternative splicing events reveals novel tumor-associated splice variants of matriptase. **Cancer Inform**. 2014 Dec 4;13:167-77. PMID: 25506199

271. Dean RA, Fam HK, An J, Choi K, Shimizu Y, **Jones SJ**, Boerkoel CF, Interthal H, Pfeifer TA. Identification of a Putative Tdp1 Inhibitor (CD00509) by in Vitro and Cell-Based Assays. **J Biomol Screen.** 2014 Dec;19(10):1372-82. PMID: 25117203.

272. Chetaille P, Preuss C, Burkhard S, Côté JM, Houde C, Castilloux J, Piché J, Gosset N, Leclerc S, Wünnemann F, Thibeault M, Gagnon C, Galli A, Tuck E, Hickson GR, Amine NE, Boufaied I, Lemyre E, de Santa Barbara P, Faure S, Jonzon A, Cameron M, Dietz HC, Gallo-McFarlane E, Benson DW, Moreau C, Labuda D; FORGE Canada Consortium, Zhan SH, Shen Y, Jomphe M, **Jones SJ**, Bakkers J, Andelfinger G. Mutations in SGOL1 cause a novel cohesinopathy affecting heart and gut rhythm. Nat Genet. 2014 Nov;46(11):1245-9. PMID: 25282101

273. Chen L, Gibbons DL, Goswami S, Cortez MA, Ahn YH, Byers LA, Zhang X, Yi X, Dwyer D, Lin W, Diao L, Wang J, Roybal JD, Patel M, Ungewiss C, Peng D, Antonia S, Mediavilla-Varela M, Robertson G, Jones S, Suraokar M, Welsh JW, Erez B, Wistuba II, Chen L, Peng D, Wang S, Ullrich SE, Heymach JV, Kurie JM, Qin FX. Metastasis is regulated via microRNA-200/ZEB1 axis control of tumour cell PD-L1 expression and intratumoral immunosuppression. **Nat Commun.** 2014 Oct 28;5:5241.PMID: 25348003

274. Cancer Genome Atlas Network. (340 Collaborators including) Ally A, Balasundaram M, Birol I, Bowlby R, Butterfield YS, Carlsen R, Cheng D, Chu A, Dhalla N, Guin R, Holt RA, **Jones SJ**, Lee D, Li HI, Marra MA, Mayo M, Moore RA, Mungall AJ, Robertson AG, Schein JE, Sipahimalani P, Tam A, Thiessen N, Wong T. 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):15544-9. PMID: 25313082

275. De La Torre AR, Birol I, Bousquet J, Ingvarsson PK, Jansson S, **Jones SJ,** Keeling CI, MacKay J, Nilsson O, Ritland K, Street N, Yanchuk A, Zerbe P, Bohlmann J. Insights into conifer giga-genomes. **Plant Physiol.** 2014 Dec;166(4):1724-32. PMID: 25349325

276. Cancer Genome Atlas Research Network. (243 Collaborators including) **Jones SJ**. Integrated genomic characterization of papillary thyroid carcinoma. **Cell**. 2014 Oct 23;159(3):676-90. PMID: 25417114

277. van den Berg S, Shen Y, **Jones SJ,** Gibson WT. Genetic Counseling in Direct-to-Consumer Exome Sequencing: A Case Report. **J Genet Couns**. 2014 Oct;23(5):742-53. PMID: 24954083

278. Alder O, Cullum R, Lee S, Kan AC, Wei W, Yi Y, Garside VC, Bilenky M, Griffith M, Morrissy AS, Robertson GA, Thiessen N, Zhao Y, Chen Q, Pan D, **Jones SJ**, Marra MA, Hoodless PA. Hippo signaling influences HNF4A and FOXA2 enhancer switching during hepatocyte differentiation. **Cell Rep**. 2014 Oct 9;9(1):261-71. PMID: 25263553

279. The Cancer Genome Atlas Research Network (223 Collaborators including) Davis CF, Ricketts CJ, Wang M, Yang L, Ally A, Balasundaram M, Birol I, Brooks D, Butterfield YS, Chuah E, Clarke A, Dhalla N, Guin R, Holt RA, Kasaian K, Lee D, Li HI, Lim E, Ma Y, Mayo M, Moore RA, Mungall AJ, Schein JE, Sipahimalani P, Tam A, Thiessen N, Wong T, **Jones SJ**, Marra MA. The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. **Cancer Cell.** 2014 Sep 8;26(3):319-30. PMID: 25155756

280. The Cancer Genome Atlas Research Network; Analysis Working Group (318 Collaborators including) **Jones SJM,** BC Cancer Agency. Comprehensive molecular characterization of gastric adenocarcinoma. **Nature.** 2014 Sep 11;513(7517):202-9. PMID: 25079317

281. Cohen AS, Townsend KN, Xiang QS, Attariwala R, Borchers C, Senger C, Picker W, Levi J, Yewchuk L, Tan J, Eydoux P, Lum A, Yong SL, McKinnon ML, Lear SA, Everett R, **Jones SJ,** Yip S, Gibson WT. Somatic mosaicism for the p.His1047Arg mutation in PIK3CA in a girl with mesenteric lipomatosis. **Am J Med Genet A**. 2014 Sep;164A(9):2360-4. PMID: 24903541

282. Cancer Genome Atlas Research Network, (307 Collaborators including) **Jones, SJ**. Multiplatform analysis of 12 cancer types reveals molecular classification within and across tissues of origin. **Cell**. 2014 Aug 14;158(4):929-44. PMID: 25109877

283. Cancer Genome Atlas Research Network. (383 Collaborators including) Robertson G, Balasundaram M, Butterfield YS, Carlsen R, Chu A, Chuah E, Dhalla N, Guin R, Hirst C, Lee D, Li HI, Mayo M, Moore RA, Mungall AJ, Schein JE, Sipahimalani P, Tam A, Varhol R, Robertson A, Wye N, Thiessen N, Holt RA, **Jones SJ**, Marra MA. Comprehensive molecular profiling of lung adenocarcinoma. **Nature**. 2014 Jul 31;511(7511):543-50. PMID: 25079552

284. Butterfield YS, Kreitzman M, Thiessen N, Corbett RD, Li Y, Pang J, Ma YP, **Jones SJ,** Birol I. JAGuaR: Junction Alignments to Genome for RNA-Seq Reads. **PLoS One.** 2014 Jul 25;9(7):e102398. PMID: 25062255.

285. Vanner RJ, Remke M, Gallo M, Selvadurai HJ, 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 SJ**, 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.

286. 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.

287. Beaulieu CL, Majewski J, Schwartzentruber J, Samuels ME, Fernandez BA, Bernier FP, Brudno M, Knoppers B, Marcadier J, Dyment D, Adam S, Bulman DE, **Jones SJ,** Avard D, Nguyen MT, Rousseau F, Marshall C, Wintle RF, Shen Y, Scherer SW; FORGE Canada Consortium, Friedman JM, Michaud JL, Boycott KM. FORGE Canada Consortium: Outcomes of a 2-Year National Rare-Disease Gene-Discovery Project. **Am J Hum Genet**. 2014 Jun 5;94(6):809-817. PMID: 24906018

288. Jamshidi F, Pleasance E, Li Y, Shen Y, Kasaian K, Corbett R, Eirew P, Lum A, Pandoh P, Zhao Y, Schein JE, Moore RA, Rassekh R, Huntsman DG, Knowling M, Lim H, Renouf DJ, **Jones SJ,** Marra MA, Nielsen TO, Laskin J, Yip S. Diagnostic Value of Next-Generation Sequencing in an Unusual Sphenoid Tumor. **Oncologist.** 2014 Jun;19(6):623-30. PMID: 24807916

289. Stival Sena J, Giguère I, Boyle B, Rigault P, Birol I, Zuccolo A, Ritland K, Ritland C, Bohlmann J, **Jones S,** Bousquet J, Mackay J. Evolution of gene structure in the conifer Picea glauca: a comparative analysis of the impact of intron size. **BMC Plant Biol.** 2014 Apr 16;14(1):95. PMID: 24734980.

290. Janbon G, Ormerod KL, Paulet D, Byrnes EJ 3rd, Yadav V, Chatterjee G, Mullapudi N, Hon CC, Billmyre RB, Brunel F, Bahn YS, Chen W, Chen Y, Chow EW, Coppée JY, Floyd-Averette A, Gaillardin C, Gerik KJ, Goldberg J, Gonzalez-Hilarion S, Gujja S, Hamlin JL, Hsueh YP, Ianiri G, **Jones S,** Kodira CD, Kozubowski L, Lam W, Marra M, Mesner LD, Mieczkowski PA, Moyrand F, Nielsen K, Proux C, Rossignol T, Schein JE, Sun S, Wollschlaeger C, Wood IA, Zeng Q, Neuvéglise C, Newlon CS, Perfect JR, Lodge JK, 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

291. Zovoilis A, Mungall AJ, Moore R, Varhol R, Chu A, Wong T, Marra M, **Jones SJ.** 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;15(4):402-10. PMID: 24534129

292. Younesy H, Möller T, Heravi-Moussavi A, Cheng JB, Costello JF, Lorincz MC, Karimi MM, **Jones SJ**. ALEA: a toolbox for allele-specific epigenomics analysis. **Bioinformatics**. 2014 Apr 15;30(8):1172-1174. PMID: 24371156.

293. Lobo Prabhu KC, Vu L, Chan SK, Phang T, Gown A, **Jones SJ,** Wiseman SM. Predictive utility of cyclo-oxygenase-2 expression by colon and rectal cancer. **Am J Surg**. 2014 May;207(5):712-6. PMID: 24791632

294. Cancer Genome Atlas Research Network. (367 Collaborators including) Mungall AJ, Robertson AG, Chu A, Ally A, Balasundaram M, Butterfield YS, Dhalla N, Hirst C, Holt RA, Lee D, Li HI, Mayo M, Moore RA, Schein JE, Sipahimalani P, Tam A, Thiessen N, Wong T, Wye N, Bowlby R, Chuah E, Guin R, **Jones SJ,** Marra MA. Comprehensive molecular characterization of urothelial bladder carcinoma. **Nature.** 2014 Mar 20;507(7492):315-22. PMID: 24476821.

295. Greenway SC, McLeod R, Hume S, Roslin NM, Alvarez N, Giuffre M, Zhan SH, Shen Y, Preuss C, Andelfinger G; FORGE Canada Consortium, **Jones SJ,** Gerull B. Exome Sequencing Identifies a Novel Variant in ACTC1 Associated With Familial Atrial Septal Defect. **Can J Cardiol.** 2014 Feb;30(2):181-7. PMID: 24461919

296. Stirling PC, Shen Y, Corbett R, **Jones SJ,** Hieter P. Genome Destabilizing Mutator Alleles Drive Specific Mutational Trajectories in Saccharomyces cerevisiae. **Genetics**. 2014 Feb;196(2):403-12.PMID: 24336748

297. Demos MK, van Karnebeek CD, Ross CJ, Adam S, Shen Y, Zhan SH, Shyr C, Horvath G, Suri M, Fryer A, **Jones SJ**, Friedman JM. A novel recurrent mutation in ATP1A3 causes CAPOS syndrome. **Orphanet J Rare Dis**. 2014 Jan 28;9:15. PMID: 24468074.

298. De Leeuw CN, Dyka FM, Boye SL, Laprise S, Zhou M, Chou AY, Boretta L, McInerny SC, Banks KG, Portales-Casamar E, Swanson MI, D'Souza CA, Boye SE, **Jones SJM**, Holt RA, Goldowitz D, Hauswirth WW, Simpson EM. Targeted CNS Delivery using human MiniPromoters and demonstrated compatibility with adeno-associated viral vectors. **Mol Ther Methods Clin Dev.** 2014 Jan 8;1:5. PMID: 24761428

299. Johnson BE, Mazor T, Hong C, Barnes M, Aihara K, McLean CY, Fouse SD, Yamamoto S, Ueda H, Tatsuno K, Asthana S, Jalbert LE, Nelson SJ, Bollen AW, Gustafson WC, Charron E, Weiss WA, Smirnov IV, Song JS, Olshen AB, Cha S, Zhao Y, Moore RA, Mungall AJ, **Jones SJ,** Hirst M, Marra MA, Saito N, Aburatani H, Mukasa A, 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):189-93. PMID: 24336570

300. Halbritter J, Bizet AA, Schmidts M, Porath JD, Braun DA, Gee HY, McInerney-Leo AM, Krug P, Filhol E, Davis EE, Airik R, Czarnecki PG, Lehman AM, Trnka P, Nitschké P, Bole-Feysot C, Schueler M, Knebelmann B, Burtey S, Szabó AJ, Tory K, Leo PJ, Gardiner B, McKenzie FA, Zankl A, Brown MA, Hartley JL, Maher ER, Li C, Leroux MR, Scambler PJ, Zhan SH, **Jones SJ**, Kayserili H, Tuysuz B, Moorani KN, Constantinescu A, Krantz ID, Kaplan BS, Shah JV; UK10K Consortium, Hurd TW, Doherty D, Katsanis N, Duncan EL, Otto EA, Beales PL, Mitchison HM, Saunier S, Hildebrandt F. Defects in the IFT-B Component IFT172 Cause Jeune and Mainzer-Saldino Syndromes in Humans. **Am J Hum Genet.** 2013 Nov 7;93(5):915-25. PMID: 24140113

301. 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

302. Yakovenko O, Morin R, Vashchenko G, and **Jones SJM.** "Theoretical Investigation of the D83V Mutation within the Myocyte-Specific Enhancer Factor-2 Beta and Its Role in Cancer," **Journal of Theoretical Chemistry**, vol. 2013, Article ID 313419, 10 pages, 2013. doi:10.1155/2013/313419. Accepted 21 October 2013

303. Tee MC, Chan SK, Nguyen V, Strugnell SS, Yang J, **Jones S**, Tiwari P, Levine DS, Wiseman SM. Incremental value and clinical impact of neck sonography for primary hyperparathyroidism: a risk-adjusted analysis. **Can J Surg**. 2013 Oct;56(5):325-31. PMID:24067517.

304. Schmouth JF, Castellarin M, Laprise S, Banks KG, Bonaguro RJ, McInerny SC, Borretta L, Amirabbasi M, Korecki AJ, Portales-Casamar E, Wilson G, Dreolini L, **Jones SJ,** Wasserman WW, Goldowitz D, Holt RA, Simpson EM. Non-coding-regulatory regions of human brain genes delineated by bacterial artificial chromosome knock-in mice. **BMC Biol**. 2013 Oct 14;11:106. PMID: 24124870

305. Cancer Genome Atlas Research Network (346 Collaborators, including) Ally A, Balasundaram M, Birol I,Butterfield SN, Chu A, Chuah E, Chun HJ, Dhalla N, Guin R, Hirst M, Hirst C, Holt RA, **Jones SJ,** Lee D, Li HI,Marra MA, Mayo M, Moore RA, Mungall AJ, Robertson AG, Schein JE, Sipahimalani P, Tam A, Thiessen N,Varhol RJ,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):1113-20. PMID: 24071849

306. Lenassi M, Gostinčar C, Jackman S, Turk M, Sadowski I, Nislow C, **Jones S**, Birol I, Cimerman NG, Plemenitas A. Whole Genome Duplication and Enrichment of Metal Cation Transporters Revealed byDe Novo Genome Sequencing of Extremely Halotolerant Black Yeast Hortaea werneckii. PLoS ONE. 2013 Aug 15 8(8): e71328. doi:10.1371/journal.pone.0071328. PMID: 23977017

307. Morin RD, Mungall K, Pleasance E, Mungall AJ, Goya R, Huff R, Scott DW, Ding J, Roth A, Chiu R, Corbett RD, Chan FC, Mendez-Lago M, Trinh DL, Bolger-Munro M, Taylor G, Hadj Khodabakhshi A, 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):1256-65. PMID: 23699601

308. Kasaian K, Wiseman SM, Thiessen N, Mungall KL, Corbett RD, Qian JQ, Nip KM, He A, Tse K, Chuah E, Varhol RJ, Pandoh P, McDonald H, Zeng T, Tam A, Schein J, Birol I, Mungall AJ, Moore RA, Zhao Y, Hirst M, Marra MA, Walker BA, **Jones SJ.** Complete Genomic Landscape of a Recurring Sporadic Parathyroid Carcinoma. **J Pathol.** 2013 Jul;230(3):249-60. PMID: 23616356

309. The Cancer Genome Atlas Research Network (200+ authors) Gordon Robertson A, Chu A, Chun HJ, Mungall AJ, Sipahimalani P, Stoll D, Ally A, Balasundaram M, Butterfield YS, Carlsen R, Carter C, Chuah E, Coope RJ, Dhalla N, Gorski S, Guin R, Hirst C, Hirst M, Holt RA, Lebovitz C, Lee D, Li HI, Mayo M, Moore RA, Pleasance E, Plettner P, Schein JE, Shafiei A, Slobodan JR, Tam A, Thiessen N, Varhol RJ, Wye N, Zhao Y, Birol I, **Jones SJ**, Marra MA. Comprehensive molecular characterization of clear cell renal cell carcinoma. **Nature.** 2013 Jul 4;499(7456):43-9. PMID:23792563

310. Maksakova IA, Thompson PJ, Goyal P, **Jones SJ**, Singh PB, Karimi MM, Lorincz MC.. Distinct roles of KAP1, HP1 and G9a/GLP in silencing of the 2-cell specific retrotransposon MERVL in mouse ES cells. **Epigenetics & Chromatin.** 2013 Jun 4;6(1):15. PMID: 23735015.

311. Birol I, Raymond A, Jackman SD, Pleasance S, Coope R, Taylor GA, Yuen MM, Keeling CI, Brand D, Vandervalk BP, Kirk H, Pandoh P, Moore RA, Zhao Y, Mungall AJ, Jaquish B, Yanchuk A, Ritland C, Boyle B, Bousquet J,Ritland K, Mackay J, Bohlmann J, **Jones SJ**. Assembling the 20 Gb white spruce (Picea glauca) genome from whole-genomeshotgun sequencing data. **Bioinformatics.** 2013 Jun 15;29(12):1492-1497. PMID: 23698863

312. Wei W, Hou J, Alder O, Ye X, Lee S, Cullum R, Chu A, Zhao Y, Warner SM, Knight DA, Yang D, **Jones SJ**, 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):2491-501. PMID: 23315977

313. The Cancer Genome Atlas Research Network which includes: Mungall AJ, Robertson A, Ally A, Balasundaram M, Birol I, Butterfield Y, Chiu R, Chu A, Chuah E, Chun HJ, Corbett R, Dhalla N, Guin R, He A, Hirst C, Hirst M, Holt RA, **Jones S,** Karsan A, Lee D, Li HI, Marra MA, Mayo M, Moore RA, Mungall K, Parker J, Pleasance E, Plettner P, Schein J, Stoll D, Swanson L, Tam A, Thiessen N, Varhol R, Wye N, Zhao Y. Genomic and epigenomic landscapes of adult de novo acute myeloid leukemia. **N Engl J Med.** 2013 May 30; 368(22): 2059-74. PMID: 23634996.

314. Hadj Khodabakhshi A, Fejes AP, Birol I, **Jones SJ**. Identifying cancer mutation targets across thousands of samples MuteProc, a high throughput mutation analysis pipeline. **BMC Bioinformatics.** 2013 May 28;14:167. PMID: 23714400.

315. Hall DE, Yuen MM, Jancsik S, Quesada AL, Dullat HK, Li M, Henderson H, Arango-Velez A, Liao NY, Docking RT,Chan SK, Cooke JE, Breuil C, **Jones SJ,** Keeling CI, Bohlmann J. Transcriptome resources and functional characterization of monoterpenesynthases for two host species of the mountain pine beetle, lodgepole pine (Pinus contorta) and jack pine (Pinus banksiana). **BMC Plant Biol.** 2013 May 16;13:80. PMID: 23679205

316. Cancer Genome Atlas Research Network (313 collaborators including) Ally A, Balasundaram M, Birol I,Butterfield YS, Carlsen R, Carter C, Chu A, Chuah E, Chuah HJ, Dhalla N, Guin R, Hirst C, Holt RA, **Jones SJ,** Lee D, Li HI, Marra MA, Mayo M, Moore RA, Mungall AJ, Plettner P, Schein JE, Sipahimalani P, Tam A, Varhol RJ,(313 collaborators). Integrated genomic characterization of endometrial carcinoma. **Nature.** 2013 May 2;497(7447):67-73. PMID: 23636398.

317. Cancer Genome Atlas Research Network (139 Collaborators including) Ally A, Balasundaram M, Birol I,Butterfield Y, Chiu R, Chu A, Chuah E, Chun HJ, Corbett R, Dhalla N, Guin R, He A, Hirst C, Hirst M, Holt RA, **Jones S**, Karsan A, Lee D, Li HI, Marra MA, Mayo M, Moore RA, Mungall K, Parker J, Pleasance E, Plettner P, Schein J, Stoll D, Swanson L, Tam A, Thiessen N, Varhol R, Wye N, Zhao Y Genomic and epigenomic landscapes of adult de novo acute myeloid leukemia. **N Engl J Med**. 2013 May 30;368(22):2059-74. PMID: 23634996

318. Clemons AM, Brockway HM, Yin Y, Kasinathan B, Butterfield YS, **Jones SJ**, Colaiácovo MP, Smolikove S. Akirin is required for diakinesis bivalent structure and synaptonemal complex disassembly at meiotic prophase I. **Mol Biol Cell**. 2013 Apr;24(7):1053-67. PMID: 23363597

319. Trinh DL, Scott DW, Morin RD, Mendez-Lago M, An J, **Jones SJ**, Mungall AJ, Zhao Y, 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):3666-74. PMID: 23460611.

320. Keeling CI, Yuen MM, Liao NY, Docking TR, Chan SK, Taylor GA, Palmquist DL, Jackman SD, Nguyen A, Li M, Henderson H, Janes JK, Zhao Y, Pandoh P, Moore R, Sperling FA, Huber DP, Birol I**, Jones SJ,** Bohlmann J. Draft genome of the mountain pine beetle, Dendroctonus ponderosae Hopkins, a major forest pest. **Genome Biol**. 2013 Mar 27;14(3):R27. PMID: 23537049.

321. Dubuc AM, Remke M, Korshunov A, Northcott PA, Zhan SH, Mendez-Lago M, Kool M, Jones DT, Unterberger A, Morrissy AS, Shih D, Peacock J, Ramaswamy V, Rolider A, Wang X, Witt H, Hielscher T, Hawkins C, Vibhakar R, Croul S, Rutka JT, Weiss WA, **Jones SJ,** 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):373-84. PMID: 23184418.

322. Tennant BR, Robertson AG, Kramer M, Li L, Zhang X, Beach M, Thiessen N, Chiu R, Mungall K, Whiting CJ, Sabatini PV, Kim A, Gottardo R, Marra MA, Lynn FC, **Jones SJ**, Hoodless PA, Hoffman BG. Identification and analysis of murine pancreatic islet enhancers. **Diabetologia.** 2013 Mar;56(3):542-52. PMID: 23238790.

323. Reipas KM, Law JH, Couto N, Islam S, Li Y, Li H, Cherkasov A, Jung K, Cheema AS, **Jones SJ**, Hassell JA, Dunn SE. Luteolin is a novel p90 ribosomal S6 kinase (RSK) inhibitor that suppresses Notch4 signaling by blocking the activation of Y-box binding protein-1 (YB-1). **Oncotarget**. 2013 Feb;4(2):329-45. PMID: 23593654.

324. Pugh TJ, Morozova O, 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 Y, 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 Jan 20. PMID: 23334666

325. Qin Z, Bilenky M, Su G, **Jones S**. MotifOrganizer: a scalable model-based motif clustering tool for mammalian genomes. **Frontiers in Bioscience** (Elite Edition). 2013 Jan 1;5:785-97. PMID: 23277033.

326. Wu C, Wyatt AW, McPherson A, Lin D, McConeghy BJ, Mo F, Shukin R, Lapuk AV, **Jones SJ**, Zhao Y, Marra MA, Gleave ME, Volik SV, Wang Y, Sahinalp SC, Collins CC. Poly-gene fusion transcripts and chromothripsis in prostate cancer. **Genes Chromosomes Cancer**. 2012 Dec;51(12):1144-53. PMID: 22927308.

327. Zhang W, Prakash C, Sum C, Gong Y, Li Y, Kwok JJ, Thiessen N, Pettersson S, **Jones SJ**, Knapp S, Yang H, Chin KC. Bromodomain-containing protein 4 (BRD4) regulates RNA polymerase II serine 2 phosphorylation in human CD4+ T cells. **J Biol Chem.** 2012 Dec 14;287(51):43137-55. PMID: 23086925.

328. Nielsen CB, Younesy H, O'Geen H, Xu X, Jackson AR, Milosavljevic A, Wang T, Costello JF, Hirst M, Farnham PJ, **Jones SJ**. Spark: A Navigational Paradigm for Genomic Data Exploration.**Genome Res** 2012 Nov;22(11):2262-9. PMID: 22960372.

329. Khodabakhshi AH, Morin RD, Fejes AP, Mungall AJ, Mungall KL, Bolger-Munro M, Johnson NA, Connors JM, Gascoyne RD, Marra MA, Birol I, **Jones SJ**. Recurrent targets of aberrant somatic hypermutation in lymphoma. **Oncotarget**. 2012 Nov;3(11):1308-19. PMID: 23131835

330. Cancer Genome Atlas Network (357 authors) including, Ally A, Balasundaram M, Butterfield YS, Carlsen R, Carter C, Chu A, Chuah E, Chun HJ, Coope RJ, Dhalla N, Guin R, Hirst C, Hirst M, Holt RA, Lee D, Li HI, Mayo M, Moore RA, Mungall AJ, Pleasance E, Robertson A, Schein JE, Shafiei A, Sipahimalani P, Slobodan JR, Stoll D, Tam A, Thiessen N, Varhol RJ, Wye N, Zeng T, Zhao Y, Birol I, **Jones SJ**, Marra MA, et al. Comprehensive molecular portraits of human breast tumours. **Nature.** 2012 Oct 4;490(7418):61-70. PMID: 23000897

331. Cancer Genome Atlas Research Network (412 authors). including, **Jones SJ**, Marra MA, et al. Comprehensive genomic characterization of squamous cell lung cancers. **Nature**. 2012 Sep 27;489(7417):519-25. PMID: 22960745

332. Shankar J, Wiseman SM, Meng F, Kasaian K, Strugnell S, Mofid A, Gown A, **Jones SJ**, Nabi IR. Coordinate Expression of Galectin-3 and Caveolin-1 in Thyroid Cancer. J Pathol. 2012 Sep;228(1):56-66. PMID: 22513979.

333. Krzywinski M, Birol I, **Jones S**, Marra M. Hive Plots – Rational Approach to Visualizing Networks. Brief Bioinform. 2012 Sep;13(5):627-44. PMID: 22155641.

334. Roberts KG, Morin RD, Zhang J, Hirst M, Zhao Y, Su X, Chen SC, Payne-Turner D, Churchman ML, Harvey RC, Chen X, Kasap C, Yan C, Becksfort J, Finney RP, Teachey DT, Maude SL, Tse K, Moore R, **Jones S**, Mungall K, Birol I, Edmonson MN, Hu Y, Buetow KE, Chen IM, Carroll WL, Wei L, Ma J, Kleppe M, Levine RL, Garcia-Manero G, Larsen E, Shah NP, Devidas M, Reaman G, Smith M, Paugh SW, Evans WE, Grupp SA, Jeha S, Pui CH, Gerhard DS, Downing JR, Willman CL, Loh M, Hunger SP, Marra MA, Mullighan CG. Genetic alterations activating kinase and cytokine receptor signaling in high-risk acute lymphoblastic leukemia. **Cancer Cell**. 2012 Aug 14;22(2):153-66. PMID: 22897847.

335. Keeling CI, Henderson H, Li M, Yuen M, Clark EL, Fraser JD, Huber DPW, Liao NY, Docking TR, Birol I, Chan SK, Taylor GA, Palmquist D, **Jones SJM** and Bohlmann J. Transcriptome and full-length cDNA resources for the mountain pine beetle, Dendroctonus ponderosae Hopkins, a major insect pest of pine forests. **Insect Biochemistry and Molecular Biology**. 2012 Aug;42(8):525-36. PMID: 22516182.

336. Northcott PA, Shih DJ, Peacock J, Garzia L, Sorana Morrissy A, Zichner T, Stütz AM, Korshunov A, Reimand J, Schumacher SE, Beroukhim R, Ellison DW, Marshall CR, Lionel AC, Mack S, Dubuc A, Yao Y, Ramaswamy V, Luu B, Rolider A, Cavalli FM, Wang X, Remke M, Wu X, Chiu RY, Chu A, Chuah E, Corbett RD, Hoad GR, Jackman SD, Li Y, Lo A, Mungall KL, Ming Nip K, Qian JQ, Raymond AG, Thiessen N, Varhol RJ, Birol I, Moore RA, Mungall AJ, Holt R, Kawauchi D, Roussel MF, Kool M, Jones DT, Witt H, Fernandez-L A, Kenney AM, Wechsler-Reya RJ, Dirks P, Aviv T, Grajkowska WA, Perek-Polnik M, Haberler CC, Delattre O, Reynaud SS, Doz FF, Pernet-Fattet SS, Cho BK, Kim SK, Wang KC, Scheurlen W, Eberhart CG, Fèvre-Montange M, Jouvet A, Pollack IF, Fan X, Muraszko KM, Yancey Gillespie G, Di Rocco C, Massimi L, Michiels EM, Kloosterhof NK, French PJ, Kros JM, Olson JM, Ellenbogen RG, Zitterbart K, Kren L, Thompson RC, Cooper MK, Lach B, McLendon RE, Bigner DD,

Fontebasso A, Albrecht S, Jabado N, Lindsey JC, Bailey S, Gupta N, Weiss WA, Bognár L, Klekner A, Van Meter TE, Kumabe T, Tominaga T, Elbabaa SK, Leonard JR, Rubin JB, Liau LM, Van Meir EG, Fouladi M, Nakamura H, Cinalli G, Garami M, Hauser P, Saad AG, Iolascon A, Jung S, Carlotti CG, Vibhakar R, Shin Ra Y, Robinson S, Zollo M, Faria CC, Chan JA, Levy ML, Sorensen PH, Meyerson M, Pomeroy SL, Cho YJ, Bader GD, Tabori U, Hawkins CE, Bouffet E, Scherer SW, Rutka JT, Malkin D, Clifford SC, **Jones SJ**, Korbel JO, Pfister SM, Marra MA, Taylor MD. Subgroup-specific structural variation across 1,000 medulloblastoma genomes. **Nature**. 2012 Aug 2;488(7409):49-5 PMID: 22832581

337. Cancer Genome Atlas Network (326 collaborators) including **Jones SJ**, Marra MA. Comprehensive molecular characterization of human colon and rectal cancer. **Nature**. 2012 Jul 18;487(7407):330-7. PMID: 22810696

338. Vrljicak P, Cullum R, Xu E, Chang ACY, Wederell ED, Bilenky M, **Jones SJM**, Marra MA, Karsan A, Hoodless PA. Twist1 Transcriptional Targets in the Developing Atrioventricular Canal of the Mouse. **PLoS One.** 2012;7(7):e40815. PMID: 22815831.

339. Doherty D, Chudley AE, Coghlan G, Ishak GE, Innes AM, Lemire EG, Rogers RC, Mhanni AA, Phelps IG, **Jones SJ**, Zhan SH, Fejes AP, Shahin H, Kanaan M, Akay H, Tekin M; FORGE Canada Consortium, Triggs-Raine B, Zelinski T. GPSM2 Mutations Cause the Brain Malformations and Hearing Loss in Chudley-McCullough Syndrome. **Am J Hum Genet.** 2012 Jul 13;91(1):209. PMID: 22578326.

340. 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):1923-4. PMID: 22563071.

341. Chiu CG, Yao R, Chan SK, Strugnell SS, Bugis S, Irvine R, Anderson D, Walker B, **Jones SJ**, Wiseman SM. Hemithyroidectomy is the preferred initial operative approach for an indeterminate fine needle aspiration biopsy diagnosis. **Can J Surg.** 2012 Jun;55(3):191-8. PMID: 22630062

342. Wu C, Wyatt AW, Lapuk AV, McPherson A, McConeghy BJ, Bell RH, Anderson S, Haegert A, Brahmbhatt S, Shukin R, Mo F, Li E, Fazli L, Hurtado-Coll A, Jones EC, Butterfield YS, Hach F, Hormozdiari F, Hajirasouliha I, 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 form of hybrid and aggressive prostate cancer. **J Pathol**. 2012 May;227(1):53-61. PMID: 22294438.

343. Chiu CG, Chan SK, Fang ZA, Masoudi H, Wood-Baker R, **Jones SJ**, Gilks B, Laskin J, Wiseman SM. Beta-catenin expression is prognostic of improved non-small cell lung cancer survival. **Am J Surg**. 2012 May;203(5):654-9. PMID: 22402266.

344. Simonis M, Atanur SS, Linsen SE, Guryev V, Ruzius FP, Game L, Lansu N, de Bruijn E, van Heesch S, **Jones SJ**, Pravenec M, Aitman TJ, Cuppen E. Genetic basis of transcriptome differences between the founder strains of the rat HXB/BXH recombinant inbred panel. **Genome Biol.** 2012 Apr 27;13(4):R31. PMID: 22541052.

345. 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):1225-33. PMID: 22267497.

346. Shah SP, Roth A, Goya R, Oloumi A, Ha G, Zhao Y, Turashvili G, Ding J, Tse K, Haffari G, Bashashati A, Prentice LM, 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 SK, Griffith M, Moradian A, Cheng SW, Morin GB, Watson P, Gelmon K, Chia S, Chin SF, Curtis C, Rueda

OM, Pharoah PD, Damaraju S, Mackey J, Hoon K, Harkins T, Tadigotla V, Sigaroudinia M, Gascard P, Tlsty T, Costello JF, Meyer IM, Eaves CJ, 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):395-9. PMID: 22495314.

347. 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):929-34. PMID: 22223660.

348. 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. PMID: 22072542

349. 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):234-42. PMID: 22187960

350. 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):110-8. PMID: 22177091

351. Chan QW, Cornman RS, Birol I, Liao NY, Chan SK, Docking TR, Jackman SD, Taylor GA, **Jones SJ,** de Graaf DC, Evans JD, Foster LJ. Updated genome assembly and annotation of Paenibacillus larvae, the agent of American foulbrood disease of honey bees. **BMC Genomics**. 2011 Sep 16;12:450. PMID: 21923906

352. Rebollo R, Karimi MM, Bilenky M, Gagnier L, Miceli-Royer K, Zhang Y, Goyal P, Keane TM, **Jones S**, Hirst M, Lorincz MC, Mager DL. Retrotransposon-induced heterochromatin spreading in the mouse revealed by insertional polymorphisms. **PLoS Genet.** 2011 Sep;7(9):e1002301. PMID: 21980304.

353. Schrader KA, Heravi-Moussavi A, Water PJ, Senz J, Whelan J, Ha G, Eydoux P, Nielsen T, Gallagher B, Oloumi A, Boyd N, Fernandez BA, Young T-L, **Jones SJM**, 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. **The Journal of Pathology.** 2011 Sep;225(1):12-8. PMID: 21792934

354. Johner A, Griffith OL, Walker B, Wood L, Piper H, Wilkins G, Baliski C, **Jones SJ**, Wiseman SM. Detection and management of hypothyroidism following thyroid lobectomy: evaluation of a clinical algorithm. **Ann Surg Oncol**. 2011 Sep;18(9):2548-54. PMID: 21547704

355. Li YY, An J, **Jones SJM**. A Computational Approach to Finding Novel Targets for Existing Drugs. **PLoS Comput Biol.** 2011 Sep;7(9):e1002139. PMID: 21909252.

356. 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

357. Karimi MM, Goyal P, Maksakova IA, Bilenky M, Leung D, Tang JX, Shinkai Y, Mager DL, **Jones S,** Hirst M, Lorincz MC. DNA Methylation and SETDB1/H3K9me3 Regulate Predominantly Distinct Sets of Genes, Retroelements, and Chimeric Transcripts in mESCs. **Cell Stem Cell**. 2011 Jun 3;8(6):676-87. PMID: 21624812.

358. Olexandr Yakovenko, Yvonne Y. Li, Alexander A. Oliferenko, Volodymyr G. Bdzhola, Ganna M. Vashchenko, and Steven **J.M. Jones.** Ab initio parameterization of YFF1, a universal force field for drug-design applications. **J Mol Model**. 2012 Feb;18(2):663-73.. PMID: 21562826.

359. Wiseman SM, Griffith OL, Gown A, Walker B, **Jones SJ**. Immunophenotyping of thyroid tumors identifies molecular markers altered during transformation of differentiated into anaplastic carcinoma. **Am J Surg**. 2011 May;201(5):578-84. PMID: 21545903.

360. Fejes AP, Hadj Khodabakhshi A, Birol I, **Jones SJ**. Human Variation Database: An open source database template for genomic discovery. **Bioinformatics**. 2011 Apr 15;27(8):1155-6. PMID: 21367872

361. Steidl C, Shah SP, Woolcock BW, Rui L, Kawahara M, Farinha P, Johnson NA, Zhao Y, Telenius A, Neriah SB, 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):377-81. PMID: 21368758

362. Geraldes A, Pang J, Thiessen N, Cezard T, Moore R, Zhao Y, Tam A, Wang S, Friedmann M, Birol I, **Jones SJ**, Cronk QC, Douglas CJ. SNP discovery in black cottonwood (Populus trichocarpa) by population transcriptome resequencing. **Mol Ecol Resour**. 2011 Mar;11 Suppl 1:81-92. PMID: 21429165

363. Zhang X, Robertson G, Krzywinski M, Ning K, Droit A, **Jones S**, and Gottardo R. PICS: Probabilistic Inference for ChIP-Seq. **Biometrics.** 2011 Mar;67(1):151-63. PMID: 20528864.

364. Gardy JL, Johnston JC, Ho Sui SJ, Cook VJ, Shah L, Brodkin E, Rempel S, Moore R, Zhao Y, Holt R, Varhol R, Birol I, Lem M, Sharma MK, Elwood K, **Jones SJ**, Brinkman FS, Brunham RC, Tang P. Whole Genome Sequencing and Social Network Analysis of a Tuberculosis Outbreak. N Engl J Med. 2011 Feb 24;364(8):730-9. PMID: 21345102

365. D'Souza CA, Kronstad JW, Taylor G, Warren R, Yuen M, Hu G, Jung WH, Sham A, Kidd SE, 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 JE, Fraser JA, Meyer W, Carter D, Schein J, Krzywinski M, Kwon-Chung KJ, Varma A, Wang J, Brunham R, Fyfe M, Ouellette BF, Siddiqui A, Marra M, **Jones S**, Holt R, Birren BW, Galagan JE, Cuomo CA. Genome variation in Cryptococcus gattii, an emerging pathogen of immunocompetent hosts.**MBio**. 2011 Feb 8;2(1):e00342-10. PMID: 21304167

366. Shin H, Lee H, Fejes AP, Baillie DL, Koo HS, **Jones SJ.** Gene Expression Profiling of Oxidative Stress Response of C. elegans aging defective AMPK Mutants Using Massively Parallel Transcriptome Sequencing. **BioMed Central.** 2011 Feb 8;4(1):34. PMID: 21303547

367. Diguistini S, Wang Y, Liao NY, Taylor G, Tanguay P, Feau N, Henrissat B, Chan SK, Hesse-Orce U, Alamouti SM, Tsui CK, Docking RT, Levasseur A, Haridas S, Robertson G, Birol I, Holt RA, Marra MA, Hamelin RC, Hirst M, **Jones SJ**, 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 S A.** 2011 Feb 8;108(6):2504-9. PMID: 21262841.

368. Liang B, Luo M, Scott-Herridge J, Semeniuk C, Mendoza M, Capina R, Sheardown B, Ji H, Kimani J, Ball BT, Van Domselaar G, Graham M, Tyler S, **Jones SJ**, Plummer FA. A comparison of parallel pyrosequencing and sanger clone-based sequencing and its impact on the characterization of the genetic diversity of HIV-1. PLoS One. 2011;6(10):e26745. doi: 10.1371/journal.pone.0026745. Epub 2011 Oct 21. PMID: 22039546

369. McLarren KW, Severson TM, du Souich C, Stockton DW, Kratz LE, Cunningham D, Hendson G, Morin RD, Wu D, Paul JE, An J, Nelson TN, Chou A, DeBarber AE, Merkens LS, Michaud JL, Waters PJ, Yin J, McGillivray B, Demos M, Rouleau GA, Grzeschik KH, Smith R, Tarpey PS, Shears D, Schwartz CE, Gecz J, Stratton MR, Arbour L, Hurlburt J, Van Allen MI, Herman GE, Zhao Y, Moore R, Kelley RI, **Jones SJ,** Steiner RD, Raymond FL, Marra MA, Boerkoel CF. Hypomorphic temperature-sensitive alleles of NSDHL cause CK syndrome. **Am J Hum Genet.** 2010 Dec 10;87(6):905-14. PMID: 21129721

370. Gao B, Griffith O, Ester M, Hui X, Qiang Z, **Jones S**. On the Deep Order-preserving Submatrix Problem: A Best-Effort Approach. **IEEE Transactions on Knowledge and Data Engineering.** 29 Nov. 2010. IEEE computer Society Digital Library. IEEE Computer Society, http://doi.ieeecomputersociety.org/10.1109/TKDE.2010.244.

371. Robertson G, Schein J, Chiu R, Corbett R, Field M, Jackman SD, Mungall K, Lee S, Okada HM, Qian JQ, Griffith M, Raymond A, Thiessen N, Cezard T, Butterfield YS, Newsome R, Chan SK, She R, Varhol R, Kamoh B, Prabhu AL, Tam A, Zhao Y, Moore RA, Hirst M, Marra MA, **Jones SJ**, Hoodless PA, Birol I. De novo assembly and analysis of RNA-seq data. **Nat Methods.** 2010 Nov;7(11):909-12. PMID: 20935650

372. 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):367-78. PMID: 21029860.

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

374. Hesse-Orce U, Diguistini S, Keeling CI, Wang Y, Li M, Henderson H, Docking TR, Liao NY, Robertson G, Holt RA, **Jones SJ**, Bohlmann J, Breuil C. Gene discovery for the bark beetle-vectored fungal tree pathogen Grosmannia clavigera.**BMC Genomics**. 2010 Oct 4;11:536. PMID: 20920358.

375. 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

376. Morozova O, Vojvodic M, Grinshtein N, Hansford LM, Blakely KM, Maslova A, Hirst M, Cezard T, Morin RD, Moore R, Smith KM, Miller F, Taylor P, Thiessen N, Varhol R, Zhao Y, **Jones S,** Moffat J, Kislinger T, Moran MF, Kaplan DR, Marra MA. System-level analysis of neuroblastoma tumor-initiating cells implicates AURKB as a novel drug target for neuroblastoma. Clin Cancer Res. 2010 Sep 15;16(18):4572-82. PMID: 20651058

377. Law JH, Li Y, Wang M, Astanehe A, Lambie K, Dhillon J, **Jones SJ,** Gleave ME, Eaves CJ, DunnSE. Molecular decoy to the Y-box binding protein-1 suppresses the growth of breast and prostate cancer cells whilst sparing normal cell viability. **PLoS One.** 2010 Sept 10;5(9). PMID: 20844853

378. Davidson WS, Koop BF, **Jones SJ,** Iturra P, Vidal R, Maass A, Jonassen I, Lien S, Omholt SW. Sequencing the genome of the Atlantic salmon (Salmo salar). **Genome Biol.** 2010 Sep 30;11(9):403. PMID: 20887641

379. Portales-Casamar E, Swanson DJ, Liu L, de Leeuw CN, Banks KG, Ho Sui SJ, Fulton DL, Ali J, Amirabbasi M, Arenillas DJ, Babyak N, Black SF, Bonaguro RJ, Brauer E, Candido TR, Castellarin M, Chen J, Chen Y, Cheng JC, Chopra V, Docking TR, Dreolini L, D'Souza CA, Flynn EK, Glenn R, Hatakka K, Hearty TG, Imanian B, Jiang S, Khorasan-zadeh S, Komljenovic I, Laprise S, Liao NY, Lim JS, Lithwick S, Liu F, Liu J, Lu M, McConechy M, McLeod AJ, Milisavljevic M, Mis J, O'Connor K, Palma B, Palmquist DL, Schmouth JF, Swanson MI, Tam B, Ticoll A, Turner JL, Varhol R, Vermeulen J, Watkins RF, Wilson G, Wong BK, Wong SH, Wong TY, Yang GS, Ypsilanti AR, **Jones SJ**, Holt RA, Goldowitz D, Wasserman WW, Simpson EM. A regulatory toolbox of MiniPromoters to drive selective expression in the brain. **Proc Natl Acad Sci U S A**. 2010 Sep 21;107(38):16589-94. PMID: 20807748

380. Liang B, Luo M, Ball TB, **Jones SJ,** Plummer FA. QUASI analysis of host immune responses to Gag polyproteins of human immunodeficiency virus type 1 by a systematic bioinformatics approach. **Biochem Cell Biol**. 2010 Aug;88(4):671-81. PMID:20651839

381. **Jones SJ,** Laskin J, Li YY, Griffith OL, An J, Bilenky M, Butterfield YS, Cezard T, Chuah E, Corbett R, Fejes AP, 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 RA, Huntsman DG, Birol I, Hirst M, Holt RA, Marra MA.. Evolution of an adenocarcinoma in response to selection by targeted kinase inhibitors. **Genome Biology.** 2010 Aug 9;11(8):R82. PMID: 20696054

382. 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 Y, Hirst M, Verchere CB, Helgason CD, Marra MA, **Jones SJ**, Hoodless PA. Locus Co-occupany, Nucleosme Positioning and H3K4me1 Regulate the Functionality of Foxa2, Hnf4a, and Pdx1 Bound Loci in Islets and Liver. **Genome Res**. 2010 Aug;20(8):1037-51. PMID: 20551221

383. Maunakea AK, Nagarajan RP, Bilenky M, Ballinger TJ, D'Souza C, Fouse SD, Johnson BE, Hong C, Nielsen C, Zhao Y, Turecki G, Delaney A, Varhol R, ThiessenN, 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 Jul8;466(7303):253-7. PMID: 20613842

384. 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):431-41. PMID: 20439774

385. Atanur SS, Birol I, Guryev V, Hirst M, Hummer O, Behmoaras J, Fernandez X, Johnson MD, McLaren W, Morrissey C, Patone G, Petretto E, Plessy C, Saar K, Zhao YJ, Carninci P*, Flicek P*, Kurtz T*, Cuppen E*, Pravenec M*, Hubner N*, **Jones SJM***, Birney E*, Aitman TJ*. The genome of the spontaneously hypertensive rat: analysis and functional significance. **Genome Research.** 2010 Jun;20(6):791-803. *These authors contributed equally to the work. PMID: 20430781

386. Swanson TW, Chan SK, **Jones SJ,** Bugis S, Irvine R, Belzberg A, Levine D, Wiseman SM. Determinants of Tc-99m sestamibi SPECT scan sensitivity in primary hyperparathyroidism. **Am J Surg.** 2010 May;199(5):614-20. PMID: 20466104

387. Chiu CG, Strugnell SS, Griffith OL, **Jones SJ**, Gown AM, Walker B, Nabi IR, Wiseman SM. Diagnostic utility of galectin-3 in thyroid cancer. **Am J Pathol.** 2010 May;176(5):2067-81. PMID: 20363921

388. Sleumer MC, Mah AK, Baillie DL, Jones SJM. Conserved Elements Associated with Ribosomal Genes and their Trans-splice Acceptor Sites in *Caenorhabditis elegans*. **Nucleic Acids Research.** 2010 May;38(9):2990-3004. PMID: 20100800

389. Leong JS, Jantzen SG, von Schalburg KR, Cooper GA, Messmer AM, Liao NY, Munro S, Moore R, Holt RA, **Jones SJ**, Davidson WS, Koop BF. Salmo salar and Esox lucius full-length cDNA sequences reveal changes in evolutionary pressures on a post-tetraploidization genome. **BMC Genomics.** 2010 Apr 30;11(1):279. PMID: 20433749

390. Malhis N, **Jones SJ**. High quality SNP calling using Illumina data at shallow coverage. **Bioinformatics**. 2010 Apr 15;26(8):1029-35. PMID: 20190250

391. **Jones SJM** and 411 Collaborators (International Cancer Genome Consortium.) International network of cancer genome projects. **Nature.** 2010 Apr 15;464(7291):993-8. PMID: 20393554.

392. Steidl C, Lee T, Shah SP, Farinha P, Han G, Nayar T, Delaney A, **Jones SJ**, Iqbal J, Weisenburger DD, Bast MA, Rosenwald A, Muller-Hermelink HK, Rimsza LM, Campo E, Delabie J, Braziel RM, Cook JR, Tubbs RR, Jaffe ES, Lenz G, Connors JM, Staudt LM, Chan WC, Gascoyne RD. Tumor-associated macrophages and survival in classic Hodgkin's lymphoma. **N Engl J Med**. 2010 Mar 11;362(10):875-85. PMID: 20220182

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

394. 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 Y, 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 **Nature Genetics**. 2010 Feb;42(2):181-5. PMID: 20081860.

395. Nielsen CB, Jackman SD, Birol I, **Jones SJ**. AbySS-Explorer: Visualizing Genome Sequence Assemblies **IEEE Trans Vis Comput. Graph**. 2009 Nov-Dec; 15(6):881-8. PMID: 19834150.

396. The MGC Project Team including: Hirst M, Zeng T, Tse K, Moksa M, Deng M, Ma K, Mah D, Pang J, Taylor G, Chuah E, Deng A, Fichter K, Go A, Lee S, Wang J, Griffith M, Morin R, Moore RA, Mayo M, Munro S, Wagner S, **Jones SJM,** Holt RA, Marra MA. The Completion of the Mammilian Gene Collection (MGC). Genome Research. 2009 Dec;19(12):2324-33. PMID: 19767417

397. 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 Tr Automation Sci and Eng. 2009, 23 Nov. 7: (3): 706-708.**

398. Birol I, Jackman SD, Nielsen C, Qian JQ, Varhol R, Stazyk G, Morin RD, Zhao Y, Hirst M, Schein JE, Horsman DE, Connors JM, Gascoyne RD, Marra MA, **Jones SJ**. De novo Transcriptome Assembly with ABySS. **Bioinformatics.** 2009 Nov. 1:25(21):2872-7. PMID: 19528083

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

400. 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 and in a lobular breast tumour profiled at single nucleotide resolution.**Nature.** 2009 Oct. 8;461(7265):809-13. PMID: 19812674

401. 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):1825-35. PMID: 19541910

402. 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 assembly of a genome sequence for the filamentous fungus, Grosmannia clavigera, assembled using Sanger, 454 and Illumina sequence data**.** **Genome Biology.** 2009 Sep 11;10(9):R94. PMID: 19747388

403. 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):1639-45. PMID: 19541911

404. Deen S, Griffith OL, Masoudi H, Gown A, **Jones SJ**, Wiseman SM. Anaplastic thyroid carcinoma exhibits intratumoral molecular homogeneity for a therapeutic target panel. **Anticancer Res**. 2009 Jul;29(7):2437-44. PMID: 19596911

405. 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 Genetics**. 2009 Jun;5 (6):e1000537. PMID: 19557190

406. Shah SP, Köbel M, Senz J, Morin RD, Clarke BA, Wiegand KC, Leung G, Zayed A, Mehl E, Kalloger SE, Sun M, Giuliany 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 Y, Zeng T, Glover JN, Vanderhyden B, Zhao C, Parkinson CA, Jimenez-Linan M, Bowtell DD, Mes-Masson AM, Brenton JD, Aparicio SA, Boyd N, Hirst M, Gilks CB, Marra M, Huntsman DG. Mutation of the FOXL2 Gene in Granulosa Cell Tumors of the Ovary. **New England Journal of Medicine.** 2009 Jun 25;360(26):2719-29. PMID: 19516027

407. Simpson JT, Wong K, Jackman SD, Schein JE, **Jones SJ,** Birol I. ABySS: A parallel assembler for short read sequence data. **Genome Res.** 2009 Jun;19(6):1117-23. PMID: 19251739.

408. An J, Lee DC, Law AH, Yang CL, Poon LL, Lau AS, **Jones SJ**. A novel small-molecule inhibitor of the avian influenza H5N1 virus determined through computational screening against the neuraminidase**.** **Journal of Medicinal Chemistry.** 2009 May 14;52(9):2667-72. PMID: 19419201

409. Wang X, Zhao YJ, 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(1):213. PMID: 19426519

410. Bovine Genome Sequencing and Analysis Consortium, et al, including Holt RA**, Jones SJ,** Marra MA, Moore R, Schein JE, The genome sequence of taurine cattle: a window to ruminant biology and evolution. **Science.** 2009 Apr 24;324 (5926):522-8. PMID: 19390049.

411. Hoffman BG, **Jones SJ.** Genome-wide identification of DNA-protein interactions using chromatin immunoprecipitation coupled with flow cell sequencing.**J Endocrinol**. 2009 Apr;201(1):1-13. PMID: 19136617.

412. Sleumer MC, Bilenky M, He A, Robertson AG, **Jones SJM.** C. elegans cisRED: A catalogue of conserved genomic elements. **Nucleic Acids Research.** 2009 Mar;37(4):1323-34. PMID: 19151087

413. McGhee JD, Fukushige T, Krause MW, Minnema SE, Goszczynski B, Gaudet J, Kohara Y, Bossinger O, Zhao YJ, 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. **Developmental Biology.** 2009 Mar 15;327(2):551-65. PMID: 1911532

414. Malhis N, Butterfield YS, Ester M, **Jones SJ**. Slider--maximum use of probability information for alignment of short sequence reads and SNP detection. **Bioinformatics.** 2009 Jan 1;25(1):6-13. PMID: 18974170

415. Wiseman SM, Melck A, Masoudi H, Ghaidi F, Goldstein L, Gown A, **Jones SJ**, Griffith OL. Molecular phenotyping of thyroid tumors identifies a marker panel for differentiated thyroid cancer diagnosis. **Ann Surg Oncol**. 2008 Oct;15(10):2811-26. PMID: 18612701.

416. Ralph SG, Chun HJ, Kolosova N, Cooper D, Oddy C, Ritland CE, Kirkpatrick R, Moore R, Barber S, Holt RA, **Jones SJ**, 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

417. Joshi B, Strugnell S, Goetz JG, Kojic LD, Cox ME, Griffith OL, **Jones S**, Leung S, Masoudi H, Leung S, Wiseman SM, Nabi IR. Phospho-caveolin-1 regulates Rho/ROCK-dependent focal adhesion dynamics and tumor cell migration. **Cancer Research.** 2008 Oct 15;68(20):8210-20. PMID: 18922892.

418. Robertson GA, 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.** Genome wide relationship between histone H3 lysine 4 mono-and tri-methylation and transcription factor binding. **Genome Research.** 2008 Dec; 18 (12) 1906-1917. PMID: 18787082.

419. 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):4549-64. PMID: 18611952.

420. Fejes AP, Robertson G, Bilenky M, Varhol R, Bainbridge M, **Jones SJM**. FindPeaks 3.1: A tool for identifying areas of enrichment from massively parallel short read sequencing technology. Application note – **Bioinformatics.** 2008 Aug 1;24(15):1729-30. PMID: 18599518

421. 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. PMID: 18611170

422. D'Souza CA, Chopra V, Varhol R, Xie YY, Bohacec S, Zhao YJ, Lee LC, 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 Neuroscience.** 2008 Jul 14; 9(1):66. doi: 10.1186/1471-2202-9-66. PMID: 18625066

423. Shin H, Hirst M, Bainbridge MN, Magrini V, Mardis E, Moerman DG, Marra MA, Baillie DL. **Jones SJ**. Transcriptome analysis for Caenorhabiditis elegans based on novel expressed sequence tags. **BMC Biol.** 2008 Jul 8;6:30. PMID: 18611272

424. Raouf A, Zhao Y, Stingl J, 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);109-18. PMID: 18593563.

425. Hoffman BG, Zavaglia B, Witzsche J, Ruiz de Algara T, Beach M, Hoodless PA, **Jones S**, Marra MA, Helgason CD. Identification of Transcripts with Enriched Expression in the Developing and Adult Pancreas. **Genome Biol.** 2008 June 14;9(6):R99. PMID: 18554416

426. Liang B, Luo M, Ball TB, Yao X, van Domselaar G, Cuff WR, Cheang M, **Jones SJM,** Plummer FA. Systematic Analysis of host immunological pressure on the envelope gene of human immunodeficiency virus type 1 by an immunological approach. **Current HIV Research.** 2008 Jun;6(4):370-9. PMID: 18691035

427. Leung SP, Griffith OL, Masoudi H, Gown A, **Jones SJ**, Phang T, Wiseman SM. Clinical Utility of Type 1 Growth Factor Receptor Expression by Colon Cancer. **The American Journal of Surgery.** 2008 May;195(5):604-10**.** PMID: 18424279.

428. Wiseman SM, Griffith OL, Melck A, Masoudi H, Gown A, Nabi IR, **Jones SJM**. Evaluation of type 1 growth factor receptor family expression in benign and malignant thyroid lesions. **The American Journal of Surgery.** 2008 May;195(5):667-73. PMID: 18424286

429. Shivaswamy S, Bhinge A, Zhao Y, **Jones SJM**, Hirst M, Iyer VR. Dynamic Remodeling of Individual Nucleosomes Across a Eukaryotic Genome in Response to Transcriptional Perturbation. **PLoS Biol**. 2008 Mar 18;6(3):e65. PMID: 18351804.

430. Chan SK, Griffith OL, Tai IT, **Jones SJM**. Meta-Analysis of Colorectal Cancer Gene Expression Profiling Studies Identifies Consistently Reported Candidate Biomarkers. **Cancer Epidemiol Biomarkers Prev**. 2008 Mar;17(3):543–52. PMID: 18349271

431. Aerts S, Haeussler M, Griffith OL, van Vooren S, **Jones SJM,** Montgomery SB, Bergman CM, The Open Regulatory Annotation Consortium. Text-mining assisted regulatory annotation. **Genome Biology.** 2008 Feb 13;9(2):R31 PMID: 18271954

432. 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 and Marra MA. ALEXA – A microarray design platform for alternative expression analysis. **Nature Methods.** 2008 Feb;5(2):118. PMID: 18235430

433. Ralph SG, Chun HJ, Cooper D, Kirkpatrick R, Kolosova N, Gunter L, Tuskan GA, Douglas CJ, Holt RA, **Jones SJ**, 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

434. Griffith OL, Montgomery SB, Bernier B, Chu B, Aerts S, Sleumer MC, Bilenky M, Haeussler M, Griffith M, Gallo SM, Giardine B, Mahony S, Hooghe B, Van Loo P, Blanco E, Ticoll A, Lithwick S, Portales-Casamar E, Donaldson IJ, Robertson G, Wadelius C, De Bleser P, Vlieghe D, Halfon MS, Wasserman W, Hardison R, Bergman CM, **Jones SJM**; The Open Regulatory Annotation Consortium. ORegAnno: an open-access community-driven resource for regulatory annotation. **Nucleic Acids Research.** 2008 Jan: 36(Database Issue):D107-13. PMID: 18006570

435. 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 labelling. **Biomarker Insights.** 2007 Dec 11:2 447-461. PMID: 19662225.

436. Ruzanov P, **Jones SJ,** Riddle DL. Discovery of novel alternatively spliced C. elegans transcripts by computational analysis of SAGE data. **BMC Genomics.** 2007 Nov 30;8:447. PMID: 18053145

437. Peng FY, Reid KE, Liao N, Schlosser J, Lijavetzky D, Holt R, Martinez Zapater JM, **Jones S,** Marra M, Bohlmann J, Lund ST. Generation of EST's in *Vitis vinifera* Wine Grape (Cabernet Sauvingnon) 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

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

439. Bainbridge M.N, Warren R.L, He A, Bilenky M, Robertson A.G, **Jones S.** THOR: Targeted High-throughput Ortholog Reconstructor. **Bioinformatics.** 2007 Oct 1;23(19):2622-4. PMID: 17038343

440. Melck AL, Masoudi H, Griffith OL, Rajput A, Wilkins GE, Bugis S, **Jones S**, Wiseman SM. Cell Cycle Regulators Show Diagnostic and Prognostic Utility for Differentiated Thyroid Cancer. **Annals of Surgical Oncology.** 2007 Sep 20; 14(12):3403-3411.PMID: 177882495

441. Hunt Newbury R, Viveiros R, Johnsen R, Mah A, Anastis D, Fang L, Halfnight E, Lee D, Lin J, Lorch A, MacKay S, Okada M, Pan J, Shultz AK, Tu D, Wong K, Zhao Z, Aleeyenko A, Buerglin 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

442. 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): 1478-85. PMID: 17712020.

443. 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 and Zhao S. A physical map of the bovine genome. **Genome Biology.** 2007 Aug 14; 8(8):R165 PMID: 17697342

444. Wiseman SM, Griffith OL, Deen S, Rajput A, Masoudi H, Gilks B, Goldstein L, Gown A, **Jones SJM.** Identification of Molecular Markers Altered during Transformation Of Differentiated Into Anaplastic Thyroid Carcinoma. **Archives of Surgery.** 2007 Aug. 142 (8): 717-729. PMID: 17709725

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

446. Robertson G, Hirst M, Bainbridge M, Bilenky M, Zhao Y, 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):651-7. PMID: 17558387

447. Ruzanov P, Riddle DL, Marra MA, McKay SJ, **Jones SJM.** Genes that may modulate longevity in C. elegans in both dauer larvae and long-lived daf-2 adults. **Exp Gerontol.** 2007 Aug;42(8):825-39. PMID: 17543485.

448. 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):1653-74. PMID: 17606643

449. Zhao Y, Raouf A. Kent D, Khattra J, Delaney A, Schnerch A, Asano J, MacDonald H, Chan C, **Jones S**, Marra M, Eaves C. 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): 1681-9. PMID: 17412892.

450. Hu G, 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, Bakkeren G. Generation of a wheat leaf rust, *Puccinia triticina*, EST database from stage-specific cDNA libraries. **Molecular Plant Pathology.** 2007 July 8 (4), 451-467. PMID: 20507513.

451. Montgomery SB, Griffith OG, Scheutz JM, Brooks-Wilson A, **Jones SJM**. A Survey of Genomic Properties for the Detection of Regulatory Polymorphisms. **PLoS, Computational Biology.** 2007 Jun 8;3 (6) :e106 PMID: 17559298

452. 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 Y, 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 nine human embryonic stem cell lines. **Genome Biol.** 2007 Jun 14; 8(6):R113. PMID: 17570852.

453. Kelleher CT, Chiu R, Shin H, Bosdet IE, Krzywinski MI, Fjell CD, Wilkin J, Yin T, DiFazio SP, Ali J, Asano JK, Chan S, Cloutier A, Girn N, Leach S, Lee D, Mathewson CA, Olson T, O'connor K, Prabhu AL, 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 SJ**, 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 Journal.** 2007 Jun;50(6):1063-78. PMID: 17488239

454. Quayle AP, Siddiqui AS, **Jones SJM**. Perturbation of Interaction Networks for Application to Cancer Therapy. Cancer Informatics. 2007;5:45-65. PMID: 19390668.

455. Rhesus Macaque Genome Sequencing and Analysis Consortium (incl. Schein, J, **Jones, S**). Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. **Science.** 2007 Apr 13;316(5822):222-34. PMID: 17431167.

456. Warren RL, Sutton GG, **Jones SJM** and Holt RA. Assembling millions of short DNA sequences using SSAKE. **Bioinformatics**. 2007 Feb 15;23(4):500-1. PMID: 17158514

457. McGhee JD, Sleumer M, 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. **Development Biology.** 2007 Feb 15: 302(2): 627-45. PMID: 17113066

458. DiGuistini S, Ralph S, Lim Y, Holt R, **Jones S**, Bohlmann J, Breuil C. Generation and annotation of lodgepole pine and oleoresin induced expressed sequences from the blue-stain fungus Ophiostoma clavigerum, a Mountain Pine Beetle associated pathogen. **FEMS Microbiology Letters.** 2007 Feb;267(2):151-8. PMID: 17328114.

459. Khattra J, Delaney AD, Zhao Y, Siddiqui A, Asano J, McDonald H, Pandoh P, Dhalla N, Prabhu AL, Ma K, Lee S, Ally A, Tam A, Sa D, Rogers S, Charest D, Stott J, Zuyderduyn S, Varhol R, Eaves C, **Jones S**, Holt R, Hirst M, Hoodless PA, 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.

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

461. Quayle S, Hare H, Delaney A, Hwang D, Schein J, **Jones S**, Marco M, Sadar M. Novel expressed sequences identified in a model of androgen independent prostate cancer. **BMC Genomics.** 2007 Jan 26;8:32. PMID: 17257419

462. Elnitski L, Jin VX, Farnham PJ, **Jones SJM**. Locating Mammalian Transcription Factor Binding Sites: A Survey of Computational and Experimental Techniques. **Genome Res.** 2006 Dec;16(12):1455-64. PMID: 17053094.

463. Lonergan K, Chari R, deLeeuw R, Shadeo A, Chi B, Tsao M-S, **Jones S**, Marra M, Ling V, Ng R, MacAulay C, Lam S, Lam W. Identification of novel lung genes in bronchial epithelium by serial analysis of gene expression. **AJRCMB.** 2006, Dec, 235 (6): 651-61. PMID: 16809635.

464. Wang G, **Jones SJM,** Marra MA, Sadar M. Identification of genes targeted by the androgen and PKA signaling pathways in prostate cancer cells. **Oncogene.** 2006, Nov. 25:7311-23. PMID: 16751804

465. Griffith OL, Melck A, **Jones SJM**, Wiseman SM. A Meta-analysis and Meta-review of Thyroid Cancer Gene Expression Profiling Studies Identifies Important Diagnostic Biomarkers. **Journal of Clinical Investigation.** 2006 Nov 1;24 (31):5043-51 PMID: 17075124

466. McLeod MP, Warren RL, Araki N, Hsiao WWL, Miyazawa D, Myhre M, Fernandes C, Morin RD, Wong W, Lillquist AL, Wang D, Petrescu A, Yang G, Stott JM, Schein JE, Shin H, Khattra J, Smailus D, Butterfield Y, 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. **PNAS.** 2006 Oct 17;103(42):15582-7. PMID: 17030794

467. Bainbridge MN, Warren RL, Hirst M, Romanuik T, Zeng T, Go A, Delany 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. **BMC Genomics.** 2006, Sept. 7:246. PMID: 17010196

468. 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. **AJHG.** 2006 Sept. 79(3):500-13. PMID: 16909388

469. Quayle AP, Siddiqui AS, **Jones SJM**. Preferential perturbation and network topology. **Physica A**. 2006 Sept. 371, 823-840**.**

470. Tuskan G, DiFazio S, Bohlmann J, Grigoriev I, Hellsten U, Jansson S,. Putnam N, Ralph S, Rombauts S, Salamov A, Schein J, Sterck L, Aerts A, Bhalerao R.R, Bhalerao R.P, Blaudez D, Boerjan W, Brun A, Brunner A, Busov V, Campbell M, Carlson J, Chalot M, Chapman J, Chen G.-L, Cooper D, Coutinho P, Couturier J, Covert S, Cronk Q, Cunningham R, Davis J, Degroeve S,. Déjardin A, dePamphilis C, Detter J, Dirks B, Dubchak I, Duplessis S, Ehlting J, Ellis B, Gendler K, Goodstein D, Gribskov M, Grimwood J, Groover A, Gunter L, Hamberger B, Heinze B, Helariutta Y, Henrissat B, Holligan D, Holt R, Huang W, Islam-Faridi N, **Jones S**, Jones-Rhoades M, Jorgensen R,. Joshi C, Kangasjärvi J, Karlsson J, Kelleher C, Kirkpatrick R, Kirst M, Kohler A, Kalluri U, Larimer F, Leebens-Mack J, Leplé J, Locascio P, Luo Y, Lucas S, Martin F, Montanini B, Napoli C, Nelson D.R., Nelson C, Nieminen K, Nilsson O, Peter G, Philippe R, Pilate G, Poliakov A, Razumovskaya J, Richardson P, Rinaldi C, Ritland K, Rouzé P, Ryaboy D, Schmutz J, Schrader J, Segerman B, Shin H, Siddiqui A., Sterky F, Terry A, Tsai C, Uberbache E, Unneberg P, Vahala J, Wall K, Wessler S, Yang G, Yin T, Douglas C, Sandberg G, Van de Peer Y, Rokhsar D. The genome of black cottonwood, *Populus trichocarpa* (Torr. & Gray ex Brayshaw) **Science.** 2006 Sep 15; 313(5793):1596-604. PMID: 16973872.

471. Bakkeren G, Jiang G, Warren RL, 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 Genetics & Biology.** 2006 Sept 43: (9) 655-666. PMID: 16793293.

472. Ralph SG, Yueh H, Friedmann M, Aeschliman D, Zeznik JA, Nelson CC, Butterfield YSN, Kirkpatrick R, Liu J, **Jones SJM**, Marra M, Douglas CJ, Ritland K, Bohlmann J. Conifer defence 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 and Environment .** Aug (2006) 29, 1545–1570. PMID: 16898017

473. Gao BJ, Griffith OL, Ester M, **Jones SJ**. Discovering significant OPSM subspace clusters in massive gene expression data. Proceedings of the 12th ACM SIGKDD international Conference on Knowledge Discovery and Data Mining (Philadelphia, PA, USA, August 20 - 23, 2006). KDD '06. ACM Press, New York, NY, 922-928.

474. Siddiqui A, Delaney A, Schnerch A, Griffith O, **Jones S**, Marra M. Sequence biases in large scale gene expression profiling data. **Nucleic Acids Res.** 2006 Jul 13;34(12):e83. PMID: 16840527

475. 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 ND, Mayo M, Schmutz J, Beland J, Park M, Gibson S, Olson T, Bouffard GG, Tsai M, Featherstone R, Chand S, Siddiqui AS, Jang W, Lee E, Klein SK, Blakesley RW, Prange C, Myers RM, Green ED, Wagner K, Gerhard DS, Marra MA, **Jones SJM**, Holt RA. Sequencing and analysis of 10967 full-length cDNA clones from *Xenopus laevis* and *Xenopus tropicalis*. **Genome Res.**, Jun 2006; 16: 796 – 803. PMID: 16672307

476. 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 AA, Marra MA, Wilson RK, **Jones SJM**. Physical map-assisted whole-genome shotgun sequence assemblies. **Genome Res.** 2006 Jun.16 (6):768-775. PMID: 16741162

477. Sundaram B, Chapman BM, Li B, Mayo M, Siddiqui A, **Jones S.** Sun Grid Engine Package for OSCAR – A Google Summer of Code 2005 Project. **Proceedings of 4th Annual OSCAR Symposium (OSCAR 2006).** Added to IEEE Xplore: 30 May 2006. Page 41. **DOI:** 10.1109/HPCS.2006.42

478. Quayle AP, Siddiqui AS, **Jones SJM**. Modeling network growth with assortative mixing. **European Physical Journal B.** 2006 Apr*:*50(4), 617-630, 2006

479. 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 deltoides*) 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. **Molecular Ecology.** Apr. 2006 15, 1275–1297. PMID: 16626454

480. Li YY, **Jones SJM**, Cherkasov A. Selective Targeting of Indel-Inferred Differences in Spatial Structures of Homologous Proteins. **J Bioinform Comput Biol.** 2006 Apr;4(2):403-14. PMID: 16819791.

481. Ruzanov P, **Jones SJM**. An interactive tool for visualization of relationships between gene expression profiles. **BMC Bioinformatics.** 2006 Apr 6;7(1):193. PMID: 16600045

482. Montgomery SB, Griffith OL, Sleumer MC, Bergman CM, Bilenky M, Pleasance ED, Prychyna Y, Zhang X, **Jones SJ**. ORegAnno: An open access database and curation system for literature-derived promoters, transcription factor binding sites and regulatory variation. **Bioinformatics.** 2006 Mar 1; 22(5):637-40. PMID: 16397004

483. Wilson GM, 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):173-81. PMID: 16365383.

484. Robertson G, Bilenky M., Lin K, He A, Yuen W, Dagpinar M, Varhol R, Teague K, Griffith OL, Zhang X, Pan Y, Hassel M., Sleumer MC, Pan W, Pleasance ED, Chuang M., Hao H, Li YY, Robertson N, Fjell C, Li B, Montgomery SB, Astakhova T, Zhou J, Sander J, Siddiqui AS, **Jones SJM**. cisRED: A Database System for Genome Scale Computational Discovery of Regulatory Elements. **Nucleic Acids Res.** 2006 Jan 1;34(Database issue):D68-73. PMID: 16381958

485. Siddiqui AS, Khattra J, Delaney AD, Zhao Y, Astell C, Asano J, Babakaiff R, Barber S, Beland J, Bohacec S, Brown-John M, Chand S, Charest D, Charters AM, Cullum R, Dhalla N, Featherstone R, Gerhard DS, Hoffman B, Holt RA, Hou J, Kuo BY-L, Lee LLC, Lee S, Leung D, Ma K, Matsuo C, Mayo M, McDonald H, Prabhu A-L, Pandoh P, Riggins GJ, Ruiz de Algara T, Rupert JL, Smailus D, Stott J, Tsai M, Varhol R, Vrljicak P, Wong D, MK Wu, 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 U S A.** 2005 Dec 20;102(51):18485-90. PMID: 1635271.

486. 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):2029-43. PMID: 16339721

487. Cherkasov A, Shi Z, Li Y, **Jones SM**, Fallahi M, Hammond GL. 'Inductive' Charges on Atoms in Proteins: Comparative Docking with the Extended Steroid Benchmark Set and Discovery of a Novel SHBG Ligand. **Chem Inf Model.** 2005 Nov 28;45(6):1842-1853. PMID; 16309292

488. Griffith OL, Pleasance ED, Fulton DL, Oveisi M, Ester M, Siddiqui AS, **Jones SJ**. Assessment and integration of publicly available SAGE, cDNA microarray, and oligonucleotide microarray expression data for global coexpression analyses. **Genomics**. 2005 Oct;86(4):476-488. PMID: 16098712

489. Ng SH, Artieri CG, Bosdet IE, Chiu R, Danzmann RG, Davidson WS, Ferguson MM, Fjell CD, Hoyheim B, **Jones SJ**, 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

490. Montgomery SB, Fu T, Guan J, Lin K, **Jones SJM**. An application of peer-to-peer technology to the discovery, use and assessment of bioinformatics programs. **Nature Methods.** 2005 Aug;2(8):563. PMID: 16094378

491. Blacque OE, Perens EA, Boroevich KA, Inglis PA, Li C, Warner A, Khattra J, Holt RA, Ou G, 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):935-41. PMID: 15916950

492. Warren RL, Butterfield YS, Morin RD, Siddiqui AS, Marra MA, **Jones SJM**. Management and visualization of whole genome shotgun assemblies using SAM. **Biotechniques.** 2005 May;38(5):715-6, 718, 720. PMID: 15945370

493. 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):603-15. Epub 2005 Apr 18. PMID: 15837805

494. Lian T, Simmer MI, 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 Mar: 55 (5): 1452-72. PMID: 15720553

495. Sonnichsen B, Koski LB, Walsh A, Marschall P, Neumann B, Brehm M, Alleaume AM, Artelt J, Bettencourt P, Cassin E, Hewitson M, Holz C, Khan M, Lazik S, Martin C, Nitzsche B, Ruer M, Stamford J, Winzi M, Heinkel R, Roder M, Finell J, Hantsch H, **Jones SJ**, Jones M, Piano F, Gunsalus KC, Oegema K, Gonczy P, Coulson A, Hyman AA, Echeverri CJ. Full-genome RNAi profiling of early embryogenesis in *Caenorhabditis elegans*. **Nature.** 2005 Mar 24;434(7032):462-9. PMID: 15791247

496. Bajdik CD, Kuo B, Rusaw S, **Jones S**, Brooks-Wilson A. CGMIM: Automated text-mining of Online Mendelian Inheritance in Man (OMIM) to identify genetically-associated cancers and candidate genes. **BMC Bioinformatics.** 2005 Mar 29;6(1):78. PMID: 15796777

497. 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):1321-4. Epub 2005 Jan 13. PMID: 15653466

498. Snijders AM, Nowak NJ, Huey B, Fridlyand J, Law S, Conroy J, Tokuyasu T, Demir K, Chiu R, Mao JH, Jain AN, **Jones SJ**, Balmain A, Pinkel D, Albertson DG. Mapping segmental and sequence variations among laboratory mice using BAC array CGH. **Genome Res**. 2005 Feb;15(2):302-11. PMID: 15687294

499. Sander J, Ng R, Sleumer MC, Yuen MS, **Jones S**. A Methodology for Analyzing SAGE Libraries For Cancer Profiling. **ACM Trans. Inf. Syst.** 2005 Jan; 23(1)35-60. PMID: N/A

500. 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. **Emerging Infectious Diseases.** 2004 Dec;10(12):2192-2195. PMID: 15663859

501. Warren R, Hsiao WW, Kudo H, Myhre M, Donsanjh M, Petrescu A, Kobayashi H, Shimizu S, Miyauchi K, Masai E, Yang G, Stott JM, Schein JE, Shin H, Khattra J, Smailus D, Holt R, **Jones S**, Mohn WW, Brinkman FSL, Fukuda M, Davies J, Eltis LD. Functional Characterization of a Catabolic Plasmid from PCB-Degrading *Rhodococcus sp.* RHA1. **J Bacteriol.** 2004 Nov;186(22):7783-95. PMID: 15516593

502. ENCODE Project Consortium. The ENCODE (ENCyclopedia Of DNA Elements) Project. **Science.** 2004 Oct 22;306(5696):636-40. PMID: 15499007

503. The MGC Project Team. The Status, Quality and Expansion of the NIH Full-length cDNA project (MGC). **Genome Res.** 2004 Oct;14(10B):2121-7. PMID: 15489334

504. 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):2003-2092. PMID: 15489330

505. Cherkasov A, Ho Sui SJ, Brunham RC, **Jones SJ**. Structural characterization of genomes by large scale sequence-structure threading: application of reliability analysis in structural genomics. **BMC Bioinformatics.** 2004 Jul 26;5(1):101. PMID: 15147578

506. 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 Acid Research.** 2004 Jul 9; 32(12):3651-60. PMID: 15247347

507. Cherkasov AR, **Jones SJ**. An approach to large scale identification of non-obvious structural similarities between proteins. **BMC Bioinformatics.** 2004 May 17;5(1):61. PMID: 15147578

508. Montgomery SB, Astakhova T, Bilenky M, Birney E, Fu T, Hassel M, Melsopp C, Rak M, Robertson G, Sleumer M, Siddiqui AS, **Jones SJM**. Sockeye: A 3D Environment for Comparative Genomics. **Genome Res.** 2004 May; 14(5):956-62. PMID: 15123592

509. MacAulayC, 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 no-small cell lung carcinoma. **Chest**, 2004 May: 125 (5 Suppl): 97S PMID: 15136435

510. 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, Guggenheimer K, Himmelbauer H, Kreitler T, Leach S, Lee D, Lehrach H, Mayo M, Mead K, Olson T, Pandoh P, Prabhu A-L, Shin H, Tänzer S, Thompson J, Tsai M, Walker J, Yang G, Sekhon M, Hillier L, Zimdahl H, Marziali A, Osoegawa K, Zhao S, Siddiqui A, de Jong, P, Warren W, Mardis E, McPherson J, Wilson R, Hűbner N, **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):766-79. PMID: 15060021

511. Cherkasov AR, **Jones SJ**. Structural characterization of genomes by large scale sequence-structure threading**. BMC Bioinformatics.** 2004 Apr 3;5(1):37. PMID: 15274750

512. The Rat Genome Project Consortium. Genome Sequence of the Brown Norway Rat Yields Insights into Mammalian Evolution. **Nature.** 2004. Apr 1;428(6982):493-521. PMID: 15057822

513. Baross A, Schertzer M, Zuyderduyn SD, **Jones SJM**, Marra MA, Lansdorp PL. Effect of TERT and ATM on gene expression profiles in human fibroblasts. **Genes Chromosomes Cancer.** 2004 Apr;39(4):298-310. PMID: 14978791

514. 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 March:14:478-490. PMID: 14962987

515. 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 Harbor Symposia on Quantitative Biology.** 2004 Jan: 159-169. PMID: 15338614

516. 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):1336-49. PMID: 14665467

517. Kiger AA, Baum B, **Jones S**, Jones MR, Coulson A, Echeverri C, Perrimon N. A functional genomic analysis of cell morphology using RNA interference. **J Biol.** 2003;2(4):27. Epub 2003 Oct 1. PMID: 14527345.

518. Pleasance ED, Marra MA, **Jones SJM**. Assessment of SAGE in transcript identification. **Genome Res.** 2003;June13(6A):1203-15. PMID: 12743019

519. Fjell CD, Bosdet I, Schein JE, **Jones SJM**, Marra MA. Internet Contig Explorer (iCE) - A tool for visualizing clone fingerprint maps. **Genome Res.** 2003 June;13(6A):1244-9. PMID: 12799356

520. 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

521. 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):940-53. PMID: 12727910

522. 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):358-63. PMID: 12593804

523. Hsiao W, Wan I, **Jones SJ**, Brinkman FSL. IslandPath: Aiding detection of genomic islands in prokaryotes. **Bioinformatics.** 2003 Feb 12;19(3):418-20. PMID: 12584130.

524. 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):16899-903. PMID: 12477932

525. McKay SJ, **Jones SJM**. AcePrimer: automation of PCR primer design based on gene structure. **Bioinformatics.** 2002 Nov;18(11):1538-9. PMID:12424127

526. Guiliano DB, Hall N, **Jones SJM**, Clark LN, Corton CH, Barrell BG, Blaxter ML. Conservation of long-range synteny and microsynteny between the genomes of two distantly related nematodes. **Genome Biology.** 2002 Sep 26;3(10):RESEARCH0057. Epub 2002 Sep 26. PMID:12372145.

527. 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**, Marra M. Resuspension of DNA sequencing reaction products in agarose increases sequence quality on the MegaBACE 1000 automated sequencer. **Biotechniques.** 2002 Sept; 33(3):532-539. PMID: 12238763

528. 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):1386-400. PMID: 12213776

529. Schein J, 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):1445-53. PMID: 12213782

530. Phan J, Ng R, Yuen M, **Jones S**. GEA: a Toolkit for Gene Expression Analysis. **Proceedings of 2002 ACM SIGMOD**, 2002: 628. (Longer version appears in: *Proceedings of BIOKDD 2002 Workshop on Data Mining in* **Bioinformatics**, August 2002.).

531. 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):743-50. Epub 2002 Aug 4. PMID: 12181558

532. Brinkman FSL, Blanchard JL, Cherkasov A, Av-Gay Y, Brunham RC, Fernandez RC, Finlay BB, Otto SP, Ouellette BFF, Keeling PJ, Hancock REW, Rose AM, **Jones SJM**. Evidence that plant-like genes in

*Chlamydia* species reflect an ancestral relationship between *Chlamydiaceae,* cyanobacteria and the chloroplast. **Genome Res.** 2002 Aug;12(8):1159-1167. PMID: 12176923

533. 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 associated with Iron Overload and Leukopenia. **Blood.** 2002 Aug 1;100(3):1075-7. PMID: 12130528

534. Butterfield YSN, Marra MA, 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

535. 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. **7.** PMID: 12034835

536. 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

537. **Jones SJM**, Riddle DL, 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 Research.** 2001 Aug;11(8):1346-52. PMID: 11483575

538. Brinkman FSL, Wan I, Hancock REW, Rose AM, **Jones SJ**. PhyloBLAST: A tool facilitating phylogenetic analysis of BLAST results. **Bioinformatics.** 2001 Apr;17(4):385-387. PMID: 11301315

539. McPherson JD, Marra M, Hillier L, Waterston RH, Chinwalla A, Wallis J, Sekhon M, Wylie K, Mardis ER, Wilson RK, Fulton R, Kucaba TA, Wagner-McPherson C, Barbazuk WB, Gregory SG, Humphray SJ, French L, Evans RS, Bethel G, Whittaker A, Holden JL, McCann OT, Dunham A, Soderlund C, Scott CE, Bentley DR, Schuler G, Chen HC, Jang W, Green ED, Idol JR, Maduro VV, Montgomery KT, Lee E, Miller A, Emerling S, Kucherlapati, Gibbs R, Scherer S, Gorrell JH, Sodergren E, Clerc-Blankenburg K, Tabor P, Naylor S, Garcia D, de Jong PJ, Catanese JJ, Nowak N, Osoegawa K, Qin S, Rowen L, Madan A, Dors M, Hood L, Trask B, Friedman C, Massa H, Cheung VG, Kirsch IR, Reid T, Yonescu R, Weissenbach J, Bruls T, Heilig R, Branscomb E, Olsen A, Doggett N, Cheng JF, Hawkins T, Myers RM, Shang J, Ramirez L, Schmutz J, Velasquez O, Dixon K, Stone NE, Cox DR, Haussler D, Kent WJ, Furey T, Rogic S, Kennedy S, **Jones S**, Rosenthal A, Wen G, Schilhabel M, Gloeckner G, Nyakatura G, Siebert R, Schlegelberger B, Korenberg J, Chen XN, Fujiyama A, Hattori M, Toyoda A, Yada T, Park HS, Sakaki Y, Shimizu N, Asakawa S, Kawasaki K, Sasaki T, Shintani A, Shimizu A, Shibuya K, Kudoh J, Minoshima S, Ramser J, Seranski P, Hoff C, Poustka A, Reinhardt R, Lehrach H. A physical map of the human genome. **Nature.** 2001 Feb 15;409:934-941. PMID: 11237014

540. Gönczy P, Echeverri C, Oegema K, Coulson A, **Jones SJM,** Copley RR, Duperon J, Oegema J, Brehm M, Cassin E, Hannak E, Kirkham M, Pichler S, Flohrs K, Goessen A, Leidel S, Alleaume AM, Martin C, Özlü N, Bork P, Hyman AA. Functional genomic analysis of cell division in C. elegans using RNAi of genes on chromosome III. **Nature**. 2000 Nov 16;408(6810):331-336. PMID:11099034.

541. de Koning AP, Brinkman F, **Jones S,** Keeling PJ. Lateral gene transfer and metabolic adaptation in the human parasiteTrichomonas vaginalis. Molecular Biology and Evolution. 2000 Nov;17(11):1769-1773. PMID: 11070064.

542. Reinke V, Smith HE, Nance J, Wang J, Van Doren C, Begley R, **Jones SJ**, Davis EB, Scherer S, Ward S, Kim SK. A global profile of germline expression in *C. elegans*. **Molecular Cell.** 2000 Sept;6(3):605-616. PMID: 11030340.

543. Rubin GM, Yandell MD, Wortman JR, Gabor Miklos GL, Nelson CR, Hariharan IK, Fortini ME, Li PW, Apweiler R, Fleischmann W, Cherry JM, Henikoff S, Skupski MP, Misra S, Ashburner M, Birney E, Boguski MS, Brody T, Brokstein P, Celniker SE, Chervitz SA, Coates D, Cravchik A, Gabrielian A, Galle RF, Gelbart WM, George RA, Goldstein LS, Gong F, Guan P, Harris NL, Hay BA, Hoskins RA, Li J, Li Z, Hynes RO, **Jones SJ**, Kuehl PM, Lemaitre B, Littleton JT, Morrison DK, Mungall C, O'Farrell PH, Pickeral OK, Shue C, Vosshall LB, Zhang J, Zhao Q, Zheng XH, Zhong F, Zhong W, Gibbs R, Venter JC, Adams MD, Lewis S. Comparative genomics of the eukaryotes. **Science.** 2000 Mar 24;287(5461):2204-2215. PMID: 10731134

544. Johnsen R, **Jones SJM,** Rose A. Mutational accessibility of essential genes on chromasome l(left) in Caenorhabditis elegans. **Molecular & General Genetics.** 2000 Mar;263(2):239-252. PMID: 10778742

545. Simmen MW, Leitgeb S, Charlton J, **Jones SJ**, Harris BR, Clark VH, Bird A. Nonmethylated transposable elements and methylated genes in a chordate genome. **Science.** 1999 Feb 19;283(5405):1164-1167. PMID: 10024242

546. The *C. elegans* Sequencing Consortium. How the worm was won: The *C. elegans* Sequencing Project. **Trends in Genetics.** 1999 Feb;15(2):51-58. PMID: 10098407

547. The *C. elegans* Sequencing Consortium. Genome Sequence of the Nematode *C. elegans*: A platform for Investigating Biology. **Science.** 1998 Dec 11;282(5396):2012-2018. PMID: 9851916

548. Simmen MW, Leitgeb S, Clark VH, **Jones SJ**, Bird A. Gene number in an invertebrate chordate, Ciona intestinalis. **Proc Natl ACAD Sci USA.** 1998 Apr 14;95(8):4437-40. PMID: 9539755

549. van Wageningen AM, Kirkpatrick PN, Williams DH, Harris BR, Kershaw JK, Lennard NJ, Jones M, **Jones SJ**, Solenberg PJ. Sequencing and analysis of genes involved in the biosynthesis of a vancomycin group antibiotic. **Chemical Biology.** 1998 Mar 5;3:155-62. PMID: 9545426

550. **Jones SJM**, Baillie DL. *Characterisation of the let-653 gene in Caenorhabditis elegans*. **Molecular and General Genetics**. 1995 Oct 25; 248:719-726. PMID: 7476875

551. **Jones SJM**. An update and lessons from whole genome sequencing projects. **Current Opinions in Genetics and Development.** 1995 Jun 5:349-353. PMID: 7549430

## NON-PEER REVIEWED PUBLICATIONS: TOTAL 2

1. Paulin LF, Fan J, O'Neill K, Pleasance E, Porter VL, **Jones SJM**, Sedlazeck FJ. The benefit of a complete reference genome for cancer structural variant analysis. **medRxiv** [Preprint]. 2024 Mar 18:2024. 03.15.24304369. doi:10.1101/2024.03.15.24304369. PMID: 38562786
2. 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 [Preprint-not yet peer reviewed by a journal]**. 2023 Nov 5:2023. PMID: 37961641

## INVITED PRESENTATIONS: TOTAL 169

1. BioNet 2024. March 26-27, 2024. Banff, AB. Title: Long reads, phasing and epigenomics.

2. Nanopore Day. February 14, 2024. Seattle, WA. Invited Speaker. Title: Nanopore sequencing – Insights from neonatal intensive care to cancer.

3. Canadian Epigenetics, Environment and Health Research Consortium (CEEHRC) 9th Canadian Conference on Epigenetics. November 15, 2023, Banff, Alberta. Invited Speaker: Title: Epigenomics in aiding hereditary cancer predisposition and more.

4. Oxford Nanopore Technologies Webinar. November 9, 2023, Virtual. Invited Speaker: Title: Nanopore Sequencing: Driving Research Insights from Neonatal Intensive Care to Cancer.

5. 20th ICGC/ 7th ICGC-ARGO Scientific Workshop. November 9, 2023, Roosevelt Island, New York. Invited Speaker: Title: Nanopore Sequencing for Personalised OncoGenomics.

6. Nanopore Day. October 26, 2023. Toronto, Ontario. Invited Speaker: Title: Nanopore sequencing – Insights from neonatal intensive care to cancer.

7. POET 2023 Congress (Precision Oncology Experimental Therapeutics). October 12, 2023, Calgary, Alberta. Invited Speaker: Title: Machine Learning to Accelerate Clinical Interference.

8. The Centre for Applied Genomics 25th Anniversary Symposium. September 19, 2023, Toronto, Ontario. Invited Speaker: Title: Using genomics to explore the mutational landscape of cancer.

9. Rwanda Military Hospital. September 7, 2023, Kigali, Rwanda. Invited Guest Speaker: Title: Genomic Sequencing - Insights from Neonatal Intensive Care to Cancer.

10. 3rd Annual BioNet Conference. June 1, 2023, Edmonton, Alberta. Invited Keynote Speaker: Title: Studying Genomes when the Epigenome comes along for the ride.

11. Nanopore Day. April 11, 2023, Chicago, Illinois. Invited Guest Speaker: Title: Nanopore sequencing – Insights from neonatal intensive care to cancer.

12. Academic and Research Opportunities Rounds. March 24, 2023, Vancouver, British Columbia. Invited Speaker: Bioinformatics resources and research at UBC.

13. Nanopore Day. March 21, 2023, Vancouver, British Columbia. Invited Speaker: Title: Nanopore sequencing – Insights from neonatal intensive care to cancer.

14. Oxford Nanopore Population Scale Genomics Summit in Singapore, November 16, 2022, Singapore. Invited Keynote Speaker: Title: Nanopore sequencing – Insights from neonatal intensive care to cancer.

15. TFRI's 9th Scientific Meeting, BC2C Plenary Session. November 4, 2022, Vancouver, British Columbia. Invited Speaker: Title: Precision Medicine Initiatives at the BC2C.

16. Presentation to Genome BC Board of Directors, September 23, 2022, Vancouver, British Columbia. Invited Guest Speaker: Title: The Canadian BioGenome Project.

17. 2nd Annual BioNet Conference. May 27, 2022, Calgary, Alberta. Invited Keynote Speaker: Title: Adventures in Long-read sequencing.

18. Genome BC Genomics Forum 2022. May 12, 2022, (Virtual) Vancouver, British Columbia. Invited Speaker: Title: Biodiversity: The Key to the Future of Humanity.

19. Oxford Nanopore Technologies North America National Sales Meeting, April 6, 2022, Orlando, Florida. Invited Speaker: Title: Nanopore sequencing – From neonatal intensive care to cancer.

20. pHioniC Consortium Meeting (Virtual), January 28 2022, Debrecen, Hungary. Invited Spearker: Title: Big data and bioinformatic approaches to precision medicine in Cancer.

21. 15th Annual International Congerence on Genomics (Virtual) (ICG-15), October 25 2020, Wuhan, China. Invited Speaker: Title: Using genomics and transcriptomics to develop a platform for precision medicine in oncology.

22. POET (Precision Oncology Experimental Therapeutics) Virtual Conference, October 23 2020. Invited Speaker: Title: Canadian NGS programs supporting access to profiling and clinical decision making.

23. MGI Canada Virtual Symposium — CoolMPS, DNBSEQ, and more, June 3, 2020. Invited Speaker: Title: Initial experiences in using the DNBSEQ™ platform for cancer research.

24. UBC FoM and BC Centre for Disease Control, Virtual BC COVID-19 Symposium, April 9, 2020. Invited Speaker: Title: Germline analysis of COVID-19 infected hosts.

25. AGBT Annual General Meeting. Marco Island, FL. February 24 2020. Invited Speaker: Title: Initial experiences in using the DNBSEQ™ platform for cancer research.

26. Canadian Diagnostic Executive Forum, Toronto, Ontario, October 25 2019. Invited Speaker: Title: Precision Medicine: A research program firmly entrenched in cancer genomics to understand the mutational landscape of cancer.

27. Alberta Bioinformatics Network, Lethbridge, Alberta, September 21 2019. **Keynote Speaker**: Title: Computationally analysing the tumour cell – the basis of precision oncology.

28. The G10K-VGP/EBP Meeting, New York City, NY, August 30 2019. Invited Speaker: Title: The CanSeq150 project

29. Manchester Cancer Research Centre: Phase 1: Where Science becomes Medicine MCRC/ECME Conference, Manchester, UK July 15, 2019. Invited Speaker. Title: Using genomics and transcriptomics to develop precision medicine in oncology in British Columbia.

30. Precision Oncology Experimental Therapeutics (POET) Conference, Calgary, Alberta April 5 2019. Invited Speaker. Title: Marathon of Hope Initiative.

31. RiboWest Conference, University of Lethbridge, Alberta June 10, 2018. **Keynote Speaker:** Title: Using genomics and transcriptomics to develop a platform for precision medicine in oncology.

32. Precision Oncology Experimental Therapeutics (POET), Calgary, Alberta April 6, 2018. **Keynote Speaker:** Title: Precision medicine as a platform for big-data studies.

33. Michael Smith Laboratory Seminar Series, University of British Columbia, Vancouver, BC. March 21, 2018. Invited Speaker. Title: Bioinformatically interrogating tumour genomes in real-time

34. Canadian Institute for Advanced Research (CIFAR) Genetics Networks Program, Toronto, Ontario, November 9-10, 2017. Invited Speaker. Title: Interrogating the genetics of cancer for real-time therapeutic insights.

35. Livestock Gentec Conference: One Genome, One Health: Our Animals, the Environment and Us, Edmonton, Alberta, October 17-18, 2017. Invited Speaker. Title: The Role of Genomics in Precision Health Care.

36. Acuitas Science Day, University of British Columbia, Vancouver, BC. September 18, 2017. Invited Speaker. Title: The application of Genomics in Cancer treatment.

37. Cancer Genomics Canadian Bioinformatics Workshop, Toronto, ON. June 2, 2017. **Keynote Speaker**. Title: Precision Oncogenomics.

38. Princess Margaret Cancer Centre Seminar Series, Toronto, ON. May 19, 2017. Invited Speaker. Title: Predicting Drug Sensitivities from Cancer Genomes.

39. Health Genomic seminar series Dalhousie Unviersity, Halifax, Nova Scotia. January 18, 2017. **Keynote Speaker.** Title: Genome sequencing for the improvement of cancer diagnosis and treatment.

40. Functional Genomics and Beyond Symposium:“Nature Via Nurture”, Qatar National Convetion Centre, Doha, Qatar. December 13, 2016. Invited Distinguished Speaker. Title: Genomic Analysis to Personalize Cancer Treatment.

41. Terry Fox Research Institute Sumposium, Toronto, Ontario. December 5, 2016. Invited Speaker. Title: Genomic Analysis within the clinic for improved therapeutic choice.

42. Molecular & Cellular Biology Retreat, Ohio University, Athens, Ohio. November 20, 2016. Invited Lecturer. Title: Can we improve cancer outcomes through real time genomics and bioinformatics.

43. Molecular Biology and Biochemistry, Human Genetics, Simon Fraser University, BC. October 28, 2016. Invited Lecturer. Title: Next generation DNA sequencing .

44. Global Alliance for Genomics and Health (GA4GH), Vancouver, BC. October 18, 2016. Invited Speaker. Title: A Systemic Approach to Data Sharing in Translational Medicine.

45. Graph Genome Day, London, UK. September 27, 2016. Invited Speaker. Title: Mutational Tracking through Multiple Biopsies.

46. 16th International Union of Biochemistry and Molecular Biology (IUBMB) Conference, Vancouver, BC. July 18, 2016. Invited Speaker: Plenary Session. Title: Genomic Analysis for Personalized Medicine.

47. Summit for Cancer Immunotherapy Conference, Halifax, Nova Scotia. June 27, 2016. Invited Speaker. Title: Identifying Novel Mutations and Proteins in Treatment Resistant Human Cancers.

48. 1st Canadian Computational Biology Conference, Toronto, Ontario. May 15-19, 2016. **Keynote Speaker**. Title: Genomic analysis of cancer genomes to aid in clinical decision making

49. Rendez-Vous Genome Quebec Meeting, Montreal Quebec. December 4, 2015. **Keynote Speaker**. Title: Genomic Analysis to Personalize Cancer Treatment.

50. Taiwan-Canada Frontier Translational Medicine workshop, National Cheng Kung University, Tainan, Taiwan. November 23, 2015. Invited Speaker. Title: Personalized Cancer Genomics.

51. Canadian Cancer Research Conference, Montreal, Canada. November 9, 2015. Invited Speaker. Title: Bioinformatic analysis of tumour genomes for real-time clinical evaluation.

52. Illumina International Summit on Population and Medical Genomics, St. Andrew's, Scotland. June 3, 2015. Invited Speaker: Title: Using whole genome sequencing for personalized cancer treatment.

53. Society for Industrial and Applied Mathmatics (SIAM), Vancouver, BC. April 30, 2015. **Keynote Speaker**: Title: Analysis of Cancer Genomes to Aid the Therapeutic Choice.

54. Taiwan-Canada Joint Health Initiative, Vancouver, BC. April 21, 2015. Invited Speaker. Title: Production epigenomic data processing.

55. Alberta Epigenetics Network Annual Summit, Banff, Alberta. March 30th, 2015. **Keynote Speaker**. Title: Identifying novel therapeutic approaches in cancer through epigenomics.

56. First International Weaver Syndrome Conference, Vancouver, BC. November 9, 2014. Invited Speaker. Title: Epigenomics and Cancer.

57. Lady Davis Institute for Medical Research, Montreal, QC. November 5, 2014. Invited Speaker. Title: Genotype specific approaches to cancer therapy.

58. Molecular Biology & Biochemistry, Simon Fraser University, Vancouver, BC. October 24, 2014. Invited Speaker. Title: A Personalized approach to cancer therapy.

59. Chinese University of Hong Kong, China. May 22, 2014. Invited Speaker. Title: Cancer Genomics to aid in clinical decision making.

60. Canada Office, Osaka Chamber of Commerce & Industry, Osaka, Japan. December 6, 2013. **Keynote Speaker**. Title: Sequencing Cancer Genomes to Determine Optimum Therapeutic Approaches.

61. Embassy of Canada, Tokyo, Japan. December 4, 2013. **Keynote Speaker**: Title: Sequencing Cancer Genomes to Determine Optimum Therapeutic Approaches.

62. International Human Epigenome Consortium Annual Meeting & Science Days, Berlin, Germany. November 12, 2013. Invited Speaker. Title: Computational Approaches to Aid and Exploit Epigenomic Information.

63. 2nd EMBL Conference on Cancer Genomics, Heidelberg, Germany. November 3, 2013. Invited Speaker. Title: Cancer Genomcis to aid in clinical decision making.

64. Ohlson Lecutre, University of Calgary, Calgary, Alberta. October 25, 2013. Invited Lecturer. Title: Sequencing cancer genomes for clinical decision making.

65. Simon Fraser University, Molecular Biology and Biochemistry (MBB 435-Genome Biology), Vancouver, BC. June 25, 2013. Invited Lecturer. Title: Next-generation DNA sequencing.

66. 3rd Annual Scientific Summit, New Orleans, Louisianna. June 4, 2013. Invited Speaker. Title: Utilizing complete genome sequencing to inform clinical decision making in oncology.

67. University of British Columbia, Medical Genetics Seminar Series, Vancouver, BC. May 10, 2013. Invited Speaker. Title: Exploiting epigenomic mechanisms in human cancer.

68. 12th International Symposium on Mutation in the Genome, Lake Louise, Banff, Alberta. April 24, 2013. Invited Speaker. Title: Detection of somatic tumour mutations to inform therapeutic decision-making in patients with advanced malignancies.

69. Australia Wine Research Institute, Adelaide, Australia. October 19, 2012. Invited Speaker. Title: Using Next-generation sequencing to explore mammalian sized genomes and transcriptomes.

70. McGill University, Montreal, Quebec. July 5, 2012. Invited Speaker. Title: Using Cancer Genomes to Identify Novel Therapeutic Approaches.

71. Computational Biology Symposium, University of Florida, Gainesville. April 2012. Invited Speaker. Title: Genomic Approaches to Characterize Human Tumours and Develop Potential Therapies.

72. Ontario Cancer Institute, Princess Margaret Hospital, Toronto, Ontario. February 2012. Invited Speaker. Title: Genomics for Personalized Medicine in Cancer.

73. Ontario Cancer Institute, Princess Margaret Hospital, Toronto, Ontario. February 2012. Invited Speaker: Title: Genomic characterization of human tumours and clues for potential therapies.

74. Canadian Cancer Research Conference, Toronto, Ontario. November 2011. Invited Speaker. Title: Using Next-generation sequencing to identify recurrent mutational events in human cancers

75. 3rd Annual Next-generation Sequencing Congress, London, UK. November 2011. Invited Speaker. Title: Using Next Generation Sequencing to identify recurrent mutational events in human cancers

76. BC Cancer Agency Research Seminar Series, Vancouver, BC. October 2011. Invited Speaker. Title: Computational approaches to characterize human tumours and develop potential therapies.

77. Insitute for Pure and Applied Mathematics: Next Generation Sequencing Workshop. UCLA, Los Angeles, CA. October 2011. Invited Speaker. Title: Identification of Recurrent Mutational Events in Human Cancer.

78. CIHR Personalized Medicine: Metabolic Disruption and Disease Scientific Workshop, Luxembourg, Luxembourg. September 2011. Invited Speaker. Title: Bioinformatics for Personalized Medicine in Cancer.

79. National Microbiology Laboratory, Winnipeg, Manitoba. September 2011. Invited Speaker. Title: Genomic Sequencing of Human Cancers.

80. Illumina Seminar Series, San Diego, CA. June 2011. Invited Speaker. Title: Evolution of an adenocarcinoma in response to selection by targeted kinase inhibitors.

81. Genome Informatics Alliance Meeting, Verona Italy. June 2011. Invited Speaker. Title: Annotation, Analysis and Visualization of Cancer Diagnosis.

82. BC Cancer Agency Clinician-Scientist Retreat, ‘Bridging the Bench to the Bedside’, Vancouver, BC. May 2011. Invited Speaker. Title: Specific Targeting of IDH1 mutations.

83. Cold Spring Harbor Laboratory, Cold Spring Harbor, NY. April 2011. Invited Speaker. Title: Identifying oncogenically relevant events in human cancers.

84. 9th Asia Pacific Bioinformatics Conference, Seoul, South Korea, January 2011. **Keynote Speaker**. Title: Bioinformatics and Cancer Genomics.

85. Antibody Engineering Conference, San Diego, CA, December 2010. Invited Speaker. Title: Current and Emerging Technologies for Sequencing and Informatics/Data Handling.

86. Genome Biology: Beyond the Genome, Boston, MA, USA. October 2010. Invited Speaker. Title: Personalized Oncogenomics.

87. Centre for Genetic Medicine, Northwestern University, Chicago, IL, USA. September 29, 2010. Invited Speaker. Title: Analyzing cancer genomes with next-generation sequencing approaches.

88. Genomics Automation Congress, Boston, MA, USA. May 7, 2010. Invited Speaker. Title: Genomic Sequencing of Human Cancer.

89. 3rd Annual Canadian Human Genetics Conference, Saint Sauveur, Quebec. April 19, 2010. Invited Speaker. Title: Complete Genome Sequencing to identify oncogenic mutations.

90. Kentucky Biomedical Research Infrastructure Network, Bioinformatics Summit, Lake Barkley State Park, Cadiz, Kentucky. March 19, 2010. Invited Speaker. Title: Genomic Analysis of a Rare Human Tumour.

91. Genome BC Winter Symposium, Vancouver, BC, January 19, 2010. Invited Speaker. Title: DNA Technologies and translational research.

92. Deeley Research Centre, Victoria, BC, January 5, 2010. Invited Speaker. Title: Next generation sequencing and cancer genomics.

93. Bioinformatics Australia (BA-2009), Melbourne, Australia, October 29, 2009. **Keynote Speaker**. Title: Bioinformatics for Personalized onco-genomics.

94. Translational Research Excellence (TRX09) Brisbane, Australia, October 23, 2009. Invited Speaker. Title: Genomic and Bioinformatic Approaches for Personalized Medicine in Cancer.

95. Illumina Expert Sequencing Panel, Seattle, Washington, October 15, 2009. Invited Speaker. Title: De novo Trascriptome Assembly.

96. Analytical & Life Science Systems Association (ALSSA) 2009 Senior Management Conference, Laguna Beach, CA. October 5, 2009. Invited Speaker. Title: Sequencing in Cancer Diagnosis and Treatment.

97. University of Calgary, Clark H. Smith Brain Tumour Centre, Calgary, Alberta. April 27, 2009. Invited Speaker. Title: Massively parallel sequencing approaches for cancer research.

98. Simon Fraser University, Department of Biosciences, Evolutionary Genetics, Vancouver, BC. April 24, 2009. Invited Speaker. Title: Applications for massively parallel DNA sequencing technology.

99. Simon Fraser University, Medicinal Chemistry, Vancouver, BC. Jan. 22, 2009. Invited Lecturer. Title: Genomics, Virtual Screening and Drug Discovery

100. Simon Fraser University, Cancer Molecular Mechanisms, Vancouver, BC. Nov. 2008. Invited Lecturer. Title: Reading the Genome

101. Uppsala University, Uppsala Sweden. Oct. 2008. Invited Lecturer. Title: Using ChIP-Seq to Understand Gene Regulatory Control.

102. Peter MacCallum Cancer Centre Symposium, Melbourne, Australia. Oct. 2008. Invited Speaker. Title: Histone Modification and Genetic Regulatory Control.

103. 4th Barbados Workshop on computational gene regulation: genetic variation and gene regulation. Bellairs Research Institute. April 2008. Platform Speaker. Title: Correlation of Chromatin Modification and Genetic Regulation.

104. Department of Molecular Biology and Biochemistry, Simon Fraser University. Feb. 2008. Invited Speaker. Title: Application of next generation sequencing in regulatory element detection and transdriptome analysis.

105. Michael Smith Laboratories, University of British Columbia, Vancouver. Feb. 2008. Invited Speaker. Title: The Chipping news and other applications for the next generation of DNA sequencing machines.

106. Canadian-Taiwan Symposium (CCAPSC) Vancouver, BC. Oct. 2007. Invited Speaker. Title: Next Generation DNA Sequencing.

107. Tsinghua University, Beijing, China. May 2007. Invited Speaker. Title: Massively parallel sequencing approaches for the determination of histone modifications and transcription factor binding sites.

108. 16th International Congress of Cytology. Vancouver, BC. May 2007. Invited Speaker. Title: Determining genomic changes through Bioinformatics.

109. AGBT Conference, Marco Island, Florida. Feb. 2007. Invited Speaker. Title: Massively Parallel Sequencing-By-Synthesis for Detection of Genetic Aberrations in Human Cancer.

110. Monsanto, St. Louis, Missouri. Dec. 2006. Invited Speaker. Title: High-throughput computational identification of gene regulatory elements.

111. Genomics Mini Symposium, Simon Fraser University, Vancouver, BC. Dec. 2006. Invited Speaker. Title: Bioinformatics at the Genome Sciences Centre

112. Department of Biology, University of Victoria. Victoria, BC. January 2006. Invited Speaker. Title: Identifying gene regulatory control elements on a genome-wide scale.

113. Biotechnology Research Institue (BRI). Montreal, QU. September 2005. Invited speaker. Title: Identifying gene regulatory control elements on a genome-wide scale

114. European Molecular Biology Laboratory (EMBL), European Bioinformatics Institute. Hinxton, UK. July 2005. Invited speaker. Title: High-throughput approaches to the detection regulatory elements.

115. Simon Fraser University, Computing Science & Molecular Biology departments. Burnaby, BC. April 2005. Invited speaker. Title: High throughput approaches to detecting regulatory control elements on a genome-wide scale.

116. Genome BC Genomics Forum 2005. Vancouver, BC. April 2005. Invited speaker. Title: High Throughput of Regulatory Elements in Mammalian Genomes.

117. World Microarray Congress 2005. Vancouver, BC. March 2005. Invited speaker. Title: Using gene expression data and orthology to detect cis-regulatory elements across mammalian genomes.

118. 2005 AGBT Meeting. Marco Island, FL. February 2005. Plenary speaker. Title: A High-Throughput Approach for cis-Regulatory Elements Detection Across Mammalian Genomics.

119. BC Cancer Research Centre, Monday Noon Seminar Series. Vancouver, BC. February 2005. Invited speaker. Title: Identifying gene regulatory control elements on a genome-wide scale.

120. Genome Canada: National Genomics and Proteomics Symposium. Vancouver, BC. November 2004. Invited speaker. Title: Bioinformatics for high-throughput sequencing at the Genome Sciences Centre (GSC) and UBC Bioinformatics Centre (UBiC), Vancouver.

121. ENCODE Consortium meeting. Cold Spring Harbour Laboratory, NY. November 2004. Invited speaker. Title: Fingerprint Contig assembly for ENCODE regions.

122. Identification of Functional Elements in Mammalian Genomes. Cold Spring Harbor Laboratory, NY. November 2004. Platform speaker. Title: A high-throughout approach for cis-regulatory element detection across entire mammalian genomes.

123. New England Bioloabs seminar. Boston, MA. October 2004. Invited speaker. Title: Serial Analysis of Gene Expression in C. elegans.

124. Cold Spring Harbor Laboratory/Wellcome Trust Conference: Genome Informatics. Hinxton, UK. September, 2004. Platform speaker. Title: A high-throughout approach for cis-regulatory element detection across entire mammalian genomes.

125. BC Cancer Agency, 20th Annual Residents' Radiobiology Course. Vancouver, BC. June 2004. Invited lecturer. Title: Gene discovery with a view to therapy.

126. 21st Annual Meeting of the Society for Computer Applications in Radiobiology. Vancouver, BC. May 2004. Platform Speaker. Title: Open Source Software in Medicine.

127. 2nd Annual Gene Expression Conference. Vancouver, BC. March 2004. Invited speaker. Title: Integrated Approaches to regulatory element detection using the Sockeye Platform.

128. Finding the Functional Elements of the Genome. Banbury Centre Cold Spring Harbor Laboratory, NY. March 2004. Invited Speaker. Title: Integrated Approaches to regulatory element detection using the Sockeye Platform.

129. 1st Canadian Plant Genomics Workshop. Saskatoon, SK. August 2003. **Keynote Speaker**. Title: Integrated genomic approaches to interpreting gene expression data.

130. 1st Canadian Gene Expression Conference. Vancouver, BC. March 2003. Invited speaker. Title: Serial Analysis of Gene Expression in Cancer Research.

131. iCAPTURE Centre, McDonald Research Laboratories Seminar Series. Vancouver, BC. March 2003. Invited speaker. Title: Cancer Bioinformatics.

132. Automation in DNA Mapping and Sequencing, Advances in Genome Biology & Technology Conference. Marco Island, FL. February 2003. Plenary speaker. Title: High-throughput serial analysis of gene expression profiling of cancers.

133. Frontiers in Cardiovascular Science 2003. Vancouver, BC. February 2003. Invited speaker. Title: Bioinformatics in dissecting human pathogenesis: Now and over the horizon.

134. Vancouver Bioinformatics User Group (VanBUG). Vancouver, BC. December 2002. Invited speaker. Title: Bioinformatic approaches to the study of cancer.

135. New Frontiers: Italian/Canadian Genomic Population Genetics and Bioinformatic Collaborations. Montreal, PQ. December 2002. Invited speaker. Title: Cancer bioinformatics.

136. BioFuture 2002, Advancing Our Double Helix World Conference. Vancouver, BC. November 2002. Invited speaker. Title: Cancer bioinformatics.

137. BioNorth 2002. Ottawa, ON. November 2002. Invited speaker. Title: Cancer genomics.

138. Stem Cell Network Annual General Meeting. Mississauga, ON. September 2002. Invited speaker. Bioinformatics and gene expression.

139. The Pacific North-West Cell Signaling Conference. Vancouver, BC. September 2002. Invited speaker. Bioinformatics and cancer research.

140. National Research Council, Genomics Health Initiatives Annual General Meeting. Ottawa, ON. August 2002. Invited speaker. Bioinformatics of Gene Expression.

141. Canadian Laboratory Medicine Congress – Together Towards Excellence. Calgary, AB. May 2002. Invited speaker. Gene expression changes in cancer diagnosis and prognosis.

142. Molecular Biology & Biochemistry, Simon Fraser University. Burnaby, BC. April 2002. Invited speaker. Bioinformatics at the Genome Sciences Centre.

143. University of British Columbia, Statistics Department. Vancouver, BC. March 2002. Invited speaker. Identification of genes expressed in early-stage lung cancers.

144. Mentors' Network Meeting, University of British Columbia. Vancouver, BC. December 2001. Invited speaker. The CIHR Bioinformatics Training Program.

145. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. November 2001. Invited speaker. Bioinformatic approaches for lung expression analysis.

146. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. November 2001. Invited speaker. Bioinformatics of Cancer Genomics.

147. BCNet Annual General Meeting. Vancouver, BC. September 2001. Invited speaker. Bioinformatics, Genomics and the Internet.

148. StemNet National Centre of Excellence. Toronto, ON. September 2001. Invited speaker. SAGE at the BC Cancer Agency Genome Sequence Centre.

149. Cold Spring Harbor Laboratory/Wellcome Trust Conference, Genome Informatics. Hinxton, UK. August 2001. Invited speaker: Bioinformatic approaches for SAGE expression analysis.

150. BC Cancer Research Centre, Cancer Genomics seminar. Vancouver, BC. July 2001. Invited speaker. Biological inference and SAGE expression data.

151. University of California San Francisco Cancer Center. February 2001. Invited Speaker. Expression profiling using Serial Analysis of Gene Expression (SAGE) in model organisms and humans.

152. Molecular Helminthology: An Integrated Approach. Taos, NM. January 2001. Invited Speaker. Functional Genomes and C. elegans.

153. Computer Science Department, University of Saskatoon. Saskatoon, SK. January 2001. Invited speaker. Bioinformatics for Physical Mapping and DNA sequencing.

154. National Research Council, Saskatoon. Saskatoon, SK. January 2001. Invited speaker. Expression Profiling in Model Organisms.

155. Annual BC Cancer Agency Clinical Cancer Conference. Vancouver, BC. November 2000. Invited Speaker. Bioinformatics at the Genome Sequence Centre.

156. The First Canadian Working Conference on Computational Biology – CCCB 2000. Toronto, ON. November 2000. Platform Presentation. Expression Analysis Using SAGE Data.

157. First Canadian Lung Cancer Research Workshop, Princess Margaret Hospital. Toronto, ON. June 2000. Invited Speaker. Studying gene expression profiling in a model organism.

158. 5th Annual International Human Genome Meeting. Vancouver, BC. April 2000. Platform presentation. Pathogenomics: Bioinformatic approaches to determine host and pathogen molecular interactions.

159. North Carolina State University Genomics Symposium. April 2000. Invited Speaker. The informational content of the C.elegans genome and its exploitation.

160. University of British Columbia, Computer Science Department. March 2000. Invited Speaker. The Organization of Genetic Information in the C.elegans Genome.

161. Vancouver Linux Users Group (VanLUG) Spring Seminars. January 2000. Invited Speaker. Linux at the BC Genome Sequence Centre.

162. Simon Fraser University, Biostat Seminar Series. January 2000. Invited Speaker. Bioinformatics in the Genome Sequence Centre and beyond.

163. Centre for Molecular Medicine and Therapeutics, University of British Columbia. September 1999. Invited Speaker. Computational analysis of the C. elegans Genome.

164. University of British Columbia Graduate Student Society. August 1999. Invited Speaker. Interpreting our Inheritance.

165. Genome Analysis: Strategies, Medical and Industrial Applications. Jena, Germany. September 1997. **Jones S**. Platform Presentaion. The C. elegans genome: towards completion.

166. Parasitic Helminths from Genomes to Vaccines. Edinburgh, Scotland. September 1997. Invited Speaker. Keynote lecture. The C. elegans genome:From sequence to Biology.

167. Genome Sequencing and Mapping. Cold Spring Harbor 1997. **Jones S**. Platform Presentation. The C. elegans genome sequencing project.

168. Tenovus Scotland: Eukaryotic Gene Biology. Glasgow 1997. **Jones S**. Platform presentation. The C. elegans genome sequencing project.

169. 6th International workshop on the identification of transcribed sequences. Edinburgh, Scotland. October 1996. Platform Presentation. Gene Prediction in the C. elegans genomic sequencing project.

## ABSTRACTS AND POSTERS: TOTAL 601

1. ISMB 2024, July 12-16, 2024, Montreal, Canada. The Canadian Genomic Data Commons (CGDC): A Platform for National Genomic Data Sharing. Jordan Lerner-Ellis, Erika Frangione, Selina Casalino, Radhika Mahajan, Navneet Aujla, Lochana Jayachandran, Anthony Philippakis, Heidi Rehm, Marc Fiume, Vincent Ferretti, Yann Joly, Patrick Frosk, Sherryl Taylor, Kym Boycott, **Steven J.M. Jones**.

2. BC Cancer Summit, November 16-18, 2023, Vancouver, BC. Benefits of integrating an open-source knowledgebase in a precision oncology workflow. Cameron J. Grisdale, Erin Pleasance, Connor Frey, Caralyn Reisle, Laura M. Williamson, Veronika Csizmok, Kathleen Wee, Yaoqing Shen, Melika Bonakdar, Greg Taylor, Kilannin Krysiak, Jason Saliba, Arpad M. Danos, Adam C. Coffman, Susanna Kiwala, Joshua F. McMichael, Janessa Laskin, Malachi Griffith, Obi L. Griffith, **Steven J.M. Jones. Poster presentation.**

3. BC Cancer Summit, November 16-18, 2023, Vancouver, BC. Immune profiling tools in whole genome and transcriptome analysis of metastatic tumours inform immunotherapy clinical trial design. Kathleen Wee, Erin Pleasance, Emma Titmuss, Laura Williamson, Yaoqing Shen, Karen Mungall, Eric Chuah, Andrew Mungall, Melika Bonakdar, Greg Taylor, Veronika Csizmok, Cameron J Grisdale, Melissa McConechy, Jing Xu, John H Dupuis, Richard D Corbett, Jessica Nelson, Stephen Yip, Sophie Sun, Howard Lim, Daniel Renouf, **Steven JM Jones**, Marco A Marra, Janessa Laskin. **Poster presentation.**

4. BC Cancer Summit, November 16-18, 2023, Vancouver, BC. Nanopore sequencing of advanced cancers identifies haplotype specific promoter methylation associated with clinically relevant HRD phenotype. Veronika Csizmok, Erin Pleasance, Laura Williamson, Kieran O'Neill, Vahid Akbari, Glenn Chang, Andrew Galbraith, Janessa Laskin, Marco A. Marra, **Steve J.M. Jones**. **Poster presentation**.

5. BC Cancer Summit, November 16-18, 2023, Vancouver, BC. Formalin-Fixed, Paraffin-Embedded Tumour Specimens for Whole Genome and Transcriptome Analysis in Precision Oncology. Connor Frey, Jing Xu, Erin Pleasance, Laura Williamson, Richard Corbett, Angela Tam, Carrie Hirst, Andrew Mungall, Karen Mungall, Jessica Nelson, Melissa McConechy, Stephen Yip, **Steven Jones**, Marco Marra, Janessa Laskin. **Poster presentation**.

6. BC Cancer Summit, November 16-18, 2023, Vancouver, BC. Precision Cancer Medicine: The Personalized OncoGenomics Program. Erin Pleasance, Laura Williamson, Yaoqing Shen, Veronika Csizmok, Kathleen Wee, Gregory A Taylor, Cameron Grisdale, Jing Xu, Melissa McConechy, John H Dupuis, Karen L Mungall, Eric Chuah, Richard Moore, Andrew J Mungall, Jessica Nelson, Stephen Yip, Kasmintan Schrader, Dean Regier, Sophie Sun, Howard Lim, Daniel J Renouf, **Steven JM Jones**, Marco A Marra, Janessa Laskin. **Poster presentation**.

7. CEEHRC 9th Annual Canadian Conference on Epigenetics, November 13-16, 2023, Banff, Alberta. Pan-Cancer Characterization of Allele-Specific Methylation using Nanopore Sequencing. Andrew Galbraith, Vahid Akbari, Glenn Chang, Veronika Csizmok, Kieren O'Neill, Erin Pleasance, **Steven J.M. Jones**. **Poster Presentation.**

8. Canadian Cancer Research Conference, November 12-14, 2023. Halifax, Nova Scotia. Nanopore sequencing of advanced cancers identifies haplotype specific promoter methylation associated with clinically relevant HRD phenotype. Veronika Csizmok, Erin Pleasance, Laura Williamson, Kieran O'Neill, Vahid Akbari, Glenn Chang, Andrew Galbraith, Janessa Laskin, Marco A. Marra, **Steve J.M. Jones**. **Lightening presentation AND poster presentations.**

9. Biodiversity Genomics conference, October 2-6, 2023, Virtual. Canadian Earth Biogenome project assembly pipeline. Solenne Correard, Sreeja Leelakumari, Samantha J. Jones, Hesther Yueh, Tara Paton,

Karen Ho, Haig Djambazian, Pierre Berube, Anne-Laure Ferchaud, Louis Bernatchez, Nathalie Vachon, Marc-Antoine Couillard, Stephen W. Scherer, Ioannis Ragoussis, **Steven J.M. Jones**. **Oral presentation**.

10. AGBT Precision Health Conference, September 7-9, 2023, San Diego, California, USA. Benefits of integrating an open-source knowledgebase in a precision oncology workflow. Cameron J. Grisdale, Erin Pleasance, Connor Frey, Caralyn Reisle, Laura M. Williamson, Veronika Csizmok, Kathleen Wee, Yaoqing Shen, Melika Bonakdar, Greg Taylor, Kilannin Krysiak, Jason Saliba, Arpad M. Danos, Adam C. Coffman, Susanna Kiwala, Joshua F. McMichael, Janessa Laskin, Malachi Griffith, Obi L. Griffith, **Steven J.M. Jones**. **Poster presentation**.

11. AGBT Precision Health Conference, September 7-9, 2023, San Diego, California, USA. Immune profiling tools in whole genome and transcriptome analysis of metastatic tumours inform immunotherapy clinical trial design. Kathleen Wee, Erin Pleasance, Emma Titmuss, Laura Williamson, Yaoqing Shen, Karen Mungall, Eric Chuah, Andrew Mungall, Melika Bonakdar, Greg Taylor, Veronika Csizmok, Cameron J Grisdale, Richard D Corbett, Jessica Nelson, Stephen Yip, Sophie Sun, Howard Lim, Daniel Renouf, **Steven JM Jones**, Marco A Marra, Janessa Laskin. **Poster presentation**.

12. Intelligent Systems for Molecular Biology, July 23-27, 2023, Lyon, France. Machine Learning Derived Transcriptional Signatures in Cancer. Faeze Keshavarz, Erin Pleasance, **Steven J.M. Jones**. **Poster Presentation.**

13. RiboWest 2023, Western Canada's Premier RNA Conference, June 15, 2023, Virtual.Nanopore-based native RNA sequencing of human transcriptomes reveals the complexity of mRNA modifications and crosstalk between RNA regulatory features. Yerin Kim, Kieran O'Neill, Jean-Michel Garant, Simon Haile Merhu, Maryam Ghashghaei, **Steven J.M. Jones***, Ly Vu* **Oral Presentation**.

14. Precision Health Summit, February 2, 2023, Vancouver, BC. Precision Cancer Medicine: The Personalized OncoGenomics Program. 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. **Poster presentation**.

15. Precision Health Summit, February 2, 2023, Vancouver, BC. Nanopore Long-Read Sequencing of Advanced Tumours from the Personalized OncoGenomics and Marathon of Hope Cancer Centres Network Study. 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, Janessa Laskin, Marco Marra, **Steven Jones**. **Poster presentation**.

16. Nanopore Community Meeting, December 5-7, 2022 (Virtual). Simultaneous haplotyping and parent-of-origin assignment of homologous chromosomes without parental sequence data using nanopore sequencing and strandseq. Vahid Akbari, Vincent C. T. Hanlon, Kieran O'Neill, Louis Lefebvre, Kasmintan A. Schrader, Peter M. Lansdorp, **Steven J.M. Jones**.. **Oral Presentation.**

17. BC Cancer Summit, November 24-26, 2022, Vancouver, British Columbia. Characterization of the epitranscriptomics landscape of acute myeloid leukemia using nanopore direct RNA sequencing. Yerin Kim, Kieran O'Neill, Jean-Michel Garant, Simon Haile Merhu, Maryam Ghashghaei, **Steven J.M. Jones**, Ly P. Vu. **Poster Presentation.**

18. BC Cancer Summit, November 24-26, 2022, Vancouver, British Columbia. Benefits of integrating an open-source knowledgebase in a precision oncology workflow. Cameron J. Grisdale, Erin Pleasance, Caralyn Reisle, Laura M. Williamson, Kilannin Krysiak, Jason Saliba, Arpad M. Danos, Adam C. Coffman, Susanna Kiwala, Joshua F. McMichael, Malachi Griffith, Obi L. Griffith, **Steven J.M. Jones**.. **Poster Presentation**.

19. UBC Department of Medical Genetics Research Day, November 4, 2022, Vancouver, British Columbia. Chromosome-scale haplotyping and parent-of-origin assignment of homologous chromosomes in a single sample without parental sequencing data. Vahid Akbari, Vincent C. T. Hanlon, Kieran O'Neill, Louis Lefebvre, Kasmintan A. Schrader, Peter M. Lansdorp, **Steven J.M. Jones.**. **Oral Presentation.**

20. TFRI's 9th Scientific Meeting, November 3-6, 2022, Vancouver, British Columbia. Personalized Oncogenomics (POG) Program. Janessa Laskin, Laura Williamson, Erin Pleasance, Daniel Renouf, Dean Regier, Kasmintan Schrader, Sophie Sun, Howard Lim, Stephen Yip, Robert Holt, Samuel Aparicio, Nadine Caron, **Steven Jones**, Marco Marra. **Poster presentation.**

21. TFRI's 9th Scientific Meeting. November 3-6, 2022, Vancouver, British Columbia. The precision oncology for young people (PROFYLE) program: A national precision oncology program for children, adolescents and young adults with hard-to-cure cancer in Canada. Stephanie A. Grover, Lesleigh Abbott, Jason N. Berman, Guillaume Bourque, Jennifer A. Chan, Avram E. Denburg, Rebecca J. Deyell, Conrad V. Fernandez, Cynthia Hawkins, Jan-Willem Henning, Meredith S. Irwin, Nada Jabado, **Steven J.M. Jones**, Philipp F. Lange, Paul Moorehead, Michael F. Moran, Daniel A. Morgenstern, Sapna Oberoi, Antonia Palmer, Shahrad R. Rassekh, Donna L. Senger, Adam Shlien, Daniel Sinnett, Caron Strahlendorf, Patrick J. Sullivan, Michael D. Taylor, Suzanne Vercauteren, Anita Villani, Stephanie Villeneuve, James A. Whitlock, David Malkin, on behalf of the Terry Fox PROFYLE Consortium. **Poster Presentation.**

22. 13th Annual Meeting of the Cancer Genomics Consortium (CGC), July 31 – August 3, 2022, St. Louis, Missouri. Benefits of integrating an open-source knowledgebase in a precision oncology workflow. Cameron J. Grisdale, Erin Pleasance, Caralyn Reisle, Laura M. Williamson, Kilannin Krysiak, Jason Saliba, Arpad M. Danos, Adam C Coffman, Susanna Kiwala, Joshua F. McMichael, Malachi Griffith, Obi L. Griffith, **Steven J.M. Jones**. **Poster presentation.**

23. London Calling, May 18-20, 2022 (Virtual). DNA methylation analysis in human tumour samples using nanopore sequencing. Vahid Akbari, Kieran O'Neill, Richard Corbett, Vanessa L. Porter, Erin Pleasance, Pawan Pandoh, Richard Moore, Marco Marra, Martin Hirst, **Steven J.M. Jones**. **Poster presentation.**

24. BIG22, March 11, 2022, Vancouver, British Columbia. A Random Forest derived p53 transcriptional signature in cancer. Faeze Keshavarz-Rahaghi, Erin Pleasance, Tyler Kolisnik, **Steven J. M. Jones**. **Poster Presentation.**

25. BC Cancer Summit. November 18-19, 2021 (Virtual). Benefits of integrating an open-source knowledgebase in a precision oncology workflow. Cameron J. Grisdale, Erin Pleasance, Laura M. Williamson, Caralyn Reisle, Melika Bonakdar, Gregory A. Taylor, Jason Saliba, Arpad M. Danos, Adam C. Coffman, Lana Sheta, Susanna Kiwala, Joshua F. McMichael, Kilannin Krysiak, Malachi Griffith, Obi L. Griffith, **Steven J. M. Jones**. **Poster Presentation.**

26. International Papillomavirus Conference (IPVC) November 15-19, 2021 (Virtual). Analysis of cervical cancers with long-read technology delineates novel genomic structures and regulation patterns at HPV integration events. Vanessa L. Porter, Kieran O'Neill, Ka Ming Nip, Luka Culibrk, Vahid Akbari, Simon K. Chan, Marissa Iden, Shirng-Wern Tsaih, Richard Corbett, Karen L. Mungall, Andrew J. Mungall, Inanc Birol, **Steven J. M. Jones**, Janet S. Rader, Marco A. Marra. **Poster Presentation.**

27. CEEHRC 7th Annual Canadian Conference on Epigenetics November 3-5, 2021 (Virtual). Detection of Imprinted DNA Methylation Using Nanopore Long-Read Sequencing. Vahid Akbari, Jean-Michel Garant, Kieran O'Neill, Pawan Pandoh, Richard Moore, Marco Marra, Martin Hirst, **Steven J.M. Jones**. **Poster presentation**.

28. CEEHRC 7th Annual Canadian Conference on Epigenetics November 3-5, 2021 (Virtual). A compendium of uniformly processed public mouse hematopoietic RNA-seq data for data mining. Misha Bilenky, Donald Ng, **Steven Jones**, Martin Hirst. **Poster presentation.**

29. ISMB/ECCB 2021 July 25 – 30, 2021 (Virtual). Investigating tumor genome instability with Ploidetect. Luka Culibrk, Erin Pleasance, Karen Mungall, Janessa Laskin, Marco Marra and **Steven Jones**. **Poster Presentation.**

30. Bioinformatics Open Source Conference (BOSC) July 29-30, 2021 (Virtual). Robust variant interpretation in precision oncology using a graph knowledge base. Caralyn Reisle, Laura Williamson, Erin Pleasance, Dustin Bleile, Anna Davies, Brayden Pellegrini, Karen Mungall, Eric Chuah, Martin Krzywinski, Raphael Matiello Pletz, Jacky Li, Ross Stevenson, Hansen Wong, Abbey Reisle, Matthew Douglas, Eleanor Lewis, Melika Bonakdar, Jessica Nelson, Cameron Grisdale, Ana Fisic, Teresa Mitchell, Daniel Renouf, Stephen Yip, Janessa Laskin, Marco Marra and **Steven Jones**. **Oral Presentation.**

31. Pathology Day, University of British Columbia May 28, 2021. Deep-Learning Based Classification Distinguishes Sarcomatoid Malignant Mesotheliomas from Benign Spindle Cell Mesothelial Proliferations. Julia R. Naso, Adrian B Levine, Hossein Farahani, Lucian R. Chirieac, Sanja Dacic, Joanne L. Wright, Chi Lai, Hui-Min Yang, **Steven J.M. Jones,** Ali Bashashati, Stephen Yip, Andrew Churg. **Oral Presentation.**

32. London Calling 19-21, May 2021 (Virtual). Genome-wide detection of imprinting control regions using nanopore sequencing. Vahid Akbari, Jean-Michel Garant, Kieran O'Neill, Pawan Pandoh, Richard Moore, Marco Marra, Martin Hirst, **Steven J.M. Jones**. **Poster presentation.**

33. Curating the Clinical Genome Conference (Virtual) May 12-14, 2021. De novo heterozygous POLR2A mutation associates with complex autism spectrum disorder (ASD), epilepsy, strabismus, hypotonia and self-injurious behaviours. Ying Qiao, Sally Martell, Kristina Calli, **Steven Jones**, Stephen W. Scherer, M. E. Suzanne Lewis. **Poster Presentation.**

34. ASPHO American Society of Pediatric Hematology/Oncology Conference April 21 - 24, 2021, Portland, Oregon. Childhood leukemia long-read transcriptomics based point of care diagnosis. Cielle Wachnian, Amanda Lorentzian, Ann Van Eyssen Pediatric, **Steven Jones,** Caron Strahlendorf. **Poster Presentation.**

35. ACMG American College of Medical Genetics and Genomics Annual Clinical Genetics Meeting, April 13-16, 2021, Virtual. Ethical Considerations in the Application of Advanced Genomic Testing for a Donor-Conceived Child. Stephanie Huynh, Alexandra Olmos Perez, Alice Virani, Cornelius F. Boerkoel, **Steven JM Jones**, Hui-Lin Chin. **Poster Presentation.**

36. ASCO GI Virtual Conference January 15-17, 2021. Beyond BRCA? Clinical Utility of Homologous Recombination Deficiency in Gastrointestinal Cancers. Erica S. Tsang, Veronika Csizmok, Laura M. Williamson, Erin Pleasance, James Topham, Joanna Karasinska, Emma Titmuss, Intan Schrader, Fergus Cafferty, Stephen Yip, Basile Cloutier, Karen Mungall, Tony Ng, Sophie Sun, Howard J. Lim, Jonathan M. Loree, Janessa Laskin, Marco Marra, **Steven Jones,** David F. Schaeffer, Daniel J. Renouf. **Poster Presentation.**

37. 10th Annual Conference on Head and Neck Cancer, Chicago, July 18-22, 2020. Development and validation of a miRNA-based prognostic signature in oral squamous cell carcinoma. Doha Itani, Mehul Kumar, Misha Bilenky, Steven C. Nakoneshny, Yussanne Ma, Andrew J. Mungall, Shamir Chandarana, Robert Hart, Thomas Wayne Matthews, **Steven J. M. Jones**, Joseph C. Dort, Pinaki Bose. **Poster Presentation.**

38. 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)**

39. International Society for Autism Research (INSAR) Annual Meeting May 6 – 9, 2020, Seattle, Washington, USA. Bringing Whole Genome Sequencing to the clinic: The iTARGET Autism Initiative (Individualized Treatments for Autism Recovery using Genetic-Environment Targets). Kristina Calli, Ying Qiao, Sally Martell, Heather MacRitchie, Jen Howe, Ali Sourkhou, **Steven Jones**, Michael Gallad, Stephen W. Scherer, Evica Separovic, Suzanne Lewis. **Poster Presentation.**

40. International Society for Autism Research (INSAR) Annual Meeting May 6 – 9, 2020, Seattle, Washington, USA. DNA copy number variants analysis from whole genome sequencing in families with non-syndromic Autism Spectrum Disorders. Ying Qiao, Kristina Calli, Sally Martell, Heather MacRitchie, Chieko Chiiwa, **Steven Jones**, Evica Rajcan-Separovic, Stephen W. Scherer, and Suzanne M. Lewis. **Poster Presentation.**

41. Single Cell Biology: Pushing New Frontiers in the Life Sciences. Florence, Italy, May 04 - 08, 2020. A high-throughput strand-specific protocol for full-length total RNA sequencing from single cells. Haile S, Corbett RD, LeBlanc VG, Wei L, Pleasance S, Bilobram S, Brown K, Trinh E, Smith J, Bala M, Chuah E, Mungall K, Moore RA, Mungall AJ, Coope RJ, Zhao Y, **Jones SJ**, Trinh DL, and Marra MA. **Poster Presentation.**

42. Sixth AACR-IASLC International Joint Conference: Lung Cancer Translational Science from the Bench to the Clinic, San Diego, California, January 11-14, 2020. Selectively targeting lung cancer with a novel small molecule that induces synthetic lethality through dual inhibition of disulfide reductases. Fraser D. Johnson, Sophie Jansen, Alvin Liu, Christina Brandstädter, Daniel Lu, Amy Nagelberg, Dylan Farnsworth, Tianna Sihota, Jianghong An, Giovanni C Forcina, Anna Prudova, Jennifer Luu, Poul H. Sorensen, Harold Varmus, Romel Somwar, Scott J. Dixon, **Steven J.M. Jones**, Katja Becker, Gregg B. Morin, William W. Lockwood. **Poster Presentation.**

43. CSHL Genome Informatics, Cold Spring Harbor, NY, November 6 – 9, 2019. Kwan H, Pleasance E, Titmuss E, Williamson L, Zhao E, Culibrk L, Bowlby R, Shen Y, Ashkani J, Mungall K, Chuah E, Moore R, Mungall A, Nelson J, Yip S, **Jones SJ**, Laskin J, Marra MA. The POG570 Cohort: An inquiry into the genomic landscape of treated advanced tumors. **Poster Presentation.**

44. Summit for Cancer Immunotherapy, Victoria, BC, October 20 – 23, 2019. Ashkani J, Titmuss E, Pleasance E, Pender A, Lavoie J, Williamson L, Jones M, Shen Y, Mungall K, Chuah E, Mungall A, Moore R, Zhao Y, Laskin J, Marra MA, **Jones SJ.** Biomarkers of Resistance to Immune-Checkpoint Inhibitors: Antibody-Drug Conjugate Target Discovery. **Poster Presentation.**

45. AGBT Precision Health, La Jolla, CA, September 5 – 7, 2019. Erin Pleasance*, Emma Titmuss*, Laura Williamson*, Harwood Kwan, Eric Zhao, Katherine Dixon, Kevin Fan, Luka Culibrk, Reanne Bowlby, Martin R Jones, Yaoqing Shen, Jasleen Grewal, Jahanshah Ashkani, Kathleen Wee, Cameron Grisdale, My Linh Thibodeau, Zoltan Bozoky, Hillary Pearson, Elisa Majounie, Tariq Vira, Reva Shenwai, Karen Mungall, Eric Chuah, Joshua Davies, Mya Warren, Caralyn Reisle, Melika Bonakdar, Gregory A Taylor, Veronika Csizmok, Simon Chan, Stuart Zong, Steve Bilobram, Amir Zadeh, Darryl D'Souza, Richard Corbett, Daniel MacMillan, Marcus Carreira, Caleb Choo, Dustin Bleile, Sara Sadeghi, Wei Zhang, Tina Wong, Dean Cheng, Richard Moore, Andrew Mungall, Yongjun Zhao, Jessica Nelson, Alexandra Fok, Robyn Roscoe, Yussanne Ma, Michael Lee, Jean-Michel Lavoie, Joanna Karasinska, Balvir Deol, Ana Fisic, David Schaeffer, Stephen Yip, Kasmintan Schrader, Dean Regier, Stephen Chia, Karen Gelmon, Anna Tinker, Sophie Sun, Howard Lim, Daniel Renouf, **Steven JM Jones**, Janessa Laskin, Marco A Marra. *These authors contributed equally. Cancer Genome Landscapes Shaped By Prior Therapy: The POG570 Cohort. **Poster Presentation.**

46. ISMB/ECCB 2019, Basel, Switzerland, July 12 – July 25, 2019. Emre Erhan, Karen Mungall, Richard Moore, Andrew J Mungall, Janessa Laskin, Marco Marra, **Steven JM Jones**. Support vector machines predict cancer patient therapy response from bulk RNA-seq. **Poster Presentation.**

47. ISMB Annual Meeting, Basel, Switzerland, July 21 - July 25, 2019. Luka Culibrk, Jasleen Grewal, Erin D Pleasance, Richard D Corbett, Karen L Mungall, Janessa Laskin, Marco A Marra, **Steven JM Jones**. Ploidetect: Interpretable detection of tumour purity and aneuploidy from whole-genome sequence data. **Poster Presentation.**

48. ISMB/ECCB 2019, Basel, Switzerland, July 21-25, 2019. Grewal JK, **Jones SJM.** Learning biologically meaningful representations of cancer transcriptomes with hierarchical Variational Bayes. **Oral Presentation**.

49. ASCO Annual Meeting, Chicago, IL, May 31 – Jun 4, 2019. Eric Y Zhao, Xiaolan Feng, Erin Pleasance, Tony Ng, Jasleen Grewal, Nissreen Mohammad, Sara Taylor, Christine Simmons, Amirrtha Srikanthan, Rod Rassekh, Rebecca Deyell, Yaoqing Shen, Emma Titmuss, Howard Lim, Daniel Renouf, Karen Gelmon, Stephen Yip, **Steven J.M. Jones**, Marco Marra and Janessa Laskin. The Whole Genome Landscape of Adult Metastatic Sarcoma. **Poster Presentation**.

50. ASCO Annual Meeting, Chicago, IL, May 31 – Jun 4, 2019. Jean-Michel Lavoie, Veronika Csizmok, Gang Wang, Laura Williamson, Marco Marra, Janessa Laskin, **Steven J.M. Jones,** Daniel J. Renouf and Christian K. Kollmannsberger. Whole genome and transcriptome analysis (WGTA) of metastatic adrenocortical carcinoma (mACC). **Poster Presentation.**

51. ASCO Annual Meeting, Chicago, IL, May 31 – Jun 4, 2019. Erica S. Tsang, Erin Pleasance, Cam Grisdale, Stephen Yip, Basile Cloutier, Karen Mungall, Tony Ng, Jessica Nelson, Sophie Sun, Howard J. Lim, Daniel J. Renouf, Janessa Laskin, Marco Marra, **Steven Jones**, Jonathan M. Loree. Uncovering Clinically Relevant Gene Fusion Events with Integrated Genomic and Transcriptomic Profiling. **Poster Presentation**.

52. 2nd ICGC-ARGO Meeting/Workshop (5th ICGC Scientific Workshop) Glasgow, Scotland, May 27-29, 2019. Emma Titmuss, Erin Pleasance, Laura Williamson, **Steven JM Jones,** Janessa Laskin, Marco A Marra. Pan-cancer analysis of advanced patient tumours reveals interaction between therapy and genomic landscapes. **Poster Presentation.**

53. 2nd ICGC-ARGO Meeting/Workshop (5th ICGC Scientific Workshop), Glasgow, Scotland, May 27-29, 2019. Deirdre Weymann, Janessa Laskin, **Steven J.M. Jones,** Howard Lim, Daniel J. Renouf, Robyn Roscoe, Kasmintan A. Schrader, Sophie Sun, Stephen Yip, Marco A. Marra, Dean A. Regier. An introduction and illustrative example of matching methods in precision oncology. **Poster Presentation.**

54. 2nd ICGC-ARGO Meeting/Workshop (5th ICGC Scientific Workshop), Glasgow, Scotland, May 27-29, 2019. Deirdre Weymann, Janessa Laskin, Howard Lim, Daniel J. Renouf, Robyn Roscoe, Kasmintan A. Schrader, Sophie Sun, Stephen Yip, Marco A. Marra, Dean A. Regier. Early-stage economic evaluation of whole-genome and transcriptome analysis to guide advanced cancer care. **Poster Presentation.**

55. 2nd ICGC-ARGO Meeting/Workshop (5th ICGC Scientific Workshop), Glasgow, Scotland, May 27-29, 2019. Veronika Csizmok, Erin Pleasance, Laura Williamson, Greg Taylor, Melika Bonakdar, Yaoqing Shen, Emma Titmuss, Kathleen Wee, Caralyn Reisle, Simon Chan, Wei Zhang, Sara Sadeghi, Reanne Bowlby, Dustin Bleile, Karen Mungall, Eric Chuah, Tina Wong, Richard Corbett, Richard Moore, Andrew Mungall, **Steven Jones**, Howard Lim, Daniel Renouf, Janessa Laskin, Marco Marra. Personalized oncogenomics: whole genome and transcriptome sequencing informs treatment decisions in the cancer clinic. **Poster Presentation.**

56. Keystone Conference on Cancer Immunotherapy, Whistler, BC Canada March 10 – 14, 2019. Emma Titmuss, Kevin Fan, Erin Pleasance, Laura Williamson, Hillary Pearson, James Topham, **Steve Jones**, Janessa Laskin, Marco Marra. Integrated genomic profiling of metastatic tumours to identify biomarkers of response to immune checkpoint inhibitors. **Poster Presentation**.

57. Keystone Conference on Cancer Immunotherapy, Whistler, BC Canada March 10 – 14, 2019. James T. Topham, Laura Williamson, Erin Pleasance, Luka Culibrk, Joanna M. Karasinska, Michael K.C. Lee, Emma Titmuss, Andrew J. Mungall, Richard A. Moore, Janessa Laskin, Marco A. Marra, **Steven J. Jones**, David F. Schaeffer, Daniel J. Renouf. Increased ERV expression is associated with predicted immunogenicity in a subset of metastatic cancers. **Poster Presentation.**

58. International Society for Autism Research (INSAR) Annual Meeting, Montreal, Canada, May 1 - May 4, 2019. Ying Qiao, Kristina Calli, Sally Martell, Simone Race, Chieko Chijiwa, Armanza Glodjo, Pat Mirenda, **Steven Jones**, Stephen W. Scherer, Evica Separovic, Suzanne Lewis. Contribution of multiple inherited and shared rare variants to Autism Spectrum Disorder (*ASD*) in a family with 3 affected siblings.

59. BC Cancer Summit, Vancouver, BC Canada November 23 – 24, 2018. Jasleen Grewal, **Steven Jones.** Bayesian Modelling Generates Compact Sample Representations that Recapitulate Gene Behaviour from Cancer Transcriptomes. **Poster Presentation**

60. BC Cancer Summit, Vancouver, BC Canada November 23 – 24, 2018. Grisdale C, Shen Y, Lai YY, Bose P, Lever J, 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**. Gene Expression And Tumour Microenvironment In Glioblastoma. **Poster Presentation.**

61. BC Cancer Summit, Vancouver, BC Canada November 23 – 24, 2018. Harwood Kwan, Erin Pleasance, Laura Williamson, Emma Titmuss, Mya Warren, Yaoqing Shen, Reanne Bowlby, Zoltan Bozoky, Jasleen Grewal, Joshua Davies, Amir Zadeh, Daryl D'Souza, Karen L Mungall, Eric Chuah, Richard A Moore, Andrew J Mungall, Jessica Nelson, Katherine Mui, Karen Gelmon, Anna Tinker, Sophie Sun, Howard Lim, Daniel Renouf, Janessa Laskin, Stephen Yip, Marco A Marra, **Steven JM Jones**. Exploratory Analysis of Recurrent Mutations Associated with Treatment in Metastatic Cancers. **Poster Presentation.**

62. BC Cancer Summit, Vancouver, BC Canada November 23 – 24, 2018. Kevin Fan, Erin Pleasance , Laura Williamson, Emma Titmuss, Hillary Pearson, Steve Bilobram, Simon Chan, Janessa Laskin, Marco Marra, **Steven Jones**. Genomic analysis of tumour-immune landscape and determinants of response to immune checkpoint inhibitors in Personalized OncoGenomics patients. **Poster Presentation.**

63. BC Cancer Summit, Vancouver, BC Canada November 23 – 24, 2018. Erin Pleasance, Laura Williamson, Martin Jones, Yaoqing Shen, Eric Zhao, Harwood Kwan, Reanne Bowlby, Emma Titmuss, Kevin Fan, Jasleen Grewal, Jahanshah Ashkani, Joshua Davies, Kevin Fan, Elisa Majounie, Zoltan Bozoky, Melika Bonakdar, Caralyn Reisle, Greg Taylor, Simon Chan, Stuart Zong, Amir Zadeh, Darryl D'Souza, Karen Mungall, Eric Chuah, Richard Moore, Andrew Mungall, Jessica Nelson, Katherine Mui, Yussanne Ma, Stephen Yip, Karen Gelmon, Anna Tinker, Sophie Sun, Howard Lim, Daniel Renouf, **Steven JM Jones,** Janessa Laskin, Marco Marra. Cancer genome landscapes shaped by prior therapy: The POG500 cohort. **Poster Presentation.**

64. American Association of Human Genetics (ASHG), San Diego, California, October 14 – 21, 2018. Jasleen Grewal, Sitanshu Gakkhar, Yussanne Ma, Yongjun Zhao, Andrew Mungall, Richard Moore, Howard Lim, Daniel Renouf, Karen Gelmon, Stephen Yip, Janessa Laskin, Marco Marra, **Steven JM Jones**. The transcriptome as a diagnostic aid - a pan cancer method for identifying the site of origin of complex metastases. **Poster Presentation.**

65. European Conference on Computational Biology (ECCB), Athens, Greece, September 8-12, 2018. Jasleen Grewal, **Steven Jones**. Inferring biological programs from cancer transcriptomes using Bayesian modeling. **Poster Presentation.**

66. AGBT 2018 Precision Health Meeting, La Jolla, California, 6-8 September, 2018. Elisa Majounie, Erin Pleasance, Martin Jones, Yaoqing Shen, Laura Williamson, Mya Warren, Jasleen Grewal, Harwood Kwan, Reanne Bowlby, Zoltan Bozoky, Emma Titmuss, Melika Bonakdar, Caralyn Reisle, Greg Taylor, Simon Chan, Stuart Zong, Amir Zadeh, Daryl D'Souza, Karen L Mungall, Eric Chuah, Richard A Moore, Andrew J Mungall, Jessica Nelson, Katherine Mui, Yussanne Ma, Stephen Yip, Karen Gelmon, Anna Tinker, Sophie Sun, Howard Lim, Daniel Renouf, **Steven JM Jones,** Janessa Laskin, Marco A Marra. Whole genome and transcriptome landscape of incurable pre-treated cancers is shaped by prior therapy and reveals unanticipated therapeutic targets. **Poster Presentation.**

67. American Society of Clinical Oncology (ASCO) Annual Meeting June 1-5, 2018. Chicago, Illinois.Tanya Skamene; Lillian L. Siu; Daniel Renouf; Janessa Laskin; Philippe Bedard; **Steven Jones**; Christiano Ferrario; Jim Whitlock; Joan Petrie; Patrick Sullivan; Eoghan Malone; Dora Nomikos; Bingshu Chen; Janet Dancey. Canadian profiling and targeted agent utilization trial (captur/): a phase ii basket trial.

68. International Association for Aquatic Animal Medicine (IAAAM) Meeting and Conference May 19 - 23, 2018, Renaissance Long Beach in Long Beach, California. Martin Haulena,* Samantha J. Jones, Greg A. Taylor, Dustin Bleile, Morgan Bye, An He, Richard Corbett, Caleb Choo, Eric Chuah, Karen Mungall, Graham W. Slack, Barbara Linnehan, Karisa Tang, Stephen Raverty, Andrew Mungall, Richard Moore, Robin Coope, Yongjun Zhao, Yussanne Ma, Marco Marra, and **Steven J.M. Jones**. MOLECULAR CHARACTERIZATION OF LYMPHOMA IN NORTHERN SEA OTTERS (*Enhydra lutris kenyoni*)

69. RECOMB April 21-24, 2018, Paris, France. Jackman SD, Coombe L, Chu J, Warren RL, Vandervalk BP Yeo S, Xue , Mohamadi H, Bohlmann J, **Jones SJM**, Birol I. Tigmint: correct assembly errors using linked reads from large molecules [version 1; not peer reviewed]. F1000Research 2018, 7:481 (poster) (doi: 10.7490/f1000research.1115395.1)

70. AACR Annual Meeting, April 14-18, 2018. Chicago, Illinois, USA. Martin R Jones, Yaoqing Shen, Erin Pleasance, Elisa Majounie, Laura Williamson, Eric Zhao, Eric Chuah, Karen L. Mungall, Andrew J. Mungall, Richard A. Moore, Yussanne Ma, Stephen Yip, Howard Lim, Daniel Renouf, **Steven J.M. Jones**, Janessa Laskin, Marco A. Marra. Integrating whole genome and transcriptome analysis to inform treatment decisions in the metastatic cancer clinical setting. **(Poster Presentation).**

71. 107th United States and Canadian Academy of Pathology Annual Meeting (USCAP), March 17-23 2018 Vancouver, BC.. Basile Tessier-Cloutier, Jasleen Grewal, Martin Jones, Erin Pleasance, Ellia Zhang, Karen Mungall, Tae Hoon Lee, Ellen Cai, Brandon S Sheffield, Cheng Han Lee, Lien Hoang, Brian Skinnider, Tyler Smith, David F Schaeffer, Anna Lee, Tony Ng, Diana Ionescu, Torsten Nielsen, Chris Dunham, **Steven Jones**, Janessa Laskin, Marco Marra, Stephen Yip. Genomic Integrative Pathology: A Large Scale Tumour Next Generation Sequencing Initiative. (**Poster Presentation).**

72. 18th Annual AGBT: General Meeting, February 12-15, 2018. Orlando, Florida, USA. Martin R. Jones, Yaoqing Shen, Erin Pleasance, Eric Zhao, Karen L. Mungall, Andrew J. Mungall, Richard A. Moore, Yussanne Ma, **Steven J.M. Jones,** Janessa Laskin, Marco A. Marra: Whole genome and transcriptome analysis in a metastatic cancer clinical setting. **(Poster Presentation).**

73. 4th Canadian Cancer Research Conference November 5 – 7, 2017, Vancouver, BC. Cameron Grisdale, Yaoqing Shen, Pinaki Bose, Jake Lever, Natalie Grinshtein, Eric Zhao, Yuk Yin Lai, Yussanne Ma, Andrew J. Mungall, Richard A. Moore, Donna L. Senger, Stephen M. Robbins, H. Artee Luchman, Samuel Weiss, Jennifer A. Chan, Michael D. Blough, Gregory Cairncross, David Kaplan, Marco A. Marra, **Steven JM**

**Jones**. Patterns of gene expression and somatic variation in matched tumours and tumour-derived model systems of Glioblastoma

74. 4th Canadian Cancer Research Conference November 5 – 7, 2017, Vancouver, BC. Jasleen Grewal, Sitanshu Gakkhar, Yussanne Ma, Yongjun Zhao, Andrew Mungall, Richard Moore, Howard Lim, Daniel Renouf, Karen Gelmon, Stephen Yip, Janessa Laskin, Marco Marra, **Steven Jones.** Using machine learning to identify the site of origin of metastatic tumours

75. 4th Canadian Cancer Research Conference November 5 – 7, 2017, Vancouver, BC. Jianghong An, Julie Rousseau, Zhengxing Zhang, Kuo-Shyan Lin, Francois Benard, **Steven Jones**. In silico evaluation and optimization of matriptase-binding compounds as radio-labeling candidates for PET imaging of invasive cancer

76. 4th Canadian Cancer Research Conference November 5 – 7, 2017, Vancouver, BC. Hillary Pearson, Erin Pleasance, Scott Brown, Emma Titmuss, Martin Jones, Stuart Zong, Payal Sipahimalani, Yussanne Ma. Robert Holt, **Steven Jones**, Stephen Yip, Howard Lim, Daniel Renouf, Marco Marra, Janessa Laskin. Genomic biomarkers of response to checkpoint inhibitor immunotherapy in the Personalized OncoGenomics cohort

77. 4th Canadian Cancer Research Conference November 5 – 7, 2017, Vancouver, BC . Yaoqing Shen, Yuk Yin Lai, Pinaki Bose, Cameron Grisdale, Natalie Grinshtein, Eric Zhao, Yussanne Ma, Andrew J. Mungall, Richard A. Moore, Donna L. Senger, Stephen M. Robbins, H. Artee Luchman, Samuel Weiss, Jennifer A. Chan, Michael D. Blough, Gregory Cairncross, David Kaplan, Marco A. Marra, **Steven JM Jones.** Comprehensive genomic profiling of matched glioblastoma tumours, cell-lines, and xenografts

78. 4th Canadian Cancer Research Conference November 5 – 7, 2017, Vancouver, BC. Sreeja Leelakumari, Oleksandr Yakovenko, Jianghong An, Andy Mungall, Keith Humphries, **Steven Jones**. Identification and Characterization of Small Molecules which modulate Epigenetic Reprogramming of BPTF in MLL2 mutant Lymphomas.

79. 4th Canadian Cancer Research Conference November 5 – 7, 2017, Vancouver, BC**.** Jahanshah Ashkani, D Dargahi, PJ Bergqvist, I Samudio, PHW Chan, J Rousseau, **SJ Jones.** Pan-Cancer Identification And Prioritization Of Cancer-Associated Genes: A Biomarker Discovery Application.

80. 4th Canadian Cancer Research Conference November 5 – 7, 2017, Vancouver, BC**.** Laura Williamson, Hui-li Wong, Eric Zhao, Martin Jones, Caralyn Reisle, Peter Eirew, Erin Pleasance, Joanna Karasinska, Steve Kalloger, Howard Lim, Yaoqing Shen, Stephen Yip Jenessa Laskin, Marco Marra, **Steven Jones**, Kasmintan Schrader, David Schaeffer, Daniel Renouf.

81. 4th Canadian Cancer Research Conference November 5 – 7, 2017, Vancouver, BC**.** Chun Hye-Jung E; Johann Pascal D; Bilenky Mikhail; Lim Emilia; Heravi-Moussavi Alireza; Cheng Dean; Cheng Young; Wong Tina; Chuah Eric; Thiessen Nina; Ma Yussanne; Gerhard Daniela S; Mungall Andrew J; Moore Richard A; **Jones Steven JM**; Perlman Elizabeth J; Hirst Martin; Huang Annie; Kool Marcel; Marra Marco A. Extra-cranial rhabdoid tumours exhibit molecular similarities to the MYC-subgroup of AT/RTs

82. 4th Canadian Cancer Research Conference November 5 – 7, 2017, Vancouver, BC**.** Emily Yun-Chia Chang, Carolina A. Novoa, Maria J. Aristizabal, Yan Coulombe, Mr. Romulo Segovia, Yaoqing Shen, Christelle Keong, **Steven J.M. Jones,** Jean-Yves Masson, Michael S. Kobor, Peter C. Stirling. Understanding the role of DNA repair factors in regulating R-loop-mediated cancer genome instability.

83. 4th Canadian Cancer Research Conference November 5 – 7, 2017, Vancouver, BC**.** Martin Jones, Yaoqing Shen, Erin Pleasance, Laura Williamson, Eliza Majounie, Melika Bonakdar, Simon Chan, Carolyn Ch'ng, Caralyn Reisle, Greg Taylor, Reanne Bowlby, Brandon Peirce, Sara Sadeghi, Amir Zadeh, Wei Zhang,

Karen Mungall, Nina Thiessen, Andy Mungall, Richard Moore, Yussanne Ma, **Steven Jones**, Janessa Laskin, Marco Marra. Taking whole genomes to the cancer clinic: Integrative analysis for interpretation and communication of whole genome and transcriptome analysis.

84. 4th Canadian Cancer Research Conference November 5 – 7, 2017, Vancouver, BC. Romulo Segovia, Yaoqing Shen, **Steven Jones**, Peter Stirling. Quantifying gene-drug interactions by synthetic hypermutation and deep sequencing.

85. 4th Canadian Cancer Research Conference November 5 – 7, 2017, Vancouver, BC. My Linh Thibodeau, Melika Bonakdar, Karen L. Mungall, Nina Thiessen, Andrew J. Mungall, Yussanne P. Ma, Martin R. Jones, Daniel J. Renouf, Howard J. Lim, Stephen Yip, Tony Ng, Cheryl Ho, Janessa Laskin, Marco A. Marra, Kasmintan A. Schrader, **Steven J.M. Jones**. Whole-Genome and Whole-Transcriptome Profiling of a Metastatic Eccrine Porocarcinoma.

86. 8th TFRI Annual Scientific Meeting November 4, 2017, Vancouver, BC . Cameron Grisdale, Yaoqing Shen, Pinaki Bose, Jake Lever, Natalie Grinshtein, Eric Zhao, Yuk Yin Lai, Yussanne Ma, Andrew J. Mungall, Richard A. Moore, Donna L. Senger, Stephen M. Robbins, H. Artee Luchman, Samuel Weiss, Jennifer A. Chan, Michael D. Blough, Gregory Cairncross, David Kaplan, Marco A. Marra, Steven JM Jones. Patterns of gene expression and somatic variation in matched tumours and tumour-derived model systems of Glioblastoma

87. TFRI ASM (TFRI 8th Annual Scientific Meeting) held in Vancouver, Canada, November 4, 2017. Ashkani J, Dargahi D, Bergqvist PJ, Samudio I, Chan PHW, Rousseau J, **Jones SJ**. Pan-Cancer Identification And Prioritization Of Cancer-Associated Genes: A Biomarker Discovery Application. **Rapid-fire talk**

88. AACR-NCI-EORTC International Conference on Molecular Targets and Cancer Therapeutics: Discovery, Biology, and Clinical Applications, Philadelphia, PA Oct 26-30, 2017. Yaoqing Shen, Martin R. Jones, Erin Pleasance, Melika Bonakdar, Carolyn Ch'ing, Caralyn Reisle, Laura Williamson, Elisa Majounie, Greg Taylor, Simon Chan, Young Song, Brandon Pierce, Wei Zhang, Amir Muhammadzadeh, Eric Y. Zhao, Dustin Bleile, Karen Mungall, Nina Thiessen, Eric Chuah, Tina Wong, Richard Corbett, Yussanne Ma, Richard A. Moore, Andrew J. Mungall, Yongjun Zhao, Stephen Yip, Anna F. Lee, Rod Rassekh, Rebecca Deyell, Howard Lim, Daniel Renouf, Robyn Roscoe, **Steven J. M. Jones**, Janessa Laskin, Marco A. Marra. Clinical application of whole genome and transcriptome sequencing in cancer care. **Poster Presentation.**

89. The International Conference of Physics Students, Turin, Italy. August 7-14, 2017. Jenny Yang, Jasleen Grewal, **Steven Jones.** Identifying Functional Clusters of Genes from Energy Landscapes in Autoencoders for Personalized Therapy in Medicine.

90. ISMB/ECCB 2017, 21-25th July, Prague, Czech Republic. Jasleen Grewal, Sitanshu Gakkhar, Yussanne Ma, Yongjun Zhao, Andrew Mungall, Richard Moore, Howard Lim, Daniel Renouf, Karen Gelmon, Stephen Yip, Janessa Laskin, Marco Marra, **Steven J.M. Jones**. Using machine learning to identify site of origin of metastatic tumours. **Poster Presentation**

91. BioNLP Workshop, Association of Computational Linguistics 2017 Conference, Vancouver, BC, July 30 - August 4 2017. Jake Lever and **Steven Jones**. Painless Relation Extraction with Kindred. **Poster Presentation.**

92. Summit4CI (Summit for Cancer Immunotherapy by BioCanRx) held in Ottawa, Canada, June 25-28, 2017. Ashkani J, Dargahi D, Bergqvist PJ, Samudio I, Chan PHW, Rousseau J, **Jones SJ**. Pan-Cancer Identification And Prioritization Of Cancer-Associated Genes: A Biomarker Discovery Application. **Poster presentation**

93. Personalized Medicine Summit 2017. Sunday June 11th-Tuesday June 13th, 2017 Vancouver, Canada**.** Erin Pleasance, Martin Jones, Yaoqing Shen, Laura Williamson, Melika Bonakdar, Carolyn Ch'ing, Caralyn Reisle, Elisa Majounie, Greg Taylor, Young Song, Simon Chan, Wei Zhang, Amir Zadeh, Brandon Pierce, Sara Sadeghi, Reanne Bowlby, Dustin Bleile, Karen Mungall, Nina Thiessen, Eric Chuah, Tina Wong, Richard Corbett, Yussanne Ma, **Steven Jones**, Howard Lim, Daniel Renouf, Janessa Laskin, Marco Marra. Personalized oncogenomics: whole genome and transcriptome sequencing informs treatment decisions in the cancer clinic.

94. Graspods Annual Research Day, June 5th, 2017, BC Cancer Research Centre (Vancouver). Jasleen Grewal, Sitanshu Gakkhar, Yussanne Ma, Yongjun Zhao, Andrew Mungall, Richard Moore, Howard Lim, Daniel Renouf, Karen Gelmon, Stephen Yip, Janessa Laskin, Marco Marra **Steven J.M. Jones**. Using machine learning to identify site of origin of metastatic tumours. **Poster Presentation**

95. Genome BC 15th Annual Genomics Forum: The Genome Engineering Revolution (CRISPR and SYNBIO), May 25th, 2017, UBC (Vancouver). Jasleen Grewal, Sitanshu Gakkhar, Yussanne Ma, Yongjun Zhao, Andrew Mungall, Richard Moore, Howard Lim, Daniel Renouf, Karen Gelmon, Stephen Yip, Janessa Laskin, Marco Marra **Steven J.M. Jones**. Using machine learning to identify site of origin of metastatic tumours. **Poster Presentation**

96. The Canadian Associate of Medical Oncologists (CAMO) Annual Scientific Meeting, Toronto, Ontario, April 27, 2017. Negar Chooback, Cheryl Ho, Yaoqing Shen, Erica Tsang, Yongjun Zhao, Andrew Mungall, Richard Moore, Howard Lim, Daniel Renouf , Karen Gelmon, Stephen Yip, **Steven J.M. Jones**, Janessa Laskin, Marco Marra. Whole genome sequencing (WGS) analysis of lung adenocarcinoma: elucidating the molecular signature.

97. AACR Annual Meeting, April 1-5, 2017 Washington, DC. Eric Y Zhao, Yaoqing Shen, Erin Pleasance, Katayoon Kasaian, Martin Jones, Carolyn Ch'ng, Caralyn Reisle, Peter Eirew, Karen L Mungall, Nina Thiessen, Yussanne Ma, Alexandra Fok, Andrew J Mungall, Yongjun Zhao, Richard A Moore, Diego Villa, Tamara Shenkier, Caroline Lohrisch, Stephen Chia, Stephen Yip, Karen Gelmon, Howard Lim, Sophie Sun, Kasmintan A Schrader, Sean Young, Aly Karsan, Robyn Roscoe, Janessa Laskin, Marco A Marra, **Steven JM Jones.** Breast Cancer Whole Genomes Link Homologous Recombination Deficiency (HRD) with Therapeutic Outcomes

98. Biocuration 2017, Stanford University, California, March 26th - 29th 2017. Jake Lever, Obi Griffith, Malachi Griffith and **Steven Jones**. CIViCmine: Assisting curation of the CIViC resource using relation extraction. **Oral Presentation.**

99. 7th Annual Bioinformatics and Integrative Genomics Research Day, March 9th, 2017, UBC, Vancouver. Jasleen Grewal, Sitanshu Gakkhar, Yussanne Ma, Yongjun Zhao, Andrew Mungall, Richard Moore, Howard Lim, Daniel Renouf, Karen Gelmon, Stephen Yip, Janessa Laskin, Marco Marra, **Steven J.M. Jones**. Using machine learning to identify site of origin of metastatic tumours. **Poster Presentation.**

100. Keystone Symposia, Whistler, BC March 5-9, 2017. Karasinska JM, Kalloger SE, Wong H, Jones M, Eirew P, Shen Y, Reisle C, Taylor G, Chan S, Ch'ng C, **Jones SJ**, Laskin J, Marra MA, Schaeffer DF, Renouf DJ. Prognostic metabolic signature associated with mutant *KRAS* copy gain in pancreatic ductal adenocarcinoma. **Poster Presentation.**

101. 17th Annual AGBT: General Meeting, February 13-16, 2017. Hollywood, Florida, USA. Martin Jones, Yaoqing Shen, Erin Pleasance, Melika Bonakdar, Carolyn Ch'ing, Caralyn Reisle, Young Song, Greg Taylor, Simon Chan, Wei Zhang, Amir Zadeh, Karen Mungall, Nina Thiessen, Eric Chuah, Tina Wong, Richard Corbett, Yussanne Ma, **Steven Jones**, Janessa Laskin, Marco Marra. Taking whole genomes to the cancer clinic: Integrative analysis for interpretation and communication of whole genome and transcriptome analysis at a tumour board. **(Oral Prentation.)**

102. 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.

103. 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.

104. CSCI-CITAC Annual Scientific Meeting. Toronto, ON. Nov 22-23, 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.

105. 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.

106. 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

107. The American Society of Human Genetics, (ASHG) October 20, 2016, Vancouver, Canada. Thibodeau M.L., Peters C.H., Townsend K., Shen Y., Hendson G., Adam S., Selby K., Macleod P.M., Gershome C., Ruben P., **Jones S.,** the FORGE Canada Consortium, Friedman J.M., Gibson W., Horvath G., Compound heterozygous *TRPV4* mutations causing severe intellectual disability, neuropathy, myopathy and skeletal involvement. **Poster Presentation.**

108. Till & McCulloch Meetings, Whistler, BC October 24 -26, 2016. Davide Pellacani, Misha Bilenky, Nagarajan Kannan, Alireza Heravi-Moussavi,David J.H.F. Knapp, Sitanshu Gakkhar, Michelle Moksa, Annaick Carles, Richard Moore, Andrew Mungall, Marco A. Marra, **Steven J.M. Jones**, Samuel Aparicio, Martin Hirst, Connie J Eaves. Human Mammary cell transcription factor networks predicted from analyses of differences in enhancer states.

109. American Society of Human Genetics (ASHG) Conference. Vancouver, Canada 18th-22th October 2016. Jake Lever & **Steven JM Jones**. A fast and easy to use framework for automatic biological knowledge base construction. **(Poster Presentation)**

110. 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.

111. 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, Roscoe R, Laskin J, Marra MA, **Jones SJM**. Guiding Platinum-based Chemotherapy with a Somatic Mutation Signature of BRCA1/2 Impairment.

112. AGBT: Precision Health Meeting , September 22-24, 2016. Scottsdale, Arizona, USA. Martin Jones, Yaoqing Shen, Erin Pleasance, Carolyn Ch'ng, Caralyn Reisle, Melika Bonakdar, Simon Chan, Greg Taylor, Young Song, Richard Corbett, Karen L Mungall, Nina Thiessen, Eric Chuah, Tina Wong, Alexandra Fok, Richard A Moore, Andrew J Mungall, Yongjun Zhao, Stephen Yip, Karen Gelmon, Howard Lim, Daniel Renouf, Anna Tinker, Sophie Sun, Robyn Roscoe, Yussanne Ma, **Steven JM Jones**, Janessa Laskin, Marco A Marra. A Bioinformatics Pipeline to Facilitate Interpretation and Delivery of Personalized OncoGenomic Data to Assist in Clinical Decision Making **(POSTER)**

113. Canadian Conference on Epigenetics/CEEHRC annual meeting, Esterel, Quebec. September 18-21, 2016. M Bilenky, S Gakkhar, **S Jones,** M Hirst. FindER: A Sensitive Analytical Tool to Study Epigenetic Modifications and Protein-DNA Binding from ChIP-Seq data

114. Canadian Conference on Epigenetics/CEEHRC annual meeting, Esterel, Quebec. September 18-21, 2016. Davide Pellacani, Misha Bilenky, Nagarajan Kannan, Alireza Heravi-Moussavi,David J.H.F. Knapp, Sitanshu Gakkhar, Michelle Moksa, Annaick Carles, Richard Moore, Andrew Mungall, Marco A. Marra, **Steven J.M. Jones**, Samuel Aparicio, Martin Hirst*, Connie J Eaves*. Derivation of transcription factor networks from analyses of active enhancer states in different subsets of normal human mammary cells. * *co-last authors*

115. Cold Spring Harbor Laboratory Meeting on Epigenetics & Chromatin. New York, NY. Sep 13-17, 2016. Chun H-J E, 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)**

116. BLUEPRINT / IHEC meeting Brussels, Belgium. September 4-10, 2016. CJ Eaves, D Pellacani, M Bilenky, N Kannan, A Heravi-Moussavi, DJHF Knapp, S Gakkhar, M Moksa, A Carles, R Moore, A Mungall, MA Marra, **SJM Jones,** S Aparicio & M Hirst· Molecular determinants of functionally distinct normal human mammary cell types.

117. BLUEPRINT / IHEC meeting Brussels, Belgium. September 4-10, 2016. M Bilenky, S Gakkhar, **S Jones,** M Hirst. FindER: A Sensitive Analytical Tool to Study Epigenetic Modifications and Protein-DNA Binding from ChIP-Seq data

118. BioNLP Workshop at Association of Computational Linguistics Conference. Berlin, Germany August 12-13, 2016. Jake Lever & **Steven JM Jones**. VERSE: Relation and Event Extraction in the BioNLP 2016 Shared Task. **(Poster and Oral Presentation)**

119. International Conference on Biological Ontology & BioCreative. Corvallis, Oregon, USA August 1, 2016. Jake Lever, Martin Jones & **Steven JM Jones**. CancerMine: Knowledge base construction for personalised cancer treatment. (**Oral Presentation.)**

120. 16th IUBMB Conference. Vancouver, BC. July17-21, 2016. **Jones SJM** on behalf of BC Cancer Agency's Personalized OncoGenomics Project. Cancer Genomics and Personalized Medicine **(Platform presentation)**

121. Intelligent Systems for Molecular Biology (ISMB) Conference Orlando, Florida, July 8-12, 2016. Celia Siu, Sitanshu Gakkhar, Alireza Heravi-Moussavi, Misha Bilenky, Annaick Carles, Thomas Sierocinski, Angela Tam, Eric Zhao, Katayoon Kasaian, Richard Moore, Andy Mungall, Blair Walker, Thomas Thomson, Sam Wiseman, Marco Marra, Martin Hirst, **Steven Jones**. Bioinformatic characterization of the normal thyroid reference epigenome.

122. Regulatory Genomics Special Interest Group Conference, Orlando, Florida, July 8-12, 2016. Celia Siu, Sitanshu Gakkhar, Alireza Heravi-Moussavi, Misha Bilenky, Annaick Carles, Thomas Sierocinski, Angela Tam, Eric Zhao, Katayoon Kasaian, Richard Moore, Andy Mungall, Blair Walker, Thomas Thomson, Sam

Wiseman, Marco Marra, Martin Hirst, **Steven Jones**. Bioinformatic characterization of the normal thyroid reference epigenome.

123. High Throughput Sequencing Conference, Orlando, July 8 – 12, 2016. Jackman SD, Warren RL, Gibb E, Vandervalk BP, Mohamadi H, Chu J, Raymond A, Pleasance S, Coope R, Wildung MR, Ritland C, Bousquet J, **Jones SJM,** Bohlmann J, Birol I**.** Organellar Genomes of White Spruce (Picea glauca): Assembly and Annotation

124. 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, Renouf DJ. Comprehensive genomic analysis in metastatic pancreatic ductal adenocarcinoma (PDAC). (ASCO Annual Meeting Proceedings. 2016; 34 (4_suppl): 285. )

125. TFRI 7th Annual Scientific Meeting. Vancouver, BC. May 12-14, 2016. Chun H-Y E, 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.

126. AACR 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)

127. AACR 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.

128. AACR 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.

129. VanBug Seminar, Vancouver, BC, March 2016. Chun H-Y, Lim EL, Heravi-Moussavi A, Modaber SS, 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". **Oral Presentation.**

130. 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)**

131. 7th International Conference on Drug Discovery and Therapy, University of Sharjah, Sharjah, UAE, February 2016. Sreeja Leelakumari, Oleksandr Yakovenko, Mor Ngom, Jianghong An, Andy J. Mungall, R. Keith Humphries and **Steven J.M. Jones.** The generation of an artificial triple complex to orchestrate the epigenetic reprogramming of BPTF in MLL2 mutant lymphomas (**Poster Presentation)**

132. The 16th Annual AGBT Meeting. Orlando, FL. Feb 10-13, 2016. Moore RA, Shen Y , 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. **Poster Presentation**

133. The 16th Annual AGBT: General Meeting, February 10-13, 2016. Orlando, Florida, USA. Martin Jones, Yaoqing Shen, Erin Pleasance, Carolyn Ch'ng, Caralyn Reisle, Melika Bonakdar, Young Song, Richard Corbett, Karen L Mungall, Nina Thiessen, Eric Chuah, Tina Wong, Katayoon Kasaian, Sreeja Leelakumari, Peter Eirew, Alexandra Fok, Richard A Moore, Jacquie Schein, Andrew J Mungall, Yongjun Zhao, Stephen Yip, Karen Gelmon, Howard Lim, Daniel Renouf, Anna Tinker, Sophie Sun, Robyn Roscoe, Yussanne Ma, **Steven JM Jones**, Janessa Laskin, Marco A Marra. Utilization of Whole Genome Analysis Approaches for Personalized Therapy Decision Making in Patients with Advanced Malignancies **(Poster Presentation)**

134. 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. **Poster Presentation**

135. 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 RNASeq Pipeline Allows High Throughput Processing of Low Input Samples. **Poster Presentation**

136. 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. **Poster Presentation**

137. 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. **Poster Presentation**

138. 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. **Poster Presentation**

139. BC Cancer Research Centre Thursday Oncology Seminar Series. Vancouver, BC. Nov 2015. Chun H-Y, 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 subgroup. **(Oral presentation)**

140. 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)**

141. The Canadian Cancer Research Conference 2015; November 8-11, 2015; Montreal, QC. **S Jones**, J Voong, R Thomas, A English, J Schuetz, GW Slack, J Graham, JM Connors and A Brooks-Wilson. Non-random occurrence of Hodgkin lymphoma, non-Hodgkin lymphoma, myeloma and chronic lymphocytic leukemia in lymphoid cancer families. **Poster Presentation.**

142. 6th Annual Gained in Translation Summit Meeting. Portland, USA. October 24, 2015. de Leeuw CN, Korecki AJ, Berry GE, Hickmott JW, Lam SL, Lengyell TC, Bonaguro RJ, Borretta L, Chou AY, D'Souza CA, Kaspieva O, Laprise S, McInerny SC, Portales-Casamar E, Swanson-Newman MI, Wong K, Yang GS, Zhou M, **Jones SJM**, Holt RA, Asokan A, Goldowitz D, Wasserman WW and Simpson EM. rAAV-Compatible MiniPromoters with restricted expression in the Brain and Eye; including ganglion, bipolar, and Müller glia cells

143. American Society for Human Genetics Annual Meeting; Oct. 6-10, 2015; Baltimore, MD, USA. **Jones S**, Voong J, Thomas R, English A, Schuetz J, Slack GW, Graham J, Connors JM and A Brooks-Wilson. Non-random occurrence and early age of onset of diverse lymphoid cancers in families supports the existence of genetic risk factors for multiple lymphoid cancers

144. Canadian Association of Genetic Counselors Annual Meeting; September 9-12, 2015; Ottawa, ON. Thomas R, **Jones S**, Voong J, English A, Schuetz J, Slack G, Graham J, Connors J, Brooks-Wilson A. Analysis of inheritance patterns of lymphoid cancer in Canadian families. **(Poster Presentation).**

145. Intelligent Systems for Molecular Biology / European Conference on Computational Biology, Dublin July 2015. Warren RL, Vandervalk BP, Yang C, **Jones SJM**, Birol I. "Scaffolding draft genomes with long reads."

146. High Throughput Sequencing Conference, Dublin, July 2015. Warren RL, Vandervalk BP, Yang C, **Jones SJM**, Birol I. "Scaffolding draft genomes with LINKS."

147. In Proceedings of 5th Symposium on Biological Data Visualization (BioVis 2015), Dublin, Ireland July 10-11, 2015. Hamid Younesy, Torsten Möller, Matthew C Lorincz, Mohammad M Karimi, and **Steven JM Jones**. VisRseq: R-based visual framework for analysis of sequencing data. **Oral Presentation. Published Aug. 13, 2015**

148. InterLymph Annual Meeting, Groningen, NL. June 22-25, 2015. **S Jones**, J Voong, R Thomas, A English, J Schuetz, GW Slack, J Graham, JM Connors and A Brooks-Wilson. Non-random occurrence of lymphoid cancers in families. **(Poster)**

149. 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.

150. 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.

151. ISSCR Stockholm, Sweden, June 2015. Heravi-Moussavi A, Raghavan K, Bilenky M, Carles A, Moore R, Mungall A, **Jones S**, Marrra MA, Larocque N, Fisher SJ, Costello JF, Hirst M. "Expression and Epigenetic States of Human Embryonic Stem Cells Under Endogenous Oxygen Tension". **(Poster)**

152. 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).

153. 9th Annual Canadian Neuroscience Meeting, Vancouver, BC. May 25, 2015. Korecki, A.J., de Leeuw, C.N., Lam, S., Berry, G.E., Hickmott, J.W., Lengyell, T.C., Bonaguro, R.J., Borretta, L., Chou, A.Y., Kaspieva, O., Laprise, S., McInerny, S.C., Portales-Casmar, E., Swanson, M.I., Wong, K., Yang, G.S., Zhou, M., Holt, R.A., **Jones, S.J.M.,** Wasserman, W.W., Asokan, A., Goldowitz, D., and Simpson, E.M. AAV-compatible MiniPromoters Target Specific Celltypes of the Central Nervous System (Poster).

154. Genome British Columbia 13th Annual Genomics Forum. University of British Columbia Pharmaceutical Building, 8th May 2015. Jennifer Asano, Naz AzRahimi, Sundeep Chahal, Stephanie Cho, Merinda Deng, Baljit Kamoh, Amy Leung, Diana Mah, Corey Matsuo, Nasrin M. Mawji, Ken Thorne, Eva K. Trinh, Adrian Ally, Noreen Dhalla, Angela Tam, Rob Holt, **Steven J. Jones,** Marco A. Marra, Andrew J. Mungall. Preparing for the Deluge-Developments in High-Throughput Sample Preparation and Library Construction.

155. 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)**

156. 2015 AACR annual meeting, Philidelphia, Pennsylvania April 18 – 22, 2015. Daryanaz Dargahi, Leanna Yee, Peter J. Bergqvist, Richard D. Swayze, Edie M. Dullaghan, Jianghong An, Bradley J. Hedberg, Ryan Dercho, Christopher Bond, John S. Babcook, **Steven J.M. Jones.** Pan-Cancer Identification and Prioritization of Cancer-Associated Differentially Expressed Genes: A Biomarker Discovery Application. **Poster Presentation.**

157. The Canadian Human and Statistical Genetics Meeting; April 18-21, 2015; Vancouver, BC. D Liu, **S Jones,** R Thomas, GW Slack, JM Connors, A Brooks-Wilson and J Graham. Is There Anticipation in the Age at Onset of Familial Lymphoid Cancers?

158. The Canadian Human and Statistical Genetics Meeting; April 18-21, 2015; Vancouver, BC. C Nieuwoudt, **S Jones**, R Thomas, GW Slack, JM Connors, A Brooks-Wilson and J Graham*. Prioritizing rare variants in lymphoid cancer families. **(Poster)**

159. The Canadian Human and Statistical Genetics Meeting; April 18-21, 2015; Vancouver, BC**. S Jones**, J Voong, R Thomas, A English, J Schuetz, GW Slack, J Graham, JM Connors and A Brooks-Wilson. Non-random occurrence of lymphoid cancers in 141 lymphoid cancer families. **(Poster)**

160. 204th 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 Intergation of Next Generation Sequencing With Glass-Based Histomorphology and Immunohistochemistry. (Mod Pathol. 2015 Feb; 28:465A Suppl 2)

161. 2015 AGBT Meeting. Marco Island, Florida, February 25-28, 2015. Mungall A, Ben-Neriah S, Boyle M, Corbett R, Costa S, Cromwell I, Docking R, Fok A, Hother C, Hung S, Kasaian K, Leelakumari S, Meissner B, Mungall K, Pleasance E, Roos A, Scott D, Shen Y, Swanson L, Tam A, Thiessen N, Tse K, Yang L, Zeng T, Zhao Y, Ma Y, Moore R, Roscoe R, Schein J, **Jones S**, Laskin J, Peacock S, Steidl C, Gascoyne R, Karsan A, Connors J, Marra M. Generating targeted and genome-wide data for cancer patients in a clinically meaningful timeframe. **( Poster Presentation)**

162. Clinical Investigator Trainee Association of Canada, Toronto, Canada, November 24 – 26, 2014. Zhao EY, 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 Y, Moore RA, Wilson S, Villa D, Shenkier T, Lohrisch C, Chia S, Yip S, Gelmon K, Lim H, Renouf D, Sun S, Roscoe R, Laskin J, Marra MA, **Jones SJM**. Searching for Targetable Mutation Signatures in a Mixed Cancer Cohort. **Poster Presentation**.

163. 4th Annual TFRI BC Node Research Day, Vancouver, Canada, November 13, 2014. Kasaian K, Shen Y, Leelakumari S, Eirew P, Li Y, Pleasance E, Corbett R, Mungall K, Schein J, Mungall A, Zhao Y, Moore R, Yip S, Gelmon K, Lim H, Renouf D, Roscoe R, Ma Y, Marra M, Laskin J, **Jones S.** Bioinformatic analyses approaches for personalized Oncogenomics. **Poster Presentation**

164. Beyond the Genome, Boston, USA, October 8-10, 2014. Kasaian K, Shen Y, Leelakumari S, Pleasance E, Jones M, Li YY, Mungall KL, Schein J, Mungall AJ, Zhao Y, Moore RA, Ma Y, Yip S, Gelmon K, Lim H, Renouf D, Laskin J, Marra MA, **Jones SJM**. Bioinformatics Analyses Approaches for Personalized Oncogenomics**. Oral Presentation.**

165. Genome Informatics, Cambridge, UK, September 19- 24, 2014. , Daryanaz Dargahi, Leanna Yee, Peter J. Bergqvist, Richard D. Swayze, Edie M. Dullaghan, Jianghong An, Bradley J. Hedberg, Ryan Dercho, John S. Babcook, **Steven J.M. Jones.** Pan-cancer analysis of alternative splicing events reveals novel commonly altered splicing patterns. **Oral Presentation.**

166. Genome Informatics, Cambridge, UK, September 19 – 24, 2014. Shen Y, Kasaian K, Leelakumari S, Pleasance E, Jones M, Bose P, Eirew P, Corbett R, Mungall KL, Thiessen N, Ma Y, Fok A, Schein J, Mungall AJ, Zhao Y, Moore RA, Yip S, Gelmon K, Lim H, Renouf D, Sun S, Roscoe R, **Jones SJM**, Laskin J, Marra MA. Utilization of Whole Genome Analysis Approaches for Personalized Therapy Decision Making in Patients with Advanced Malignancies. **Oral Presentation.**

167. Canadian Association of General Surgeons (CAGS), Vancouver, Canada, September 17 – 20, 2014. Moore SE, Kasaian K, **Jones S**, Melck A, Wiseman SM. Papillary Thyroid Cancer: Epidemiology and clinical implications of bilateral disease. **Oral Presentation.**

168. ISMB Conference, Boston, Mass. July 10 – 15, 2014. Daryanaz Dargahi, Leanna Yee, Peter J. Bergqvist, Richard D. Swayze, Edie M. Dullaghan, Jianghong An, Bradley J. Hedberg, Ryan Dercho, John S. Babcook, **Steven J.M. Jones.** Pan-cancer analysis of alternative splicing events reveals novel tumor biomarkers shared by different tumor types. **Poster Presenation.**

169. ISSCR 12th Annual Meeting, June 18 – 21, 2014, Vancouver, BC. Heravi-Moussavi Alireza, Raghavan Karthika, Bilenky Misha, Carles Annaick, Moore Richard, Mungall Andy, **Jones Steven,** Marra Marco A., LaRoque Nick, Fisher Susan, Costello Joseph F., Hirst Martin J. Epigenetic Profiling of Human Embryonic Stem Cells at Endogenous Oxygentension.

170. ASGCT 17th Annual Meeting, May 21-24, 2014 in Washington, DC. Elizabeth M. Simpson, Charles N. de Leeuw, Siu Ling Lam, Andrea J. Korecki, Russell J. Bonaguro, Kaelan Wong, Michelle Zhou, Garrett E. Berry, Tess C. Lengyell, Olga Kaspieva, Stéphanie Laprise, Lisa Borretta, Simone C. McInerny, Alice Y. Chou, Elodie Portales-Casamar, Cletus A. D'Souza, Magdalena I. Swanson, George S. Yang, **Steven J.M. Jones**, Robert A. Holt, Aravind Asokan, Wyeth W. Wasserman, Ph.D. and Daniel Goldowitz. **Title:** Regional-CNS MiniPromoters for AAV are Identified in a High Through-put Pipeline. **(Poster Presentation).**

171. 2nd International Conference on Intergrative Salmonid Biology (ISISB), June 10 – 12, 2014, Vancouver, BC. Ben Koop, Jong Leong, David Minkley, Gret Taylor, **Steven Jones.** Gene and transposable element evolution in the restabilization of the Atlantic salmon genome. **(Oral presentation).**

172. ASCO Annual Meeting, May 30 – June 3, 2014. Chicago, Illinois. Simon Daniel Baxter, Howard John Lim, Yaoqing Shen, Janessa J. Laskin, Daniel John Renouf, Stephen Yip, David Huntsman, Stephen K. L. Chia, Yvonne Li, Katayoon Kasaian, Peter Eirew, Sreeja Leelakumari, Yussanne Ma, Samuel Aparicio, **Steven Jones**, Marco Marra. Whole genome DNA and RNA sequencing in patients with metastatic colorectal cancer (mCRC).

173. TCGA Third Annual Scientific Symposium, Bethesda, USA, May 2014. Mungall AJ, Shen Y, Kasaian K, Mungall KL, Corbett R, Eirew P, Fok A, Leelakumari S, Li YY, Pleasance E, Thiessen N, Tse K, Zeng T, Zhao Y, Gelmon K, Karsan A, Lim H, Ma Y, Moore RA, Renouf DJ, Roscoe R, Schein J, Sun S, Yip S, **Jones SJM**, Laskin JJ, Marra MA. Using TCGA data to inform on precision medicine in late-stage cancer settings. **Oral Presentation.**

174. Genome BC 12th Annual Genomics Forum, Vancouver, Canada, May 2014. Kasaian K, Shen Y, Leelakumari S, Eirew P, Li Y, Pleasance E, Corbett R, Mungall K, Schein J, Mungall A, Zhao Y, Moore R, Yip S, Gelmon K, Lim H, Renouf D, Roscoe R, Ma Y, Marra M, Laskin J, **Jones S**. Bioinformatic analyses approaches for personalized Oncogenomics. **Poster award.**

175. Keystone Symposia on Molecular and Cellular Biology. (Autophagy:Fundamentals to Disease) May 23-28, 2014. Austin, Texas. A Hannigan, J An, J Xu, L Vezenkov, C Choutka, A Leung, S Kovacic, D Bosc, S. Bortnik, N Honson, T Pfeifer, R Young, **S Jones**, S Gorski. AI4-28: a first-in-class small molecule inhibitor of Atg4B autophagy activity.

176. Annual Meeting of the American Scociety of Gene & Cell Therapy (ASGCT) May 20 – 24, 2014. Washington, DC. Elizabeth M. Simpson, Charles N. de Leeuw, Siu Ling Lam, Andrea J, Korecki, Russell J. Bonaguro, Kaelan Wong, Michelle Zhou, Garrett E. Berry, Tess C, Lengyell, Olga Kaspieva, Stéphanie Laprise, Lisa Borretta, Simone C. McInerny, Alice Y. Chou, Elodie Portales-Casamar, Cletus A. D'Souza, Magdalena I, Swanson, George S. Yang, **Steven J.M. Jones**, Robert A. Holt, Aravind Asokan, Wyeth W. Wasserman and Daniel Goldowitz. Regional-CNS MiniPromoters for AAV are Identified in a High Through-put Pipeline.

177. United States and Canadian Academy of Pathology Meeting, San Diego, USA, March 2014. Ng TL, Kasaian K, Thomson T, Yip ST, Zhao Y, Schein J, Moore RA, **Jones SJ,** Marra MA, Laskin J, Ho C. Genomic Analyses of Head and Neck Cancers Illustrate Novel and Confirmatory Molecular Genetic Findings with Potential Therapeutic Impact: Experience From the Personalized Oncogenomics Project. **Poster Presentation**

178. 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)**

179. 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)**

180. 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)**

181. ASCO 2014 Gastrointestinal Cancers Symposium, San Francisco, CA. January 16-18, 2014. Daniel John Renouf, Janessa J. Laskin, Howard John Lim, Stephen Yip, David Schaeffer, David Huntsman, Ryan Morin, Yvonne Li, Yaoqing Shen, Yongjun Zhao, Katayoon Kasaian, Sreeja Leelakumari, Richard Corbett, Peter Eirew, Karen Mungall, Andy Mungall, Jacquie Schein, Robyn Roscoe, **Steven Jones**, Marco Marra. Detailed genomic analysis in patients with pancreatic ductal adenocarcinoma (PDAC).

182. Pacific Symposium on Biocomputing, Big Island, USA, January 2014. Kasaian K, Mungall KL, Schein J, Zhao Y, Moore RA, Hirst M, Marra MA, Walker BA, Wiseman SM, **Jones SJM**. Transcriptomic Analysis of Benign and Malignant Thyroid Nodules. **Poster Presentation**.

183. The 12th Asia Pacific Bioinformatics Conference, Shanghai, China, January 2014. Shing Zhan, **Steven Jones.** Computational Analysis of Immune Escape Strategies in Non-Small Cell Lung Cancers.

184. NIH Roadmap project annual conference in Boston, Oct. 20-21, 2013. Li L, Bilenky M, Carles A, Hong C, Maire C, Tam A, Kamoh B, Cho S, Cheung D, Wong T, Nagarajan R, Mungall AJ, Moore R, Wang T, **Jones SJM**, Ligon K. Marra MA, Costello J, Hirst M. "DNA Methylation Analysis of Fetal Brain from Monozygotic Twins". **Poster Presentation.**

185. 3rd Annual TFRI–BC Node Research Day, Vancouver, BC, October 2013. Annaick Carles, Misha Bilenky, Alireza Heravi-Moussavi, Dean Cheng, Irene Li, Richard Varhol, Richard Corbett, Kelsey Zhu, Liza Chui Shan Leung, William Long, Yussane Ma, Eric Chuah, **Steven Jones**, Martin Hirst. Whole Genome Bisulfite Sequencing Quality Control Pipeline

186. 3rd Annual TFRI–BC Node Research Day, Vancouver, BC, October 2013. Misha Bilenky, Sitanshu Gakkhar, Annaick Carles, Brad Davis, Joseph F. Costello, **Steven J.M. Jones**, Martin Hirst. FindER: analysis and QC tool for ChIP-Seq experiments.

187. The 15th Australian Wine Industry Technical Conference. Sydney, Australia, 13 – 18, July 2013. Simon A. Schmidt, Anthony R. Borneman, Justin Chu, Paul J. Chambers, Peter Dry, Nick Dry, Mike McCarthy, Hendrick J.J. van Vuuren, Jörg Bohlmann, **Steven J.M. Jones**, Samantha Turner, Isak S. Pretorius, Daniel Johnson. Chardonnay clonal variation – A comparative genomic and phenotypic evaluation. (**Poster Presentation).**

188. The Endocrine Society's 95th Annual Meeting & Expo, San Francisco. June 15 – 18, 2013. Choi H, Kasaian K, Kowal J, **Jones S**, White A, Wiseman S. Differentiated Thyroid Cancer: Clinical Presentation as Prognostic Variable.

189. Tree Biotechnology Conference. Asheville, North Carolina, May May 27 – 28, 2013. Inanc Birol, Anthony Raymond, Shaun D Jackman, Stephen Pleasance, Robin Coope, Greg A Taylor, Macaire Man Saint Yuen, Christopher I Keeling, Dana Brand, Benjamin P Vandervalk, Heather Kirk, Pawan Pandoh, Richard A Moore, Yongjun Zhao, Andrew J Mungall, Detlef Weigel, Margarete Hoffman, Barry Jaquish, Alvin Yanchuk, Carol Ritland, Brian Boyle, Jean Bousquet, Kermit Ritland, John MacKay, Jörg Bohlmann, **Steven JM Jones**. Shotgun sequencing and assembly of the 20 Gb white spruce (*Picea glauca*) genome

190. 12th International Symposium on Mutation in the Genome, Lake Louise, Banff, Alberta. April 22 – 26, 2013. **Steven Jones**, Howie Lim, Karen Gelmon, Daniel Renouf, Stephen Yip, David Huntsmen, Anna Tinker, Cheryl Ho, Erin Pleasance, Yvonne Li, Yaoqing Shen, Katayoon Kasaian, Richard Corbett, Jasleen Grewal, Sreeja Leelakumari, Alexandra Fok, Pawan Pandoh, Helen McDonald, Simon Haile Merhu, Katty Cruz, Peter Eirew, Karen Mungall, Yongjun Zhao, Andy Mungall, Jacquie Schein, Robyn Roscoe, Janessa Laskin, Marco Marra. Detection of somatic tumour mutations to inform therapeutic decision-making in patients with advanced malignancies.

191. Canadian Association for Neuroscience Meeting; Toronto, Ontario. May 21-24, 2013. Elizabeth M. Simpson, Charles N. de Leeuw, Frank M. Dyka, Sanford L. Boye, Stéphanie Laprise, Michelle Zhou, Alice Y. Chou, Lisa Borretta, Simone C. McInerny, Elodie Portales-Casamar, Magdalena I. Swanson, Cletus A. D'Souza, **Steven J.M. Jones**, Robert A. Holt, Daniel Goldowitz,William W. Hauswirth, Wyeth W. Wasserman. Human MiniPromoters for the Brain, Eye, and Spinal Cord; Developed in the Mouse Genome but Delivering the Same Restricted Expression in the AAV Genome. (Poster presentation).

192. American Society of Gene & Cell Therapy (ASGCT) Annual Meeting, Salt Lake City, Utah. May 15-18, 2013. Elizabeth M. Simpson, Charles N. de Leeuw, Frank M. Dyka, Sanford L. Boye, Stéphanie Laprise, Michelle Zhou, Alice Y. Chou, Lisa Borretta, Simone C. McInerny, Elodie Portales-Casamar, Magdalena I. Swanson, Cletus A. D'Souza, **Steven J.M. Jones,** Robert A. Holt, Daniel Goldowitz,William W. Hauswirth, Wyeth W. Wasserman. New MiniPromoters with Restricted-Retinal Expression when Docke in the Mouse Genome Show the Same Expression when Delivered in AAV. **(Poster presentation).**

193. American Society of Clinical Oncology (ASCO) Annual Meeting, Chicago, USA. May 31, 2013. Janessa J. Laskin, Howard John Lim, Karen A. Gelmon, Cheryl Ho, Daniel John Renouf, Stephen Yip, David Huntsman, Anna Tinker, Erin Pleasance, Yvonne Li, Yaoqing Shen, Katayoon Kasaian, Richard Corbett, Karen Mungall, Andrew Mungall, Yongjun Zhao, Jacquie Schein, Robyn Roscoe, **Steven Jones,** Marco Marra. Practical application of whole genome and transcriptome tumour analysis to guide chemotherapy decision-making for patients with advanced cancers.

194. American Association for Cancer Research (AACR) Annual Meeting, Washington, DC, USA. April 6-10, 2013. Janessa Laskin, Howie Lim, Karen Gelmon, Daniel Renouf, Stephen Yip, David Huntsmen, Anna Tinker, Cheryl Ho, Erin Pleasance, Yvonne Li, Yaoqing Shen, Katayon Kasaian, Richard Corbett, Karen Mungall, Yongjun Zhao, Andy Mungall, Jacquie Schein, Robyn Roscoe, **Steven Jones,** Marco Marra. Genome analysis informs chemotherapy decision-making in patients with advanced malignancies. (**Poster presentation).**

195. Joint Conference of HGM 2013 & 21st International Congress of Genetics, Singapore, Singapore. April 13 – 18, 2013. F. Zahir, Y. Shen, S. Adam, FORGE Canada Consortium, M. Marra, **S. Jones**, J. Friedman. Whole Genome Sequencing for Siblings with Severe Interlectual Disability.

196. BC Surgical Society Annual Spring Meeting, Sun Peaks. March 21 – 23, 2013. Moore S, Kasaian K, Kowal J, **Jones S**, Wiseman S. Epidemiology and Clinical Implications of Papillary Thyroid Carcinoma Bilaterality.

197. 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)**

198. 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)**

199. 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)**

200. Terry Fox Research Institute: BC Node Research Day, Vancouver, BC. November 2012. Misha Bilenky, Annaick Carles, Joseph F. Costello, **Steven J. M. Jones**, Martin Hirst. Finder: An Improved Analysis Tool for High-throughput Chip-Seq Experiments.

201. American Society of Human Genetics Annual Meeting, San Francisco. November 2012. Dan Doherty, Albert E. Chudley, Gail Coghlan, Gisele E. Ishak, A. Micheil Innes, Edmond G. Lemire, R. Curtis Rogers, Aizeddin A. Mhanni, Ian G. Phelps, **Steven J. M. Jones**, Shing H. Zhan, Anthony P. Fejes, Hashem Shahin, Moien Kanaan, Hatice Akay, Mustafa Tekin, Barbara Triggs-Raine, Teresa Zelinski. Mutations in *GPSM2* Cause the Brain Malformations and Hearing Loss of Chudley-McCullough Syndrome.

202. NeuroDevNet Third Annual Brain Development Conference, Toronto, ON.September 2012. Farah Zahir, Yaoqing Shen, Shelin Adams, Nancy Makela, Chandree Beaulieu, William Gibson, Milan Patel, Gabriela Horvath, Marco Marra, **Steven Jones,** Jan Friedman. Whole exome sequencing of additional family members in identifiation of causative mutations for severe intelectual disability in affected siblings.

203. 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. **(Oral presentation)**

204. Model Organisms to Human Biology- Cancer Genetics Conference. Washington, DC. June 17-20 2012. Pon J, 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)**

205. Keystone Symposia: Advances in Islet Biology, Montreray, California. March 2012. Bryan R. Tennant, A. Gordon Robertson, Mike Beach, Leping Li, Xuekui Zhang, Cheryl J. Whiting, Ada Kim, Shing H Zhang, Raphael Gottardo, Marco A. Marra, **Steven J.M. Jones** and Pamela A. Hoodless, Brad G. Hoffman. Identification and analysis of pancreatic islet enhancers.

206. The BC Cancer Agency Annual Cancer Conferernce, Vancouver, BC. December 2011. Jianghong An, Adrienne Hannigan, Jing Xu, Thanh-Giau Nguyen, Suganthi Chittaranjan, Robert Young, Sharon Gorski, **Steven Jones**. Identification of ATG4B Inhibitors for Novel Cancer Therapies by a Molecular Docking-Based Ligand Screening Approach.

207. The BC Cancer Agency Annual Cancer Conferernce, Vancouver, BC. December 2011. Yvonne Y Li, Jennifer Law, Kristen Reipas, Amarpal Cheema, Huifang Li, Artem Cherkasov, **Steven Jones**, and Sandra Dunn. Combining Virtual and High-Throughput Screening to Reposition Existing Drugs for Triple Negative Breast Cancer.

208. The BC Cancer Agency Annual Cancer Conferernce, Vancouver, BC. December 2011. Shing H. Zhan, Anthony P. Fejes, Nina Thiessen, Alireza H. Khodabakhshi, An He, Inanc Birol, **Steven J.M. Jones**. Will All the Passengers Please Sit Down?

209. Society for Neuroscience Meeting, Washington, DC. November 2011. Charles N. de Leeuw, Stephanie Laprise, Kathleen G. Banks, Elodie Portales-Casamar, Magdalena I. Swanson, Douglas J. Swanson, Li Liu, Lisa Dreolini, **Steven J.M. Jones,** Robert A. Holt, Daniel Goldowitz, Wyeth W. Wasserman, Elizabeth M. Simpson. New Pleiades Minipromoters for Brain and Eye.

210. 42nt Union World Conference on Lung Health, Lille, France. October 2011. Marcus Lem, Jennifer L. Gardy, James C. Johnston, Patrick Tang, Victoria J. Cook, Shirley Rempel, April MacNaughton, Elizabeth Brodkin, Shannan J. Ho Sui, **Steven Jones**, Lena Shah, Meenu K. Sharma, R. Kevin Elwood, Fiona S.L. Brinkman,

Robert C. Brunham. Programme Implications of Genomic Epidemiological Analysis of Tuberculosis (TB) Transmission Patterns.

211. American Society of Human Genetics, Montreal, Canada. October 2011. K. Schrader, A. Heravi-Moussavi, P. Waters, J. Senz, J. Whelan, G. Ha, P. Eydoux, T. Nielsen, B. Gallagher, A. Oloumi, N. Boyd, B.A. Fernandez, T.L. Young, **S.J.M. Jones,** M. Hirst, S.P. Shah, M.A. Marra, J. Green, D.G. Huntsman. A next-generation sequencing approach to diagnosis of a family's skeletal abnormalities and retinitis pigmentosa**.**

212. American Society of Human Genetics, Montreal, Canada. October 2011. W. Gibson, J. Soul, S. Gyawali, A. Fam, R. Billings, S.L. Babich, L. Musa1, J. Friedman1, S. Lear, **S. Jones**, D.D. Weaver, K. Boycott, P. Eydoux, FORGE Consortium Canada. Detailed Metabolic Studies Identify Endophenotypes in Rare Obesity and Overgrowth Disorders.

213. The 27th Annual meeting of The International Society of Chemical Ecology, Simon Fraser University, Burnaby. July 2011. Keeling, CI, Henderson H, Li M, Yuen M, Dullat HK, Huber DPW, **Jones SJ**, Bohlmann J. Mountain Pine Beetle Genomics.

214. NeuroDevNet Brain Development Conference, Vancouver, BC. June 2011. Charles N. de Leeuw, Kathleen G. Banks, Stephanie Laprise, Elodie Portales-Casamar, Douglas J. Swanson, Li Liu, Lisa Dreolini, Magdalena I. Swanson, **Steven J.M. Jones**, Robert A. Holt, Daniel Goldowitz, Wyeth W. Wasserman, Elizabeth M. Simpson. Expansion of the Pleiades Promoter Toolset: Adding New Promoters with Brain, Eye and Embryonic Expression.

215. The Genetics Society of American Conferences, Washington, DC. June 2011. EM Simpson,C de Leeuw, KG Banks, S Laprise, RJ Bonaguro, A McLeod, L. Dreolini,DJ Swanson, L Liu, E Portales-Casamar, MI Swanson, **SJM Jones,** RA Holt, WW Wasserman, D Goldowitz. Pleiades and CanEuCre: MiniPromoters, Cre/ERT2-Driver Mice, and Cre Adeno-Associated Viruses Designed for Selected Expression in the Brain, Eye, and Spinal Cord.

216. 9th Annual Genomics Forum & Poster Competition, Vancouver, BC. May 2011. Hamid Younesy, Torsten Möller, Cydney Nielsen, and Steve Jones. User Guided Pattern Discovery in CHiP-Seq Data.

217. Advances in Genome Biology & Technolgy (AGBT) Conference Marco Island, Florida. Feb. 2011. Ryan D. Morin, Maria Mendez-Lago, Andrew J. Mungall, Rodrigo Goya, Nathalie A. Johnson, Tesa M. Severson, Karen L. Mungall, Readman Chiu, Matthew Field, Shaun Jackman, Martin Krzywinski, David Scott, Diane L. Trinh, Malachi Griffith, Richard Corbett, Susanna Chan, Eric Zhao, Duane Smailus, Michelle Moksa, Lisa Rimsza, Angela Brooks-Wilson, Barbara Meissner, Bruce Woolcock, Merrill Boyle, Helen McDonald, Angela Tam, Yongjun Zhao, Allen Delaney, Thomas Zeng, Kane Tse, Yaron Butterfield, Inanc Birol, Rob Holt, Jacqueline Schein, Douglas E. Horsman, Richard Moore, **Steven J.M. Jones,** Joseph M. Connors, Martin Hirst, Randy D. Gascoyne, Marco A. Marra. Genome, Exome and Transcriptome sequencing reveals genes involved in histone modification and B-cell-receptor signalling are frequently mutated in non-Hodgkin lymphoma.

218. Advances in Genome Biology & Technolgy (AGBT) Conference Marco Island, Florida. Feb. 2011. Martin Hirst, Yongjun Zhao, Cydney Nielsen, Angela Tam, Baljit Kamoh, Adrian Ally, Allen Delaney, Dorothy Cheung, Richard Varhol, Mahvash Sigaroudinia, Philippe Gascard, Thea Tlsty, Yun Choi, Michael McManus, Raman Nagarajan, Chibo Hong, Lorigail Echipare, Henriette O'Geen, Peggy Farnham, Hunter Richards Ting Wang, David Haussler, Arthur Weiss, Richard Moore, **Steven JM Jones**, Joe Costello, Marco A. Marra. Reference Human Epigenomes**.**

219. 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

220. 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.

221. 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.

222. 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.

223. BC Cancer Annual Cancer Conference.Vancouver, BC, Nov. 2010. <u>Anthony P. Fejes</u>, Jianghong An, Yvonne Li, Stephen Leach, Yongjun Zhao, Richard Varhol, Jenny Qian, Shaun Jackman, Readman Chiu, Karen Mungall, Gordon Robertson, Rong She, Martin Hirst, Inanc Birol, Marco A. Marra, Angela Brooks-Wilson, **Steven J.M. Jones**. Comparative analysis of ductal carcinoma in situ breast cancer cell-lines with 1400 samples.

224. BC Cancer Annual Cancer Conference.Vancouver, BC, Nov. 2010. <u>Jianghong An</u>, Artee Luchman, Gregory Cairncross and **Steven Jones**. Developing mutant-specific inhibitors of isocitrate dehydrogenase 1 (IDH1) for novel therapeutics of brain cancer.

225. BC Cancer Annual Cancer Conference.Vancouver, BC, Nov. 2010. Alireza Hadj Khodabakhshi*, Anthony P. Fejes*, <u>Katayoon Kasaian</u>, Inanc Birol, **Steve J.M. Jones** **authors contributed equally.*Genetic Variation database: An open source database template for genomic discovery.

226. 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.

227. ISEH, International Society of Experimental Hematology, Melbourne, Australia. September 2010. Yung E, Sekulovic S, Berg T, Nielsen C, **Jones S**, Hirst M, Humphries RK. Changes in the epigenome associated with Meis 1 induced leukemic transformation.

228. ISMB 2010, International Society for Computational Biology, Boston, Massachusetts, USA, July 2010. Birol I, Jackman SD, Robertson G, Swanson L, Mungall K, Chiu R, Field M, Lee S, Raymond A, Varhol R, Zhao YJ, Hirst M, Moore R, Marra MA, **Jones SJM,** Hoodless PA. Detecting Trans-Splicing Events and Non-co-Linear Transcripts in Transcriptome Assemblies.

229. TFRI 2nd Annual Scientific Meeting, Vancouver, BC. May 2010. Mungall, A.J., Morin, R.D., An, J., Yakovenko, A., Boyle, M, Johnson N.A., Leach, S., Mayo, M., Mendez-Lago, M., Munro, S., Zeng, T., Zhao, Y., Hirst, M., Holt, R.A., Moore, R., Schein, J.E., Gascoyne, R.D., Horsman, D.E., Connors, J.M., Jones, S.J., Marra MA. Recurrent DNA Mutations in Non-Hodgkin's Lymphomas Reveal Candidate Therapeutic Targets.

230. American Thoracic Society Inernational Conference, New Orleans, LA. May 2010. J. Johnston, J. Gardy, S. Ho Sui, **S. Jones**, F. Brinkman, R. Brunham, P. Tang. Whole Genome and Network-Based Epidemiological Investigation of a Tuberculosis Outbreak.

231. AMMI Canada - CACMID Annual Conference, Edmonton, Alberta, Canada. May 2010. Gardy J, Ho Sui S, Johnston J, **Jones S**, Brinkman F, Brunham R, Tang P. Genomic Epidemiology Reveals New Pattern of Transmission in a Tuberculosis Outbreak.

232. The 110th General Meeting of the American Soceity for Microbiology, San Diego, California. May 2010. Gardy JL, Ho Sui SJ, Johnston J, **Jones S,** Tang P, Brinkman FSL, Brunham RC. Genomic Epidemiology of a Tuberculosis Outbreak: Whole Genome Sequencing of 36 *M. tuberculosis* Isolates Identifies Novel Patterns of Transmission.

233. HUGO, 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. (**Poster Presentation)**

234. 11th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. February 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.

235. 11th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. February 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)**

236. 11th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. February 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.

237. 11th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. February 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.

238. 11th Annual Advances in Genome Biology and Technology Meeting. Marco Island, FL. February 2010. Anthony P. Fejes, Stephen Leach, Yongjun Zhao, Richard Varhol, Martin Hirst, Marco A. Marra, Angela Brooks-Wilson, **Steven J.M. Jones**. RNA-Seq Determination of Non-Synonymous Coding Mutations in 5 Breast Cancer Cell Lines and a Matched Cancer/Normal Set.

239. American Association of Endocrine Surgeons 2010 Annual Meeting. Pittsburgh, PA, USA. April 2010. Wiseman SM, Griffith OL, Deen S, Masoudi H, Goldstein L, Gown A, **Jones SJM.** 2010. Immunophenotyping of Thyroid Tumors Identifies Molecular Markers Altered During Transformation of Differentiated into Anaplastic Carcinoma. Abstract submitted. 1 Dec 2009.

240. American Association of Endocrine Surgeons 2010 Annual Meeting. Pittsburgh, PA, USA. April 2010. Johner A, Griffith OL, Wood L, Piper H, Wilkins G, Walker B, Baliski C, Bugis S, **Jones SJM,** Wiseman SM. 2010. Detection and Management of Hypothyroidism Following Total or Near Total Thyroid Lobectomy: Evaluation of a Clinical Algorithm. Abstract submitted. 1 Dec 2009.

241. Worm Breeders Gazette, November 19, 2009. Thierry-Mieg, J, Thierry-Mieg D, Kohara Y, Shin-I T, Sugano S, Suzuki Y, Salehi-Ashtiani K, Vidal M, Ramani A, Fraser An **Jones S,** Shin H, Baillie D. AceView gene models now integrate high throughput cDNA sequences.

242. The American Society of Hematology, 51st Annual Meeting, December 2009. Morin R, Johnson NA, Serverson TM, Mungal AJ, An J, Paul JE, Boyle M, Woolcock BW, Kuchengauer F, Yapp 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, Aparicio S, Schein J, Moore R, Holt R, Horsman DE, Connors JM, **Jones S**, Hirst M, Gascoyne RD, Marra MA. Tyrosine 641 in the EZH2 Oncogene is Frequently Mutated in Follicular and Diffuse Large B-cell Lymphomas of Germinal Center Origin.

243. The American Society of Hematology, 51st Annual Meeting, December 2009.Mungall AJ, Chiu R, ChuA, Corbett R, Field M, Jackman S, Mungall K, Wong K, Boyle M, Carlsen R, Chan SY, Coope R, Hirst C, Hirst M, Johnson N, Krzywinski M, Lee D, Lin J, Moore R, Simpson J, Steidel C, Severson T, 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 Arrangement Breakpoints in Follicular Lymphoma.

244. The American Society of Hematology, 51st Annual Meeting, December 2009. Johnson NA, Morin RD, Severson TM, Mungall AJ, Zhao YJ, Schein J, Boyle M, Woolcock BW, Moore R, Holt R, Horsman DE, Connors JM, **Jones S,** Hirst M, Marra MA, Gascoyne RD. FAS Mutations in Follicular Lymphoma are Rare but may be Associated with a Poor Clinical Outcome.

245. VisWeek Conference, Atlantic City, USA, October 2009. Nielsen CB, Jackman SD, Birol I, **Jones SJM**. ABySS-Explorer: Visualizing Genome Sequence Assemblies. Abstract. **Won Best Paper Award.**

246. CSHL Genome Informatics, NY, USA, October 2009. Birol Inanc, Jackman Shaun, Field Matthew, Mungall Karen, Wong Kim, Chiu Readman, Chu Andy, Corbett Richard, Hirst Carrie, Mungall Andrew J, Zeng Thomas, Tam Angela, Li Irene, Hajirasoulia Iman, Hormozdiari Fereydoun, Sahinalp Cenk S, Varhol Richard, Zhao Yongjun, Hirst Martin, Schein Jacqueline E, Horsman Doug E, Gascoune Randy D, Connors Joseph M, Marra Marco A, **Jones Steven JM**. Assembling Pooled Bac Sequences.

247. CSHL Genome Informatics, NY, USA, October 2009. Birol Inanc, Jackman Shaun, Raymond Anthony, Schein Jacqueline E, **Jones Steven JM**. Abyss V2.0: Adapting *De Novo* Assmebly Techniques to Employ Advances in Sequencing.

248. The American Society of Human Genetics 59th Annual Meeting, Hawaii. October 2009. Bretherick Karla L, Leach Stephen, Montgomery Stephen, Banath Judit P, Olive Peggy L, **Jones Steven JM**, Brooks-Wilson Angela R. A common SNP associated with non-Hodgkin Lymphoma influences protein binding at the *H2AFX* promoter.

249. Toronto International Data Release Workshop. September 2009. Birney E, Hudson TJ, Green ED, Gunter C, Eddy S, Rogers J, Harris JR, Ehrlich SD, Apweiler R, Austin CP, Berglund L, Bobrow M, Bountra C, Brookes AJ, Cambon-Thomsen A, Carter NP, Chisholm RL, Contreras JL, Cooke RM, Crosby WL, Dewar K, Durbin R, Dyke SO, Ecker JR, El Emam K, Feuk L, Gabriel SB, Gallacher J, Gelbart WM, Granell A, Guarner F, Hubbard T, Jackson SA, Jennings JL, Joly Y, Jones SM, Kaye J, Kennedy KL, Knoppers BM, Kyrpides NC, Lowrance WW, Luo J, MacKay JJ, Martín-Rivera L, McCombie WR, McPherson JD, Miller

L, Miller W, Moerman D, Mooser V, Morton CC, Ostell JM, Ouellette BF, Parkhill J, Raina PS, Rawlings C, Scherer SE, Scherer SW, Schofield PN, Sensen CW, Stodden VC, Sussman MR, Tanaka T, Thornton J, Tsunoda T, Valle D, Vuorio EI, Walker NM, Wallace S, Weinstock G, Whitman WB, Worley KC, Wu C, Wu J, Yu J. Prepublication data sharing. Nature. 2009 Sep 10;461(7261):168-70. Abstract.

250. In proceeding of the 14th International Congress on Molecular Plant-Microbe Interactions, Quebec, Canada. July 2009. DiGuistini S, Wang Y, Alamouti S, Keeling C, Hamelin R, **Jones S,** Bohlmann J, Breuil C. Identifying genes involved in *Grosmannia clavigera*'s response to pine tree defenses**.**

251. InterLymph Consortium 8th Annual Meeting, Vancouver, BC. July, 2009. Bretherick KL, Leach S, Montgomery S, Banath JP, Olive PL, **Jones SJM**, Brooks-Wilson AR. A common SNP associated with non-Hodgkin Lymphoma influences protein binding at the *H2AFX* promoter.

252. Annual Meeting of SMB, Vancouver, BC, Canada, July 2009. Inanc Birol, Shaun Jackman, Cydney Nielsen, Jenny Qian, Marco Marra, **Steven JM Jones.** *De novo* assembly of transcriptomes with ABySS.

253. 17th Annual Conference on ISMB and 8th ECCB, Stockholm, Sweden, June 2009. Inanc Birol, Shaun D Jackman, Cydney Nielsen, Jenny Q Qian, Richard Varhol, Greg Stazyk, Ryan D Morin, Yongjun Zhao, Martin Hirst, Jacqueline E Schein, Doug E Horsman, Joseph M Connors, Randy D Gascoyne, Marco A Marra, and **Steven JM Jones**. *De novo* Transcriptome Assembly with ABySS.

254. CIHR National Poster Competition, Winnipeg, Canada, June 2009. Fejes Anthony P, Cezard Timothee, Birol Inanc, Jones **Steven JM**. Vancouver Short Read Analysis Package: Tools for Genome-Wide Analysis of Transcriptome Expression, Transcription Factor Binding and Chromatin Modification.

255. 2nd International Conference on Functional Annotation of the Mammalian Genome, Banff, Alberta. April 2009. Simpson, E.M., Portales-Casamar, E., Swanson, D.J., de Leeuw, C.N., Banks, K.G., Fulton, D.L., Amirabbasi, M., Castellarin, M., Chen, J., Docking, T.R., Khorasan-zadeh, S., Liu, F., Liu, Li., Wong, B.K.Y. , **Jones, S.J.** , Holt, R.A., Goldowitz, D., and Wasserman, W.W. Pleiades Promoter Project: Anotating the regulatory genome and producing minipromoters for regional brain expression.

256. In Proceedings of the 3rd International Conference on Bioinformatics and Biomedical Engineering (Beijing, China, June 11 - 13, 2009). iCBBE 2009. Institute of Electrical and Electronics Engineers, Inc. Los Alamitos, CA, USA. p. 1-9. Griffith OL, Gao B, Bilenky M, Prychyna Y, Ester M, **Jones S**. 2009. KiWi: A Scalable Subspace Clustering Algorithm for Gene Expression Analysis. Accepted for publication.

257. Keystone Symposia, Killarney, Ireland. June 2009. Law J, Wang M, To K, Stratford AL, Li Y, **Jones SJM,** Dunn S. Development of a cell premeable peptide inhibitor that blocks phosphorylation of YB-1 at S102 by p90 RSK and suppresses cancer cell growth.

258. 3rd Annaul Canadian Neuroscience Meeting, Vancouver, BC. May 2009. Simpson, E.M., Swanson, D.J., Portales-Casamar, E., de Leeuw, C.N., Banks, K.G., Bonaguro, R.J., D'Souza, C.A., Hearty, T.G. , Milisavljevic, M., Yang, G.S., **Jones, S.J.,** Holt, R.A., Wasserman, W.W., Goldowitz, D.Pleiades Promoter Project: Large-scale Production of Minipromoters for Focused Expression in the Brain.

259. 50th American Society of Hematology, San Francisco, California. December 2008. Sitwala KV, Huang Y, Dandekar M, Robertson G, Cezard T, Bilenky M, Thiessen N, Zhao YJ, Zeng T, Hirst M, Hero A, **Jones S**, Hess J. Hoxa9 and Meis1 Bind Highly Conserved Elements near Targets Regulated in Leukemia Cells.

260. 50th American Society of Hematology, San Francisco, California. December 2008. Steidl C, Lee T, Shah SP, Han G, Nayar T, Delaney A, **Jones SJ,** Chan WC, Rosenwald A, Rimsza LM, Campo E, Jaffe ES, Staudt LM, Lenz G, Connors JM, Gascoyne RD. Genome-wide expression profiling predicts treatment outcome in classical Hodgkin lymphoma.

261. BCCA Annual Cancer Conference, Vancouver, BC. November 2008. Sleumer MC, Bilenky M, He A, Robertson AG, Thiessen N, **Jones SJM**. cisRED: A Genome-wide Catalogue of Conserved Regulatory Elements for C. elegans. Poster Presentation

262. 9th International Congress on cell Biology (ICCB), South Korea, Seoul. October 2008. Lee Hyojin, Shin Heesun, Fejes Anthony, Jones **Steven JM**, Koo Hyeon-Sook. Gene Expression Analysis of C. elegans of aak-2 Mutant Using Massively Parallel Transcriptome Sequencing. Poster Presentation.

263. 8th International Society for Transgenic Technology, Toronto, Ontario. October, 2008.Simpson EM, Banks KG, Bonaguro RJ, de Leeuw CN, Schmouth J-F, Swanson DJ, Yang GS, Amirabbasi M, Babyak N, Black SF, Candido T, Chen J, Chen Y, Driolini L, Wilson G, Hatakka K, Hearty T, Khorasan-zadeh S, Komljenovic I, Laprise S, Liu F, Liu L, Mis J, Palma B, Turner JL, Wong SH, Ypsilanti AR, **Jones SJ**, Wasserman WW, Goldowitz D, Holt RA. Pleiades Promoter Project: New Tools for Promoter and Expression Analysis Employing Knock-in at *Hprt1*. Abstract Accepted.

264. 1st INCF Congress of Neuroinformatics: Databasing and Modeling the Brain, Stockholm, Sweden. September 2008. Portales-Casamar E, Swanson M.I, Holt R.A, Goldowitz D, **Jones S**, Simpson E.M and Wasserman W.W. The Pleiades Promoter Project: Using bioinformatics to design human DNA MiniPromoters driving region-specific expression in the brain. Abstract Submitted.

265. Canadian Surgery Forum, (CAGS), Halifax, Nova Scotia. September 2008. Dickeson MRC, Chan SK, Griffith OL, Phang PT, Masoudi H, **Jones SJM**, Nabi IR, Wiseman SM. Autocrine Motility Factor Receptor Expression Predicts Rectal Cancer Patients Outcomes. Abstract Submitted.

266. Biology of Genomes, Cold Spring Harbour, New York. May 2008. Siddiqui A, Bonfield J, Alekseyev V, Marth G, Bloom T, Zimmer A, Flicek P, Glassock J, Platt D, Knight J, Sorenson J, Thayer E, Brown C, **Jones S,** Attili M, Bainbridge M, Church D, Cox A, Du L, Huang W, Malek J, Manning J, Maisinger K, Messina D, Moulton K, Quinlan A, Stewart C, Stromger M, Warren R, Wylie T. SuRFING the Genome: A Common format for DNA Sequence Data.

267. AACR Annual Meeting San Diego, California. April 2008. Wiseman S, Griffith O, Leung S, Masoudi H, Phang T, **Jones S**, Moukhles H. Syntophin Expression Predicts colon Cancer Outcome. Abstract submitted.

268. Keystone Symposium, January 2008. Wederell ED, Cullum R, Robertson G, Bilenky M, Thiessen N, Varhol R, Delaney A, Dagpinar M, Zhao YJ, Hirst M, **Jones S**, Marra M, Hoodless PA. Genome-wide analysis of FoxA2 binding sites in the mouse adult liver by ChIP-Seq.

269. BCCA Annual Cancer Conference, Vancouver, BC. November, 2007. Butterfield Y, Wong K, Krzywinski M, Pugh T, Severson T, Field M, Mathewson C, Fejes A, Ali J, Varhol R, Malhis N, Hirst M, Birol I, Holt R, Connors J, Schein J, **Jones S,** Marra M. DNA Sequencing for Detecting Genome Aberrations in Follicular Lymphoma. Abstract submitted.

270. BCCA Annual Cancer Conference, Vancouver, BC. November, 2007. Bilenky M. Dagpinar M, Thiessen N, He A, Robertson G, Fejes A, Varhol R, Marra M, **Jones S.** Bioinformatics pipeline for the genome-wide analysis of Transcription factor binding using chromatin immunoprecipitation and next generation-sequencing. Abstract submitted.

271. North Pacific Surgical Association Annual Meeting. Victoria, BC. November 2007. Leung S, Griffith OL, Phang T, Jones SJM, Masoudi H, Wiseman, S. Prognostic significance of Human Epidermal Growth factor receptor (HER) family expression in colon cancer patients: a TMA study. Abstract submitted.

272. The World Congress on Psychiatric Genetics, New York. October 2007. Simpson EM, Banks KG, Ali J, Bonaguro RJ, de Leeuw CN, Komljenovic I, Swanson M, Wilson G, D'Souza C, Yang GS, Chopra V, Portales-Casamar E, Goldowitz D, Jones SJ, Holt RA, Wasserman WW. Pleiades Promoter Project: Human MiniPromoters for Region-Specific Brain Expression and Gene Therapy.

273. CSHL-Integrative Aproaches to Brain Complexity. Hinxton, UK. September 2007. Swanson MI, Portales-Casamar E, Arenillas D, D'Souza C, Chopra V, Lee L, Varhol R, Kwon TJ, Lithwick S, Ticoll A, Holt RA, Goldowitz D, **Jones S**, Simpson EM, Wasserman WW. The Pleiades Promoter Project: A public resource of human minipromoters for region-specific expression in the brain. Abstract submitted.

274. 16th Biennial International C. elegans Conference, UCLA, California, June 28, 2007. Etchberger JF, Lorch A, Sleumer MC, Zapf R, **Jones SJ,** Marra MA, Holt RA, Moerman DG, Hobert O. The cis-regulatory logic of the ASE gustatory neuron transcriptome. Abstract.

275. 16th Biennial International C. *elegans* Conference, UCLA, California, June 2007. Sleumer MC, Bilenky M, He A, Mah AK, Robertson AG, Thiessen N, Baillie DL, **Jones SJM**. De Novo Detection of Regulatory Modules in C. elegans. Poster Presentation.

276. Finishing the Future Meeting, Santa Fe, New Mexico. June 2007. Ali J, Chun E, Liao N, Palmquist D, Huang P, Wynhoven B, Kirkpatrick R, Holt R, Marra M, **Jones S**. A high throughput cDNA finishing pipeline-*Bos Taurus* as a model.

277. First Pan American Congress in Developmental Biology, Cancun, Mexico. June 2007.Hoffman B, Kok D, Witzsche J, Hirst M, Robertson R, Hoodless PA, **Jones S**, Marra M, Helgason CD. Genome-wide analysis of Nkx2.2 binding sites using ChIP- tag sequencing (ChIP-TS)

278. C. elegans Meeting, University of California, Los Angeles, CA. June 2007. Sleumer MC, Bilenky M, He A, Mah AK, Robertson AG, Thiessen N, Baillie DL, **Jones SJM**. *de Novo* Detection of Regulatory Modules in *C. elegans.*

279. C. elegans Meeting, University of California, Los Angeles, CA. June 2007. Meissner B, Somasiri A, Warner A, Veiga M, Rogalski T, Lorch A, Zapf R, Wong K, Marra M, **Jones S,** Fox R, Miller D, Moerman D. Mapping out a muscle cell – a first step towards a full description of protein localization within a single cell type.

280. 16th International Congress of Cytology, Vancouver, BC. May 2007. Jones S. Determining genomic changes through bioinformatics.

281. 2007 Pacific Cascade Chapter Meeting of the Society for Neuroscience, University of Washington, Seattle April 2007. Simpson EM, Banks KG, Ali J, Black SF, Bonaguro RJ, Candido TR, Chen J, Chen Y, Cheng JCY, Chopra V, de Leeuw CN, Dreolini L, Flynn EK, Komljenovic I, Lee L, Lithwick S, Liu J, McConechy M, Swanson M, Ticoll A, Vermeulen J, Ypsilanti AR, D'Souza C, Yang GS, Portales-Casamar E, Goldowitz D, Jones SJ, Holt RA, Wasserman WW. Pleiades Promoter Project: Human MiniPromoters Knocked-into ESC's for Region-Specific Brain Expression.

282. 2007 Pacific Cascade Chapter Meeting of the Society for Neuroscience, University of Washington, Seattle April 2007. de Leeuw CN, Banks KG, Ali J, Black SF, Bonaguro RJ, Candido TR, Chen J, Chen Y, Cheng JCY, Dreolini L, Flynn EK, Komljenovic I, Lee L, Lithwick S, Liu J, McConechy M, Swanson M, Ticoll A, Vermeulen J, Yang GS, Ypsilanti AR, Chopra V, D'Souza C, Portales-Casamar E, Goldowitz D, **Jones SJ**, Holt RA, Wasserman WW, Simpson EM. Towards the application of Pleiades MiniPromoter resources to understand the role of *Nr2e1* in neural stem cells and mouse behaviour. Poster Presentation.

283. 98th Annual AACR Meeting, Los Angeles, CA. April 2007. Wiseman SW, Melck A, Griffith O, Rajput A, Masoudi H, **Jones S**. Evaluation of Type 1 Growth Factor Receptor Family Expression in 205 Thyroid Lesions Reveals Diagnostic Utility And Targeted Therapeutic Potential For HER1, HER3, and HER4.

284. Janelia Conference, Loudoun County, Virginia. March 2007. Simpson EM, Banks KG, Ali J, Black SF, Bonaguro RJ, Candido TR, Chen J, Chen K, Cheng JCY, Chopra V, Dreolini L, Flynn EK, Komljenovic I, Lee L, Lithwick S, Liu J, McConechy M, Swanson M, Ticoll A, Vermeulen J, Ypsilanti AR, D'Souza C, Yang GS, Portales-Casamar E, Goldowitz D, Jones SJ, Holt RA, Wasserman WW. Pleiades Promoter Project: Genomic Resources Advancing Therapies for Brain Disorders.

285. Systems Biology: Global Regulation of Gene Expression, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, March, 2007. Bilenky M, Robertson G, Dagpinar M, He A, Bainbridge M, Varhol R, Thiessen N, Teague K, Griffith OL, Sleumer MC, Li YY, Fjell C, Warren RL, Zhou J, Sander J, Marra M, and **Jones SJM**. Computational prediction and ranking of mammalian transcriptional regulatory modules using dense comparative genomics. Abstract.

286. Janelia Conference, Loudoun County, Virginia. March 2007. Portales-Casamar,E., Arenillas,D., D'Souza,C., Chopra,V., Lee,L., Varhol,R., Kwon,T.J., Lithwick,S., Swanson,M., Ticoll,A., Holt,R.A., Goldowitz,D., Jones,S., Simpson,E.M. and Wasserman,W.W. Pleiades Promoter Project: Human DNA MiniPromoters driving region-specific expression in the brain.

287. Society of Surgical Oncology's 60th Annual Cancer Symposium. Washington, DC. March 2007. Melck AL, Masoudi H, Griffith OL, Rajput A, Wilkins GE, Bugis S, Jones S, Wiseman SM. Evaluation of Cell Cycle Regulators in 205 Thyroid Lesions Reveals the Diagnostic Utility of p16, p21, cyclinD1 and cyclinE. Accepted for oral presentation.

288. Advances in Genome Biology and Technology (AGBT) Conference, Marco Island, Florida, Feb. 2007. Griffith OL, Montgomery SB, Bergman CM, Bilenky M, Chu B, Pleasance ED, Prychyna Y, Sleumer MC, Zhang X, Jones SJM. ORegAnno: A Community-Based Annotation System for Literature-Derived Regulatory Sequences. Abstract.

289. Advances in Genome Biology & Technolgy (AGBT) Conference Marco Island, Florida. Feb. 2007. **Steven J.M. Jones**, Matthew Bainbridge, Anthony P. Fejes, Rene L. Warren, Martin Hirst, Richard Moore, Martin Krzywinski, Jacqueline E. Schein, Joseph Conners, Randy Gascoyne, Robert A. Holt and Marco A. Marra. Massively parallel sequencing-by-synthesis for detection of genetic aberrations in human cancer.

290. Advances in Genome Biology and Technology (AGBT) Conference, Marco Island, Florida. 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, Dellaney 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.

291. The Fifth Asia Pacific Bioinformatics Conference. Hong Kong January 2007. Li YY, An J, Jones SJM. A Large-scale computational method for kinase-drug interaction prediction.

292. The Fifth Asia Pacific Bioinformatics Conference. Hong Kong January 2007. Li YY, An J, Jones SJM. Computational Drug Repositioning and Side Effect Prediction for Kinase Inhibitors.

293. Plant & Animal Genome XV Conference. San Diego, California January 2007. Kirkpatrick R, Jones S. Establishing a Bioinformatics Quality Programme in an Adademic Environment.

294. Prostate Cancer Research Retreat. Orangeville ON. January 2007. An J, Sadar M, Jones S. Structure Based Drug Discovery against Novel Binding Pockets of Androgen Receptors.

295. BCCA 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 AL, 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.

296. BCCA Annual Cancer Conference, Vancouver, BC. Nov. 2006. Kneller JM, **Jones S**. Identification of cancer targets by SAGE library comparison.

297. BCCA Annual Cancer Conference, Vancouver, BC. Nov. 2006. Romanuik T, Holt R, **Jones S**, Marra M, Sadar MD. Identification of novel androgen-regulated genes in LNCAP human prostate cancer cells using long serial analysis of gene expression.

298. BCCA Annual Cancer Conference, Vancouver, BC. Nov. 2006. Wang G, **Jones S**, Marra MA, Sadar MD. Dysregulation of Androgen receptor and protein kinase a pathways in the hormonal progression of prostate cancer.

299. Merck Frosst Biology Research Day. Kirkland, Quebec. October 2006. Li YY, An J, **Jones S**. A large-scale computational approach to drug repositioning.

300. American Society of Human Genetics. New Orleans, LA. October 2006. Simpson EM, Wasserman WW, Holt RA, **Jones SJ**, Goldowitz D, Ward S, Kingsley S. Pleiades Promoter Project: Genomic Resources Advancing Therapies for Brain Disorders.

301. Cold Spring Harbor Laboratory/Wellcome Trust Conference: Genome Informatics.Hinxton UK. September 2006. Shin H, Hirst M, Bainbridge MN, Warren RL, Baillie DL, Jones SJM. Transcriptome Analysis for C. Elegans Based on Novel Expressed Sequence Tags (ESTs)

302. Cold Spring Harbor Laboratory/Wellcome Trust Conference: Genome Informatics.Hinxton, UK. September 2006. Liao N, Chun E, Wynhoven B, Kirkpatrick R, Siddqui A, Jones S. An Effective Approach to EST Sequence Filtering System.

303. Genome BC Genomics Forum. Vancouver, BC. July 2006. Palmquist D, Huang P, Wynhoven B, Chun E, Kirkpatrick R, Ali J, Sidiqqui A, Holt R, Marra M, Jones S. Achieving Transparent and Consistent High Quality in cDNA Finishing

304. The Sixth Canadian Computational Chemistry Conference, Vancouver BC, July 2006. Li YY, An J, **Jones SJM**. A high throughput computational approach to find new uses for old drugs.

305. Genome BC Genomics Forum. Vancouver, BC. July 2006. Bainbridge MN, Warren RL, Delany A, Griffith M, Hirst M, Magrini V, Mardis ER, Sadar MD, Romanuik T, Siddiqui AS, Marra MA, **Jones SJM**. Analysis of the prostate cancer cell line LNCaP transcriptome using a sequencing-by-synthesis approach.

306. 2006 Annual Meeting for the American Society of Colon and Rectal Surgeons. Seattle WA. June 2006. Leung S, Griffith O, Phang T, **Jones S**, Masoudi H, Wiseman S. Additional variables other than AJCC staging show clinical utility for colon cancer patient prognostication.

307. 8th Annual Meeting of IBANGS. Vancouver BC. May 2006. 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.

308. 8th Annual Meeting of IBANGS. Vancouver BC. May 2006. Simpson E, Wasserman W, Holt R, **Jones**

**SJM**, Goldowitz D, Ward S, Kingsley S. Pleiades Promoter Project: Genomic Resources Advancing Therapies for Brain Disorders.

309. Canadian Breast Cancer Research Alliance meeting. Montreal QU. 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.

310. The Biology of Genomes. Cold Spring Harbor Laboratory, NY. May 2006. Delaney AD, Li HI, 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, **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 SMP genotype chips.

311. The Biology of Genomes. 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.

312. The Biology of Genomes. 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.

313. Finishing in the Future. Santa Fe, NM. May 2006. Ali J, Chun E, Liao N, Liu J, Palmquist D, Wynhoven B, Huang P, Kirkpatrick R, Siddiqui A, Holt R, Marra M, **Jones S**. A high throughput bovine full length cDNA sequencing pipeline.

314. Genomics Forum Research Exchange. Vancouver, BC. April 2006. Li YY, An J, **Jones SJM.** Finding new protein interactions for old drugs: inverse docking for the prediction of drug side effects.

315. 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*.

316. 2006 Genomics Forum: Student Biotechnology Network Research Exchange. Vancouver, BC. April 2006. Ruzanov P, **Jones SJ**, Moerman DG, Riddle DL. Discovery of novel alternatively spliced transcripts based on computational predictions supported by SAGE data in *C.elegans*.

317. 2006 Genomics Forum: Student Biotechnology Network Research Exchange. Vancouver, BC. April 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*

318. 2006 Genomics Forum: Student Biotechnology Network Research Exchange. Vancouver, BC. April 2006. Bainbridge MN, Warren RL, Hirst M, Romanuik T, Zeng T, Go A, Delany 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.

319. 2006 Genomics Forum: Student Biotechnology Network Research Exchange. Vancouver, BC. April 2006. Sleumer MC, Bilenky M, Dagpinar M, Griffith OL, He A, Pan W, Pleasance ED, Robertson AG, Yuen W, Zhang X, **Jones SJM**. *de Novo* Detection of Regulatory Modules in *C. elegans*.

320. 2006 Genomics Forum: Student Biotechnology Network Research Exchange. Vancouver, BC. April 2006. Montgomery SB, Bainbridge M, Griffith OL, Schinas J, Brooks-Wilson A, **Jones SJM**. In Silico approach to the Identification of Regulatory Polymorphisms within Promoter Regions of Homo Sapiens using Comparative Genomics, Regulatory Feature and Sequence Composition Metrics.

321. 2006 Genomics Forum: Student Biotechnology Network Research Exchange. Vancouver, BC. April 2006. Li YY, An J, **Jones SJM**. Finding new protein interactions for old drugs: inverse docking for the prediction of drug side effects.

322. 2006 Genomics Forum: Student Biotechnology Network Research Exchange. Vancouver, BC. April 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 M. A Sequence-ready physical map of a Follicular Lymphoma genome

323. 2006 Genomics Forum: Student Biotechnology Network Research Exchange. Vancouver, BC. April 2006.Liao N, Kirkpatrick R, Liu J, Chun E, Wynhoven B, Palmquist D, Siddiqui A, **Jones S**. A Novel Protocol for Filtering, Clustering and Analysizing EST Sequences.

324. 2006 Genomics Forum: Student Biotechnology Network Research Exchange. Vancouver, BC. April 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.

325. 2006 Genomics Forum: Student Biotechnology Network Research Exchange. Vancouver, BC. April 2006. Ali J, Wynhoven B, Palmquist D, Elizabeth Chun H-J, 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 C, 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.

326. 2006 Genomics Forum: Student Biotechnology Network Research Exchange. Vancouver, BC. April 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 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.

327. 97th Annual Meeting for the American Association for Cancer Research. Washington, DC. April 2006. Griffith OL, Wiseman SM, Jones SJM. Meta-analysis of thyroid cancers expression profiling studies – Identification of most promising biomarkers for tissue microarray analysis.

328. 3rd Canadian Developmental Biology Conference. Mont-Tremblant, QU. April 2006. Hoodless PA, Vrljicak1 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.

329. Keystone Symposia-Nuclear Receptors: Steroid Sisters. Banff, Alberta March 2006. Wang G, Jones S, Marra M, Sadar MD. Genes targeted by both the Androgen and PKA signaling pathways that dependent upon Androgen Receptor.

330. Systems Biology: Global Regulation of Gene Expression Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, March 2006. Sleumer MC, Bilenky M, Dagpinar M, Griffith OL, He A, Pan W, Pleasance ED, Robertson AG, Siddiqui AS, Yuen W, Zhang X, **Jones SJM**. *De Novo Detection of Regulatory Modules in C. elegans*., Poster Presentation.

331. 2006 AGBT Meeting. Marco Island, FL. February 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.

332. 2006 AGBT Meeting. Marco Island, FL. February 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 HI, Nayar T, Schein J, Siddiqui A, Friedman JM, Marra MA. Genome copy number analysis of idiopathic mental retardation using high-density ogligonucleotide microarrays.

333. Plant and Animal Genome XIV Conference. San Diego, CA. January 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, Marra M, **Jones S**. An efficient strategy for full length clone selection in *Bos Taurus*.

334. Plant and Animal Genome XIV Conference. San Diego, CA. January 2006. Moore SS, Luo Guan L, Lobo S, Meng Y, Taniguchi M, Wang Z, Stott J, Ali J, Kirkpatrick R, 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.

335. Plant and Animal Genome XIV Conference. San Diego, CA. January 2006. Ali J, Wynhoven B, Palmquist D, Chun HJE, 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 C, 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.*

336. PSB 2006. Maui, HI. January 2006. Griffith OL, Montgomery SB, Bilenky M, Pleasance ED, Prychyna Y, Sleumer MC, Zhang X, **Jones SJM**. ORegAnno: An open access database and curation system for literature-derived, experimentally-verified promoters, transcription factor binding sites, and regulatory variation.

337. The 15th Annual Meeting of the Society of Basic Urologic Research. Miami, Florida, USA. December 2005. Genes targeted by both the Androgen and PKA Signalling Pathways that dependent upon Androgen Receptor. Wang G, Jones S, Marra M, Sadar MD.

338. University of British Colmubia Medical Genetics Research Retreat. Vancouver BC. November 2005. Griffith OL, Jones SJM. Differential Co-Expression Analysis for the Identification of Dysregulated Genes in Prostate Cancer.

339. BC Cancer Agency Annual Cancer Conference 2005. Vancouver, BC. November 2005. 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, Wong D, Lee D, Mathewson C, Wye N,

Bosdet I, Birol I, Siddiqui A, Schein J, Jones S, Horsman D, Gascoyne R, Connors J, M Marra. A Sequence-ready physical map of a Follicular Lymphoma genome.

340. BC Cancer Agency Annual Cancer Conference 2005. Vancouver, BC. November 2005. Wang G, **Jones S**, Marra M, Sadar MD. Identification of Genes Targeted by the Androgen and PKA Signalling Pathways in Prostate Cancer Cells.

341. BC Cancer Agency Annual Cancer Conference 2005. Vancouver, BC. November 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.

342. BC Cancer Agency Annual Cancer Conference 2005. Vancouver, BC. November 2005. Morin RD, Chang E, Petrescu A, Liao N, Baross A, Hirst M, Kirkpatrick R, Griffith M, Butterfield YS, Stott J, Barber S, Babakaiff R, Matsuo C, Wong D, Yang GS, Smailus DE, Brown-John M, Mayo M, Beland J, Gibson S, Olson T, Tsai M, Featherstone R, Chand S, Siddiqui AS, Marra MA, **Jones SJM**, Holt RA. The Mammalian Gene Collection: A growing resource of clones of human, mouse, rat, xenopus and zebrafish, is rich in genes implicated in oncogenesis.

343. BC Cancer Agency Annual Cancer Conference 2005. Vancouver, BC. November 2005. Montgomery SB, Griffith O, Schinas J, Brooks-Wilson A, **Jones SJM**. In Silico Determination of Functional Non-Coding Polymorphisms.

344. BC Cancer Agency Annual Cancer Conference 2005. Vancouver, BC. November 2005. Quayle AP, Siddiqui AS, **Jones SJM**. Application of Interaction Networks for the Prediction of Drug Discovery combinations in cancer therapy.

345. BC Cancer Agency Annual Cancer Conference 2005. Vancouver, BC. November 2005. Sleumer MC, Bilenky M, Griffith OL, Pan W, Pleasance ED, Robertson AG, Zhang X, **Jones SJM**. The Search for Regulatory Elements in the model organism *C. elegans*.

346. BC Cancer Agency Annual Cancer Conference 2005. Vancouver, BC. November 2005. Romanuik T, Holt R, **Jones S**, Marra M., Sadar MD. Discovery of Genes involved in cross-talk between the androgen and PKA pathways in prostate cancer using long serial analysis of gene expression.

347. BC Cancer Agency Annual Cancer Conference 2005. Vancouver, BC. November 2005. Griffith OL, Jones SJM. Differential coexpression analysis for the identification of dysregulated genes in prostate cancer.

348. BC Cancer Agency Annual Cancer Conference 2005. Vancouver, BC. November 2005. Griffith OL, Wiseman SM, Jones SJM. Meta-analysis of thyroid cancers expression profiling studies – Identification of most promising biomarkers for tissue microarray analysis.

349. BC Cancer Agency Annual Cancer Conference 2005. Vancouver, BC. November 2005. Pleasance ED, Sleumer MC, Bilenky M, Chuang M, Dagpinar M, Griffith OL, He A, Lin K, Montgomery S, Oveisi M, Pan W, Robertson G, Robertson N, Teague K, Varhol R, Yuen W, Zhang M, Gorski SM, Siddiqui A, Jones SJM. A method for genome-wide *CIS*-Regulatory element discovery I *Drosophila Melanogaster.*

350. Genome Informatics. Cold Spring Harbour Laboratory, NY. November 2005. Kirkpatrick R, Liao N, Reid K, Peng F, Lucker J, Martin D, Lund S, Siddiqui A, **Jones S**. Genomics Studies in the Grapevine.

351. Genome Informatics. Cold Spring Harbour Laboratory, NY. November 2005. Warren RL, Varabei D, Platt D, Huang X, Messina D, Hillier L, Yang S, Wallis J, Chinwalla A, Siddiqui AA, Schein JE, Marra MA, **Jones SJM**. Real-time contiguity improvement of whole-genome shotgun assemblies using physical maps.

352. Genome Informatics, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, Nov.2005. Pleasance ED, Sleumer MC, Bilenky M, Chuang M, Dagpinar M, Griffith OL, He A, Lin K, Montgomery S, Oveisi M, Pan W, Robertson G, Robertson N, Teague K, Varhol R, Yuen W, Zhang X, Gorski SM, Siddiqui A, **Jones SJM.** A method for genome-wide cis-regulatory element discovery in Drosophila melanogaster. Abstract.

353. ISCB 2005 – Sixth Internationl Conference on Systems Biology. Boston, MA. October 2005. Quayle AP, Siddiqui AS, **Jones SJM**. Application of Interaction Networks for the Prediction of Drug Discovery combinations in cancer therapy.

354. 55th Annual Meeting of The American Society of Human Genetics. Salt Lake City, UT. October 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 S, Li I, McGillivray B, 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.

355. 2005 IEEE Computational Systems Bioinformatics Conference. August 2005. Stanford University, CA. Siddiqui A, Robertson G, Bilenky M, Astakhova T, Griffith OL, Hassel M, Lin K, Montgomery S, Oveisi M, Pleasance E, Robertson N, Sleumer MC, Teague K, Varhol R, Zhang M, **Jones S**. C*is*-regulatory element prediction in mammalian genomes. Abstract.

356. Plant Biology 2005. Seattle, WA. July 2005. Reid K, Liao N, Kirkpatrick R, Stott J, Peng F, Schlosser J, Shukin R, Bowen P, Holt R, **Jones S**, Marra M, Bohlmann J, Lund S. Development of an EST Database for Gene Discovery in Wine Grape.

357. 15th Biennial International *C.elegans* Meeting. Los Angeles, CA. June 2005. Shin H, Baillie D, **Jones S**. Analysis of conservation and frequency of the trans-splice sites in C. elegans suggests that the neurons have a significantly smaller proportion of genes with the conserved trans-splice site compared to other tissue type genes.

358. 15th Biennial International *C.elegans* Meeting. Los Angeles, CA. June 2005. Sleumer MC, Bilenky M, Griffith OL, Pleasance ED, Robertson AG, Zhang X, **Jones SJM**. The Search for Regulatory Elements in C. elegans.

359. 15th Biennial International *C.elegans* Meeting. 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.

360. 15th Biennial International *C.elegans* Meeting. 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.

361. 15th Biennial International *C.elegans* Meeting. Los Angeles, CA. June 2005. Wong K, McKay SJ, Huang P, Ruzanov P, Hogan M, Pofahl N, Green R, Mills C, Baillie DL, **Jones S**, Marra M, Moerman D. Transcription profiling of C. elegans developmental stages: A comparison of different platforms.

362. 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.

363. 15th Biennial International *C.elegans* Conference. Los Angeles, CA. June 2005. Newbury R, Johnsen R, Anastis D, Fang L, Lin J, Mah A, McKay S, Mills C, Tu D, Viveiros R, Wong K, Vaz Gomes A,

Alexeyenko A, Sonnhammer E, Bürglin TR, Wahlestedt C, Schnabel R, **Jones S**, Moerman D, Baillie D. Insight into human genes of unknown function using *C. elegans* promoter::GFP expression constructs.

364. 6th Interntational Conference: Cryptococcus & Cryptococcosis. Boston, MA. June 2005. Jung W, Bilenky M, Robertson G, **Jones S**, Kronstad J. Computational prediction of *cis*-regulatory elements in *Cryptococcus neoformans*.

365. International Society for Stem Cell Research 3rd Annual Meeting. San Francisco, CA. June 2005. Raouf A, Zhao Y, Kent D, Stingl 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.

366. 34th Annual Meeting of the American Aging Association: Aging – Mechanisms and Prevention. 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.

367. CanFly 2005, Burnaby, BC, May, 2005. Pleasance ED, Sleumer MC, Bilenky M, Robertson AG, Griffith OL, Zhang X, Lin K, He A, Astakhova T, Hassel M, Montgomery S, Oveisi M, Robertson N, Varhol R, Teague K, Gorski SM, Siddiqui A, **Jones SJM**. A method for genome-wide cis-regulatory element discovery in Drosophila melanogaster using multiple Drosophila genomes and large-scale gene expression data. Abstract.

368. Pathology Research Day, University of British Columbia, Vancouver, BC. May 2005. Wang G, **Jones S**, Sadar MD. Affymetrix GeneChip Analyisis of Androgen Regulated Genes in Prostate Cancer LNCaP Cell.

369. The Biology of Genomes. Cold Spring Harbor Laboratory, NY. May 2005. Robertson G, Bilenky M, Astakhova T, Griffith OL, Hassel M, Lin K, Montgomery S, Oveisi M, Pleasance E, Robertson N, Sleumer MC, Varhol R, Zhang M, Siddiqui A, **Jones S**, Zhou J, Sander J. High-throughout *cis*-regulatory element PREDICTION in mammalian genomes. Abstract.

370. 5th Annual BC Net Conference. Vancouver, BC. April 2005. McVicker G, He D, Montgomery S, Sawkins J, Shah S, Yuen MMS, **Jones S**, Ouellette BFF. Pegasys: software for creating and executing workflows for genome analysis.

371. Genomics Forum Research Exchange 2005. Vancouver, BC. April 2005. Pleasance ED, Gorski SM, Marra MA, **Jones SJM**. SAGE database analysis of programmed cell death in *Drosophila melanogaster* and cancer.

372. World Microarray Congress 2005. Vancouver, BC. March 2005. **Jones S**, Bilenky M, Griffith O, Lin K, Montgomery S, Oveisi M, Pan Y, Pleasance E, Robertson G, Robertson N, Sleumer M, Teague K, Varhol R, Siddiqui A. Using gene expression data and orthology to detect *cis*-regulatory elements across mammalian genomes.

373. International Workshop on Encoding Information in DNA Sequences. Okinawa, J. February 2005. Montgomery SB, **Jones SJM**. A bioinformatic approach to the identification of regulatory variation.

374. International Workshop on Encoding Information in DNA Sequences. Okinawa, J. February 2005. Griffith O, Pleasance E, Fulton D, Bilenky M, Robertson G, Oveisi M, Pan YJ, Ester M, Siddiqui A, **Jones S**. Gene expression platforms for global coexpression analyses – assessment and integration for studying of gene deregulation in cancer.

375. 2005 AGBT Meeting. Marco Island, FL. February 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.

376. 2005 AGBT Meeting. Marco Island, FL. February 2005. **Jones S**, Astakhova T, Bilenky M, Griffith O, Hassel M, Li Y, Lin K, Montgomery S, Oveisi M, Pan Y, Pleasance E, Robertson G, Robertson N, Sleumer M, Teague K, Tsang E, Varhol R, Siddiqui A. A high-throughout approach for *cis*-regulatory element detection across mammalian genomes.

377. Genome Canada: National Genomics and Proteomics Symposium. Vancouver, BC. November 2004. Siddiqui A, Butterfield Y, Guin R, Kirkpatrick R, McVicker G, Mayo M, Shah S, Warren R, Chan A, Chun E, Chui G, Li B, Liao N, Liu J, Morin R, Palmquist D, Santos J, Sawkins J, Taylor G, Xu T, Yuen M, Ouellette BFF, **Jones SJM**. Bioinformatics for high-throughput sequencing at the Genome Sciences Centre (GSC) and UBC Bioinformatics Centre (UBiC), Vancouver.

378. Genome Canada: National Genomics and Proteomics Symposium. Vancouver, BC. November 2004. **Jones S**, Astakhova T, Bilenky M, Griffith O, Hassel M, Lin K, Oveisi M, Pleasance E, Robertson G, Sleumer M, Siddiqui A. A high-throughout approach for *cis*-regulatory element detection across entire mammalian genomes.

379. Genome Canada: National Genomics and Proteomics Symposium. Vancouver, BC. November 2004. Kuo B, Wasserman WW, **Jones SJ**, Simpson EM. Genomic exploration of splicing in SAGE tags.

380. BC Cancer Agency Annual Cancer Conference 2004. Vancouver, BC. November 2004. Wang G, **Jones S**, Sadar MD. Affymetrix GeneChip Analyisis of Androgen Regulated Genes in Prostate Cancer LNCaP Cell.

381. BC Cancer Agency Annual Cancer Conference 2004. Vancouver, BC. November 2004. Quayle AP, Siddiqui AS, **Jones SJM**. Modeling Interaction for applications in Cancer Therapy.

382. BC Cancer Agency Annual Cancer Conference 2004. Vancouver, BC. November 2004. Griffith G, Pleasance E, Fulton D, Bilenky M, Robertson G, Oveisi M, Jia Pan Y, Ester M, Siddiqui A, **Jones S**. Large-Scale comparison of ublicly available SAGE, cDNA, and Oligonucleotide Microarray Expression Data for Global Co-Expression Analyses.

383. BC Cancer Agency Annual Cancer Conference 2004. Vancouver, BC. November 2004. Sleumer MC, Bilenky M, Griffith O, Hao H, Hassel M, Pleasance E, Robertson AG, **Jones SJM**. Understanding gene regulation using the model organism *C. elegan.*

384. BC Cancer Agency Annual Cancer Conference 2004. Vancouver, BC. November 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.

385. BC Cancer Agency Annual Cancer Conference 2004. Vancouver, BC. November 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.

386. BC Cancer Agency Annual Cancer Conference 2004. Vancouver, BC. November 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 trasncriptome profiling: SAGE and DNA mircoarray platforms at Canada's Michael Smith Genome Sciences Centre.

387. BC Cancer Agency Annual Cancer Conference 2004. Vancouver, BC. November 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.

388. BC Cancer Agency Annual Cancer Conference 2004. Vancouver, BC. November 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.

389. BC Cancer Agency Annual Cancer Conference 2004. Vancouver, BC. November 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.

390. Inland Northwest Cancer Conference, Spokane, WA, USA. November 2004. Wang G, **Jones S**, Sadar MD. Affymetrix GeneChip Analyisis of Androgen Regulated Genes in Prostate Cancer LNCaP Cell.

391. Identification of Functional Elements in Mammalian Genomes. Cold Spring Harbour Laboratory, NY. November 2004. Montgomery S, Fu T, Guan J, Lim J, Lin K, McVicker G, Ouellette F, Wasserman W, Siddiqui A, Jones, S. A Collaborative Framework for Regulatory Element Detection.

392. Identification of Functional Elements in Mammalian Genomes. Cold Spring Harbour Laboratory, NY. November 2004. **Jones S**, Astakhova T, Bilenky M, Griffith O, Hassel M, Lin K, Oveisi M, Pleasance E, Robertson G, Sleumer M, Siddiqui A. A high-throughout approach for *cis*-regulatory element detection across entire mammalian genomes.

393. EMBL 2nd Symposium, Heidelberg, Germany. October 2004. Mawji NR, Blaszczyk N, Masri B, Wang G, Jones S, Marra M, Sadar MD. Comparison of the Transcriptome and Proteome of Prostate Cancer Cells Treated with Osteoblast Derived Factors.

394. 54th Annual Meeting of the American Society of Human Genetics. Toronto, ON. October 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.

395. 18th International Mouse Genome Conference. Seattle, WA. October 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.

396. Neuroscience 2004. The Society for Neuroscience 34th Annual Meeting. San Diego, CA. October 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).

397. SAGE 2004 Conference. Boston, MA. September 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 Cell Lines.

398. SAGE 2004 Conference. Boston, MA. September 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*.

399. Cold Spring Harbor Laboratory/Wellcome Trust Conference: Genome Informatics.Hinxton, UK. September, 2004. **Jones S**, Astakhova T, Bilenky M, Griffith O, Hassel M, Kennedy J, Li Y, Lin K, Montgomery S, Oveisi M, Pleasance E, Robertson G, Sleumer M, Tsang E, Fu T, Siddiqui A. A high-throughout approach for cis-regulatory element detection across entire mammalian genomes. Abstract.

400. Cold Spring Harbor Laboratory/Wellcome Trust Conference: Genome Informatics.Hinxton, UK. September, 2004. Siddiqui AS, Delaney A, Khattra J, Varhol R, Leung D, Simpson EM, Helgason C, Hoodless P, Marra M **Jones S**. A Quantitative and Comprehensive Atlas of Gene Expression in Mouse Development.

401. Cold Spring Harbor Laboratory/Wellcome Trust Conference: Genome Informatics.Hinxton, UK. September, 2004. Montgomery S, Astakhova T, Fu T, Guan J, Hassel M, He D, Kennedy J, Li1 Y, Lim J, Lin K, Ouellette F, Shah S, Sleumer M, Wasserman Q, Siddiqui A, **Jones S**. A distributed, decentralized peer-to-peer platform for bioinformatics analysis.

402. Mouse Molecular Genetics Annual Meeting. Cold Spring Harbor Laboratory, NY. September 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.

403. 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 Genes with major effects on Life Span in *C. elegans* genes associated with longevity using serial analysis of gene expression (SAGE).

404. 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 Bodywall Muscle Cells.

405. 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.

406. 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, Goszcynski 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.*

407. 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.

408. 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. Trancription Profiling of *C. elegans* developmental stages using Serial Analysis of Gene Expression and Microarrays.

409. 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.

410. 63rd Annual Meeting for the Society for Developmental Biology. Calgary, AB. July 2004. Robertson G, Bilenky M, Hassel M, McKay S, Sleumer M, Fu T, Siddiqui A, **Jones S**. A discovery workspace for gene regulation motifs and modules.

411. 63rd Annual Meeting for the Society for Developmental Biology. Calgary, AB. July 2004. Robertson G, Hassel M, Bilenky M., Sleumer M, Astakhova T, Lin K, Li Y, Tsang E, Griffith O, Pleasance E, Teague K,

Robertson N, Varhol R, McKay S, Fu T, Siddiqui A, **Jones S**. A regulatory element discovery workspace and database.

412. 63rd Annual Meeting for the Society for Developmental Biology. Calgary, AB. July 2004. Mah AK, Asano J, Bilenky M, Boroevich K, Chan S, Dube N, Fang N, 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*.

413. American Aging Association Annual Meeting: Molecular Mechanisms of Aging—As Modulated by Genes, Hormones and Oxidative Events. St. Petersburg, FL. June 2004. Halaschek-Wiener J, McKay S, **Jones S**, Marra MA, Riddle D, Brooks-Wilson A. Analysis of Long Lived *C. elegans daf-2* mutants using Serial Analysis of Gene Expression.

414. CIHR Canadian Student Health Research Forum. Winnipeg, MN. June 2004.Griffith O, Pleasance E, Fulton D, Bilenky M, McKay S, Oveisi M, Ruzanov P, Wong K, Zuyderduyn S, Ester M, Siddiqui A, **Jones S**. Gene Expression Platforms for Global Co-Expression Analyses: A Comparison of spotted cDNA microarrays, Affymetrix microarrays, and SAGE.

415. The First Northern Lights Summer Conference, CFBS 47th Annual Meeting. Vancouver BC. June 2004. Wang G, **Jones S**, Sadar MD. Affymetrix GeneChip analysis of the Gene Expression during Progression of Prostate Cancer to Androgen Independence.

416. 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.

417. 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.

418. Pathology Research Day, University of British Columbia, Vancouver, BC. May 2004. Wang G, **Jones S**, Sadar MD. Affymetrix GeneChip analysis of the Gene Expression during Progression of Prostate Cancer to Androgen Independence.

419. 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.

420. OSCAR Symposium 2004. Winnipeg, MA. May 2004. Li B, Mayo M, Siddiqui A, **Jones S**. Cluster Evolution at the Genome Sciences Centre.

421. 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.

422. 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.

423. The Biology of Genomes. Cold Spring Harbor Laboratory, NY. May 2004. Schnerch A, Khattra J, 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.

424. The Biology of Genomes. Cold Spring Harbor Laboratory, NY. May 2004. Griffith O, Pleasance E, Fulton D, Bilenky M, McKay S, Oveisi M, Ruzanov P, Wong K, Zuyderduyn S, Siddiqui A, **Jones S**. Large-scale comparison of SAGE, cDNA microarray, and Affymetrix gene expression platforms for global co-expression analyses.

425. The Biology of Genomes. Cold Spring Harbor Laboratory, NY. May 2004. McKay SJ, Johnsen R, Baillie DL, **Jones SJM**, Marra M, Khattra J, Asano J, Bilenky M, Chan S, Dube N, Fang N, Goszczynski B, Halfnight B, Hassel M, Hollebakken R, Huang P, Jensen V, Lee A, Mah A, Mills C, McGhee J, Newbury R, Pouzyrev A, Riddle DL, Rogalski T, Robertson G, Ruzanov P, Tian H, Tu D, Warner A, Wong K, Wong S, Zhao Z, Moerman DG. Gene expression profiling of cells, tissues and developmental stages of the nematode *C. elegans.*

426. 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.

427. 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 AL, Tsai M, Yang G, Cooper D, Gunter D, Tuskan, Bohlmann J, Ritland K, Ellis B, Douglas C, Siddiqui A, Holt R, **Jones S**, Marra M. Gene discovery in poplar.

428. The Biology of Genomes. Cold Spring Harbor Laboratory, NY. May 2004. Marra M, Gerhardt D, Simpson E, Hoodless P, **Jones S**, Riggins G, Helgason C, Delaney A. The atlas of gene expression in mouse development.

429. 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.

430. The Biology of Genomes. Cold Spring Harbor Laboratory, NY. May 2004. McGhee JD, Robertson G, Khattra J, Moerman D, Baillie DL, **Jones S**, Marra M, S McKay. The Transcription Factor Network Regulating Development of the *Caenorhabditis elegans* Intestine.

431. The Biology of Genomes. Cold Spring Harbor Laboratory, NY. May 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.

432. 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).

433. Annual Canadian Developmental Biology Symposium. Banff, AB. April 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.

434. 2004 BCNET - WestGrid - Netera Advanced Networks Conference. Vancouver, BC. April 2004. Fu T, Astakhova T, Bilenky M, Griffith O, Hassel M, Kennedy J, Lin K, Montgomery S, Robertson G, Sleumer M, Tsang E, Fu T, Siddiqui A, **Jones S**. Sockeye – a distributed application for gene regulation analysis.

435. 2004 Genomics Forum: Genomics and the Science of Life. Vancouver, BC. March 2004. **Jones S**, Griffith O, Pleasance E, Fulton D, Oveisi M, Astakhova T, Hassel M, Sleumer M, Kennedy J, Li Y, Lin K, Roberston 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.

436. 2004 Genomics Forum: Genomics and the Science of Life. Vancouver, BC. March 2004. Varhol R, Zuyderduyn S, Oveisi-Fordoei M, Fjell C, Robertson N, Siddiqui A, **Jones S**. DISCOVERYspace: A Gene Expression Analysis Tool.

437. 2004 Genomics Forum: Genomics and the Science of Life. Vancouver, BC. March 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.

438. 2004 Genomics Forum: Genomics and the Science of Life. Vancouver, BC. March 2004. Kirkpatrick R, Liu J, Palmquist D, Butterfield Y, Siddiqui A, **Jones S**, Marra M. EST Sequencing Bioinformatics Pipeline.

439. 2004 Genomics Forum: Genomics and the Science of Life. Vancouver, BC. March 2004. 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 A, **Jones S**, Marra M. Full length cDNA sequencing Bioinformatics pipeline.

440. 2004 Genomics Forum: Genomics and the Science of Life. Vancouver, BC. March 2004. Li B, Mayo M, Brown G, Siddiqui A, Jones S. High Performance Computing and Bioinformatics.

441. 2004 Genomics Forum: Genomics and the Science of Life. Vancouver, BC. March 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.

442. 2004 Genomics Forum: Genomics and the Science of Life. Vancouver, BC. March 2004. Montgomery SB, Astakhova T, Hassel M, Kennedy J, Lim J, Lin K, Sleumer M, Wasserman WW, Fu T, Siddiqui AS, **Jones SJM**. Chinook: Peer-to-peer bioinformatics services.

443. 2004 Genomics Forum: Genomics and the Science of Life. Vancouver, BC. March 2004. Griffith O, Pleasance E, Fulton D, Bilenky M, McKay S, Oveisi M, Ruzanov P, Wong K, Zuyderduyn S, Siddiqui A, **Jones S**. Comparison of SAGE, cDNA microarray, and Affymetrix gene expression platforms for consistency and biological relevance of large-scale global co-expression analyses.

444. 2004 Genomics Forum: Genomics and the Science of Life. Vancouver, BC. March 2004. Warren R, Myhre M, Dosanjh M, Petrescu A, Yang G, Scott JM, Butterfield Y, Schein JE, Shin H, Latreille P, Khattra J, Smailus D, Siddiqui A, Holt R, **Jones S**, Marra M, Mohn WW, Fukuda M, Davies J, Eltis LD. Whole Genome Shotgun Assembly and Characterization of Rhodococcus SP. RHA1, A PCB-Degrading Actinomycete.

445. 2004 Genomics Forum: Genomics and the Science of Life. Vancouver, BC. March 2004. Sleumer MC, 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.

446. 2004 Genomics Forum: Genomics and the Science of Life. Vancouver, BC. March 2004. Pleasance ED, Gorski SM, Marra MA, **Jones SJM**. Identification of novel programmed cell death genes using large-scale gene expression data and comparative genomics approaches.

447. 2004 Genomics Forum: Genomics and the Science of Life. Vancouver, BC. March 2004. Quayle AP, Siddiqui AS, **Jones SJM**. Modelling Interaction Networks for Application to Cancer Therapy.

448. 2nd Annual Canadian Gene Expression Conference. Vancouver, BC. March 2004. **Jones S**, Griffith O, Pleasance E, Fulton E, Oveisi M, Astakhova T, Hassel M, Sleumer M, Kennedy J, Li Y, Lin K, Roberston 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.

449. 2nd Annual Canadian Gene Expression Conference. Vancouver, BC. March 2004. Griffith O, Pleasance E, Fulton D, Bilenky M, McKay S, Oveisi M, Ruzanov P, Wong K, Zuyderduyn S, Siddiqui S, **Jones S**. Gene Expression Platforms – A comparison of spotted cDNA microarrays, affymetrix oligonucleotide microarrays, and serial analysis of gene expression (SAGE) for global co-expression analyses.

450. 2nd Annual Canadian Gene Expression Conference. Vancouver, BC. March 2004. Pleasance ED, Gorski SM, Marra MA, **Jones SJM**. Identification of novel programmed cell death genes using large-scale gene expression data and comparative genomics approaches.

451. 2nd Annual Canadian Gene Expression Conference. Vancouver, BC. March 2004. Baross A, Butterfield YSN, Coughlin SM, Zeng T, Griffith M, Griffith OL, 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.

452. 2nd Annual Canadian Gene Expression Conference. Vancouver, BC, March 2004. Robertson G, Bilenky M, Hassel M, Sleumer M, McKay S, Fu T, Siddiqui A, **Jones S**. A Discovery Workspace for Gene Regulation Motifs and Modules. Abstract.

453. Systems Biology: Genomic approaches to transcriptional regulation. Cold Spring Harbor Laboratory, NY. March 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.

454. Systems Biology: Genomic approaches to transcriptional regulation. Cold Spring Harbor Laboratory, NY. March 2004. McGhee JD, Robertson G, Khattra J, Moerman D, Baillie DL, **Jones S**, Marra M, McKay S. The Transcription Factor Network Regulating Development of the *Caenorhabditis elegans* Intestine.

455. Keystone Symposia: Biological Discovery Using Diverse High-Throughput Data. Steamboat Springs, CO. March 2004,Quayle S, Hare H, Hwang D, **Jones S**, Schein J, Marra M, Sadar M.D. A custom microarray for profiling gene expression changes in advanced prostate cancer.

456. Keystone Symposia: Signaling in Vertebrate Organogenesis (C4). Santa Fe, NM. March 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.

457. GenomeBC Research Exchange, Vancouver, BC, March 26 2004. Montgomery SB, Astakhova T, Hassel M, Kennedy J, Lim J, Lin K, Sleumer M, Wasserman WW, Fu T, Siddiqui AS, **Jones SJM.** Chinook: P2P Bioinformatics Services. Abstract.

458. The ASI Exchange. Vancouver, BC. March 2004. Montgomery 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, **Jones S**. Sockeye: A platform for *cis*-regulatory element discovery. Abstract.

459. 2004 AGBT Meeting. Marco Island, FL. February 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.

460. 2004 AGBT Meeting. Marco Island, FL. February 2004. Butterfield YS, Griffith M, Griffith O, Guin R, Kirkpatrick R, Liao N, Liu J, Palmquist D, Petrescu AS, Stott JM, Yang GSH, Barber SA, 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.

461. 2004 AGBT Meeting. Marco Island, FL. February 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

462. 2004 AGBT Meeting. Marco Island, FL. February 2004. Baross A, Butterfield YSN, Coughlin SM, Griffith M, Griffith OL, Khattra J, McDonald HL, McKay SJ, 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.

463. 2004 AGBT Meeting. Marco Island, FL. February 2004. Baross A, Schertzer M, Zuyderduyn SD, **Jones SJM**, Marra MA, M. Lansdorp P. The Effect of Telomerase (hTERT) and Ataxia Telangiectasia Mutated (ATM) on Gene Expression Profiles in Human Fibroblasts.

464. 2004 AGBT Meeting. Marco Island, FL. February 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 SS, Masson A, Mayo M, McLeavy C, Olson T, Pandoh P, Prabhu A, Shin H, Spence L, Stott J, Taylor S, Tsai M, Yang G, Albertson D, Lam W, Choy C, Osoegawa K, Zhao S, de Jong PJ, Schein J, **Jones S**, Marra M. Whole Genome Mammalian Clone Sets for High-Resolution BAC Arrays.

465. 2004 AGBT Meeting. February 2004. Marco Island, FL. Raouf A, Zhao Y, Khattra J, Schnerch A, Asano J, **Jones S**, Marra M, Eaves C. Representative Amplification of RNA for the Application of Serial Analysis of Gene Expression (SAGE) to Very Small Cell Samples.

466. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. November 2003. Sleumer MC, Astakhova T, Bilenky M, Griffith O, Hassel M, Kennedy J, Lin K, Robertson G, Tsang E, Ung J, Fu T, Siddiqui A, **Jones SJM**. Sockeye: A 3D Genome Visualization Platform for Gene Regulation Analysis.

467. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. November 2003. Montgomery SB, Fu T, Siddiqui AS, **Jones SJM**. Chinook: Peer-to-peer distributed bioinformatics application server.

468. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. November 2003. Zuyderduyn S, Varhol R, Oveisi-Fordoei M, Fjell C, Robertson N, Sadiqui A, **Jones S**. DISCOVERYspace: A Gene Expression Analysis Tool.

469. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. November 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.

470. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. November 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.

471. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. November 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.

472. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. November 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.

473. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. November 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.

474. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. November 2003. Bosdet I, Mathewson C, Lee D, Chiu R, Cloutier A, Featherstone R, Fjell C, Kryzwinski 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.

475. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. November 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.

476. BC Cancer Agency Annual Cancer Conference. Vancouver, Canada. November 2003. Quayle S, Hare H, Hwang D, **Jones S**, Schein J, Marra M, Sadar M. Subtractive hybridization for identifying novel expressed sequences in prostate cancer .

477. BC Cancer Agency Annual Cancer Conference. Vancouver, Canada. November 2003. Wang G, **Jones S**, Sadar MD. Affymetrix GeneChip analysis of the Gene Expression during Progression of Prostate Cancer to Androgen Independence.

478. International Conference on Applied Genomics. Amsterdam, The Netherlands. October 2003. Quayle S, Hare H, Hwang D, **Jones S**, Schein J, Marra M, Sadar, M. Subtractive hybridization for identifying novel expressed sequences in prostate cancer.

479. University of British Columbia Genetic Students' Retreat. Vancouver, BC. October 2003. Montgomery SB, Fu T, Siddiqui AS, **Jones SJM**. Chinook: Peer-to-peer distributed bioinformatics application server.

480. 15th International Genome Sequencing and Analysis Conference. Savannah, GA. September, 2003. Holt RA, Astell CR, **Jones SJM**, Brooks-Wilson A, Marra MA. The Genome Sequence of the SARS Associated Coronavirus.

481. 1st Canadian Plant Genomics Workshop. Saskatoon, SK. August 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.

482. 10th World Congress on Lung Cancer. Vancouver, BC. August 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.

483. 10th World Congress on Lung Cancer. Vancouver, BC. August 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.

484. 10th World Congress on Lung Cancer. Vancouver, BC. August 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.

485. 94th annual meeting of the American Association for Cancer Research. Washington, DC. July 2003. Bajdik CD, Kuo B, Rusaw S, Young C, **Jones S**, Brooks-Wilson A. Data mining to identify groups of genetically-related cancers.

486. 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.*

487. 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.*

488. 14th International *C. elegans* Meeting, University of California. Los Angeles, CA. July 2003. McKay S, Johnsen R, **Jones S**, Khattra J, Marra M, Moerman D, Ouellette F, Burglin T, Sonnhammer E, Vas Gomes A, Wahlestedt C, Asano J, Chan S, Coughlin S, Fang L, Girn N, Ha E, Huang P, Kai H, Mah A, McDonald H, Pandoh P, Tu D, Warner A, Wong K, Baillie D. Gene expression profiles in cells, tissues and development of *C. elegans.*

489. XI 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, *Puccinia triticina*, EST database from stage-specific cDNA libraries.

490. Thomas L. Petty Aspen Lung Conference, 46th Annual Meeting. Aspen, CO. June 2003. MacAulay C, Longergan K, Chi B, Zuyderduyn S, Shein 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.

491. 14th International Worm Meeting. June 2003. Los Angeles, CA. Bettencourt P, Hewitson M, Stamford J, Jones M, Gonczy P, Coulson A, **Jones S**, Oegema K, Hyman A, Echeverri C. Comprehensive genome wide RNAi screen for cell division genes in C. elegans.

492. Pathology Day. Univeristy of British Columbia, Vancouver, BC. May 2003. Quayle S, Hare H, Akopian V, Hwang D, **Jones S**, Schein J, Tung S, Marra M, Sadar M. Discovery of new genes differentially expressed in androgen independent prostate cancer.

493. The Genome of Homo Sapiens. Cold Spring Harbor Laboratory, NY. May 2003. The Genome Canada *C. elegans II* Consortium including Johnsen R, Mckay S, Khattra J, Ouellette F, **Jones S**, Marra M, Moerman D, Sonnhammer E, Baillie D. Preliminary analysis of expression profiles of human ortholog genes in *C. elegans.*

494. 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.

495. 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.

496. 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*.

497. American Association of Cancer Research 94th Annual Meeting. Toronto, ON. April 2003. Bajdik CD, Brooks-Wilson A, Young C, Rusaw S, **Jones S**. Data mining to identify groups of genetically-related cancers.

498. 1st Canadian Gene Expression Conference. Vancouver, BC. March 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.

499. 1st Canadian Gene Expression Conference. Vancouver, BC. March 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.

500. The ASI Exchange. Vancouver, BC. March 2003. Saeedi P, Krzywinski M, **Jones S**, Marra MA. Automated lane tracking for DNA gel images.

501. Fungal Genetics Conference 2003. Pacific Grove, CA. March 2003. Steen BR, Zuyderduyn S, Lesiuk J, **Jones S**, Perfect J, J Kronstad. Identification of genes that may be relevant for pathogenesis of *Cryptococcus neoformans* using serial analysis of gene expression.

502. Advances in Genome Biology & Technology and Automation in Mapping & DNA Sequencing 4th Annual Meeting. Marco Island, FL. February 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, MacAuley C, Lam W, Choy CO, Osoegawa K, Zhao S, de Jong PJ, Schein J, **Jones S**, Marra M. Abstract. A set of rearrayed BAC clones spanning the human genome.

503. Advances in Genome Biology & Technology and Automation in Mapping & DNA Sequencing 4th Annual Meeting. Marco Island, FL. February 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. Abstract. Verification of *Drosophila melanogaster* sequence assembly using restriction digest BAC fingerprints derived from multiple enzymes.

504. Advances in Genome Biology & Technology and Automation in Mapping & DNA Sequencing 4th Annual Meeting. Marco Island, FL. February 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. Abstract. High-throughput serial analysis of gene expression profiling of cancers.

505. Advances in Genome Biology & Technology and Automation in Mapping & DNA Sequencing 4th Annual Meeting. Marco Island, FL. February 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. Abstract. An integrated approach to transposon-mediated full length cDNA sequencing.

506. Advances in Genome Biology & Technology and Automation in Mapping & DNA Sequencing 4th Annual Meeting. Marco Island, FL. February 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. Abstract. High-throughput gene expression analysis technologies at the British Columbia Cancer Agency.

507. TIGR/ASM Microbial Genomes 3rd Annual Conference. New Orleans, LA. January 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.

508. SAGE 2003. Amsterdam, Netherlands. January 2003. Lam W, Lonergan K, Zuyderduyn S, Shein 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.

509. SAGE 2003. Amsterdam, Netherlands. January 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.

510. SAGE 2003. Amsterdam, Netherlands. January 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.

511. SAGE 2003. Amsterdam, Netherlands. January 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.

512. The American Society for Cell Biology 42nd Annual Meeting. San Francisco, CA. December 2002. Kiger AA, Baum B, **Jones S**, Jones M, Echeverri C, Perrimon N, Functional Genomic Analysis of Cell Morphology Using High-throughput RNAi Screens.

513. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. November 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.

514. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. November 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.

515. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. November 2002. Fjell C, Astakova V, Chiu R, Flibotte S, Saeedi P, Shin H, Schein J, **Jones S**, Marra M. Bioinformatics for genetic physical mapping.

516. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. November 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.

517. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. November 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.

518. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. November 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.

519. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. November 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.

520. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. November 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, MacAuley C, Osoegawa K, Zhao S, deJong PJ, Schein J, **Jones S**, Marra M. A set of rearrayed BAC clones spanning the human genome.

521. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. November 2002. Zuyderduyn S, Varhol R, Oveisi-Fordoei M, Rusaw S, **Jones S**. Exploring gene expression with the discovery platform.

522. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. November 2002. Montgomery S, Astakhova T, Bilenky M, Rak M, Robertson G, Sleumer M, Marra M, **Jones S**. Mammalian gene expression platform.

523. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. November 2002. Rusaw S, Bajdik C, Varhol R, Zuyderdyn S, Astakhov V, **Jones S**. Using natural language processing to find relationships between genes, drugs and cancer.

524. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. November 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.

525. University of British Columbia Medical Genetics Research Day. Vancouver, BC. November 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.

526. University of British Columbia Medical Genetics Research Day. Vancouver, BC. November 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.

527. Canadian Phytopathological Society - British Columbia (CPS-BC) Regional Meeting. Summerland, BC. October 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 wheat leaf rust, Puccinia triticina, EST database from stage-specific cDNA libraries and construction of a corresponding microarray.

528. International Society for Animal Genetics Conference. Gottingen, Germany. August, 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.

529. The 10th International Conference on Intelligent Systems for Molecular Biology. Edmonton, AB. August, 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.

530. West Coast Worm Meeting. August 2002. San Diego, CA. Allan R, Barstead R, Edgley M, Gengyo-Ando K, Holmes J, **Jones S**, Kohara Y, Lansdale M, Liu L, Maydan J, Machiyama E, Mitani S, Moerman D, Moulder G, Nisha M, Noguchi S, Osborn J, Rankin A, Rezania N, Robertson J, Shen B, Tamura M, Viswanathan M, Hughes M, McKay S, Rogers B. The C. elegans Knockout Consortium: Interim Report.

531. BIOKDD 2002 2nd Workshop on Data Mining in Bioinformatics in conjunction with 8th ACM SIGKDD International Conference on Knowledge Discovery and Data Mining. Edmonton, AB. July 2002. Phan JM, Ng R, Yuen MS, **Jones S**. GEA: A Toolkit for Gene Expression Analysis.

532. Midwest Worm Meeting. June 2002. St. Louis, MO. Moulder G, Barstead R, Allan R, Edgley M, Gengyo-Ando K, Holmes J, Hughes M, **Jones S**, Kohara Y, Lansdale M, Liu L, Maydan J, McKay S, Machiyama E, Mitani S, Moerman D, Nisha M, Noguchi S, Osborn J, Rankin A, Rezania N, Robertson J, Rogers B, Shen B, Tamura M, Viswanathan M. The C. elegans Knockout Consortium: Interim Report 2002.

533. 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.

534. 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.

535. 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.

536. Pathology Day. Univeristy of British Columbia, 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.

537. American Association for Cancer Research, Oncogenomics 2002. Dublin, Ireland. May 2002. **Jones S**, Ruzanov P, Asano J, Butterfield Y, Garland E, Girn N, Guin R, Hsaio L, Krzywinski M, Lam W, Lam S, Lee S, Lonergan K, McCauly C, Olson T, Oveisi M, Pandoh P, Saeedi P, Skalska U, Spence L, Smailus D, Stott J, Teague K, Varhol R, Yang G, Zuyderdyn S, Schein J, Marra M. Gene expression profiling of early-stage lung cancers.

538. Genome Sequencing & Biology. Cold Spring Harbor Laboratory, NY. May 2002. **Jones S**, Ruzanov P, Asano J, Butterfield Y, Garland E, Girn N, Guin R, Hsaio L, Krzywinski M, Lam W, Lam S, Lee S, Lonergan K, McCauly C, Olson T, Oveisi M, Pandoh P, Saeedi P, Skalska U, Spence L, Smailus D, Stott J, Teague K, Varhol R, Yang G, Zuyderdyn S, Schein J, Marra M. Identification of genes expressed in early-stage lung cancers.

539. Genome Sequencing & Biology. Cold Spring Harbor Laboratories, NY. May 2002. Krzywinski M, **Jones S**, Bosdet I, Schein J, Marra M. A set of rearrayed BAC clones spanning the human genome.

540. Genome Sequencing & Biology. Cold Spring Harbor Laboratories, NY. May 2002. Bosdet I, Barber S, Chan S, Chiu R, Fjell C, Kryzwinski 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.

541. Genome Sequencing & Biology. Cold Spring Harbor Laboratories, 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.

542. American Association for Cancer Research 93rd Annual Meeting. San Francisco, CA. April 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.

543. 43rd Annual Drosophila Research Conference. San Diego, CA. April 2002. Kiger A, Baum B, Armknecht S, Chang M, Jones M, Coulson A, **Jones S**, Sönnichsen B, Echeverri C, Perrimon N. Functional genomic analysis of cellular morphology using high-throughput RNAi screens.

544. Worm Breeder's Gazette 17: 30. McKay S, Edgley M, Gilchrist E, **Jones S**, Moerman D. 2002. Gene Knockout Methods Available Online.

545. Physiological Genomics & Rat Models. Cold Spring Harbor, NY. December 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.

546. Northwest Urological Society 48th Annual Meeting. Vancouver, BC. December 2001. Quayle S, Hare H, Akopian V, **Jones S**, Schein J, Marra M, and Sadar M. Gene expression analysis of androgen-independent prostate cancer.

547. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. November 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.

548. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. November 2001. Fjell C, Chiu R, Saeedi P, **Jones S**, Schein J. Advances in bioinformatics for genetic physical mapping.

549. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. November 2001. Cherkasov A, **Jones S**. Bioinformatics tools for neoantigens characterization and targeting.

550. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. November 2001. Butterfield Y, Guin R, MacDonald K, Schnerch A, Skalska U, Smailus D, Zuyderduyn S, Krzywinski M, Schein J, **Jones S**. Bioinformatics for high-throughput Mu transposon sequencing.

551. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. November 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, deJong P, Schein J, **Jones S**, Marra M. Fingerprinted BAC clones for physical map construction.

552. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. November 2001. Chittaranjan S, Garland E, Freeman D, **Jones S**, Marra M, Gorski S. Transcription profiling of cell death in *drosophila melanogaster*.

553. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. November 2001. Smailus D, Asano J, Butterfield Y, Chan S, Guin R, Krzywinski M, MacDonald K, Olson T, Pandoh P, Skalska U, Scherch 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.

554. BC Cancer Agency Annual Cancer Conference. Vancouver, BC. November 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.

555. The BC Cancer Agency Annual Cancer Conference. Vancouver, BC. November 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.

556. University of British Columbia Medical Genetics Research Day. Vancouver, BC. November 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.

557. McKay S, Edgley M, Gilchrist E, **Jones S**, Moerman D. Gene knockout methods available online. *Worm Breeders Gazette 2001, (17)*

558. The BC Cancer Agency Annual Cancer Conference. Vancouver, BC. November, 2001.Quayle S, Hare H, Akopian V, **Jones S**, Schein J, Marra M, and Sadar M. Gene expression analysis of androgen-independent prostate cancer.

559. The BC Cancer Agency Annual Cancer Conference. Vancouver, BC. November, 2001.Quayle S, Hare H, Akopian V, **Jones S**, Schein J, Marra M, and Sadar M. Differential gene expression in a model of advanced prostate cancer.

560. Functional Genomics, Satellite to the 8th International Conference on Environmental Mutagens. Seattle, WA. October 2001. Quayle S, Hare H, Akopian V, **Jones S**, Schein J, Marra M, and Sadar M. Identification of new targets for the treatment of androgen-independent prostate cancer.

561. SAGE 2001 Frontiers in Transcriptome Exploration. Coronado, CA. September 2001. Lian T, Steen BR, Tangen K, MacDonald K, Zuyderduyn S, Marra M, **Jones S**, and Kronstad J. Analysis of Virulence-Related Transcription in the Human Pahtogenic Fungus *Cryptococcus neoformans* Using SAGE.

562. SAGE 2001 Frontiers in Transcriptome Exploration. Coronado, CA. September 2001. **Jones SJM**, Riddle DL, Pouzyrev AT, Velculescu VE, Hillier L, Eddy SR, Stricklin SL, Baillie DL, Waterston R, and Marra M. Changes in Gene Expression Associated with Developmental Arrest and Longevity.

563. SAGE 2001 Frontiers in Transcriptome Exploration. Coronado, CA. September 2001. Garland E, Varhol R, Zuyderduyn S, Marra M, and **Jones S**. Transcript construction for increased accuracy of tag to gene mapping in SAGE analysis.

564. SAGE 2001 Frontiers in Transcriptome Exploration. Coronado, CA. September 2001. Varhol R, Zuyderduyn S, Lypkie P, Krzywinski M, Garland E, Marra M, and **Jones S**. SAGEdb: Integrated Database for Gene Expression Analysis.

565. SAGE 2001 Frontiers in Transcriptome Exploration. Coronado, CA. September 2001. Zuyderduyn S, Varhol R, Garland E, Krzywinski M, Marra M, and **Jones S**. SAGEspace: Interrogating and Visualizing SAGEdb.

566. International Society for Trace Elements in Humans 2001 Meeting. Quebec City, PQ. Septemeber 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).

567. 13th International *C. elegans* international meeting. Los Angeles, CA. June 2001. Price NL, Brinkman FSL, **Jones SJ**, Greberg H, Finlay BB, and Rose AM. Pathogenomics: *Caenorhabditis elegans* as a model to investigate host and pathogen molecular interactions.

568. 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, and Marra MA. Changes in gene expression associated with developmental arrest and longevity in *C. elegans*.

569. 13th International C. elegans international Meeting. Los Angeles, CA. June, 2001. Barstead RJ, Dsouza A, Edgley ML, Gengyo-Ando K, Gilchrist EJ, Holmes J, **Jones S**, Kohara Y, Lansdale M, McKay S, Machiyama E, Mitani S, Moerman DG, Moulder GL, Noguchi S, Osborn J, Shen B, Tamura M, Viswanathan M. The C elegans Knockout.

570. 13th International *C. elegans* international meeting. Los Angeles, CA. June 2001. Barstead R, Dsouza A, Edgley M, Gengyo-Ando K, Gilchrist E, Holmes J, **Jones S**, Kohara Y, Lansdale M, McKay S, Machiyama E, Mitani S, Moerman D, Moulder G, Noguchi S, Osborn J, Shen B, Tamura M, and Viswanathan M. The *C. elegans* Knockout Consortium: Interim Report.

571. 13th International *C. elegans* international meeting. Los Angeles, CA. June 2001. Holt SJ, Riddle DL, **Jones SJ**. A bin's-worth of bounty: SAGE data mining in dauer larvae and mixed-stage transcript profiles.

572. 13th International *C. elegans* international meeting. Los Angeles, CA. June 2001. **Jones S** and McKay S. Automation of PCR primer design for the *C. elegans* knockout project.

573. Genome Sequencing and Mapping. Cold Spring Harbor, NY. June 2001. Ness S, Fjell C, Chiu R, Saeedi P, Fuhrmann D, Schein J, **Jones S** and Marra M. Developing computational strategies for constructing and analyzine physical maps of large genomes.

574. Genome Sequencing and Mapping. Cold Spring Harbor, NY. June 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.

575. Genome Sequencing and Mapping. Cold Spring Harbor, NY. June 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.

576. Genome Sequencing and Mapping. Cold Spring Harbor, NY. June 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 and Marra M. A fingerprinted BAC clone physical map of the mouse genome.

577. The Fifth Annual International Conference on Computational Molecular Biology. Montreal, PQ. April 2001. Thorne M, Marra M, **Jones S**. Cataloguing candidate elements involved in transcriptional regulation in the *Caenorhabditis elegans* genome.

578. ASM and TIGR Conference on Microbial Genomes. Monterey, CA. January 2001. Brinkman FSL, Greberg H, Wan I, Av-Gay Y, Baillie DL, Brunham R, Fernandez RC, Finlay BB, Hancock REW, de Koning A, Keeling P, Macfarlane E, Moerman DG, Otto SP, Ouellette BF, Yan H, Rose AM, and **Jones SJ**. Cross-domain and within-domain horizontal gene transfer: Implications for bacterial pathogenicity and tools to aid identification.

579. 21st Fungal Genetics Conference. Pacific Grove, CA. March 2001. Steen BR, Tangen K, MacDonald K, Lian TS, Marra M, **Jones S**, and Kronstad J. Genome wide analysis of *Cryptococcus neoformans*.

580. Mouse Molecular Genetics. Cold Spring Harbor, NY. August 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.

581. The Third International Symposium on Fungal Genomics: Novel Developments in Functional, Evolutionary and Computational Genomics. Atlanta, GA. July 2000. Steen BR, Tangen K, MacDonald K, Marra M, **Jones S**, and Kronstad J. Genome analysis and infection regulated gene expression in *Cryptococcus neoformans*.

582. Midwest Worm Meeting. June 2000. Minneapolis, MN. Shen B, Lansdale M, Viswanathan M, **Jones S**, Moerman DG, Mullen GP, Edgley ML, Dsouza A, Barstead RJ, Kotarska M, Gilchrist EJ, Moulder GL. Knockouts In C. elegans: Madness and Methodology.

583. European Worm Meeting. Blankenberge, Belgium. May, 2000. Echeverri C, **Jones S**, Leidel S, Coulson AR, Kirkham M, Goessen A, Hannak E, Cassin E, Flohrs K, Oegema K, Pichler SC, Gonczy P, Brehm M, Hyman AA. Genome-wide RNAi-based screen to identify genes required for cell division processes in C. elegans.

584. Genome Sequencing and Mapping. Cold Spring Harbor, NY. 2000. Fuhrmann DR, Marra MA, Chinwalla A, **Jones S**, and Waterston R. Poster and Abstract. Automated image analysis for DNA restriction mapping.

585. Genome Sequencing and Mapping. Cold Spring Harbor, NY. 2000. **Jones SJM**, Brinkman FSL, Wan I, Av-Gay Y, Baillie DL, Brunham R, Butland S, Fernandez RC, Finlay BB, Hancock REW, Haywood-Farmer C, Keeling P, de Koning A, Moerman DG, Otto SP, Ouellette BF, Taylor IEP, and Rose AM. Pathogenomics: Bioinformatic approaches to determine host and pathogen molecular interactions.

586. 5th Annual International Human Genome Meeting. Vancouver, BC. April 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**, and Marra M. Fingerprinted BAC clones for sequencing the genome of the mouse.

587. Genomes 2000. Paris, France. April 2000. Brinkman FSL, **Jones SJ**, Av-Gay Y, Baillie DL, Brunham R, Butland S, Fernandez RC, Finlay BB, Hancock REW, Haywood-Farmer C, Keeling P, de Koning A, Moerman DG, Otto SP, Ouellette BF, Taylor IEP, and Rose AM. Pathogenomics: An interdisciplinary approach for the study of infectious disease.

588. 12thInternational C. *elegans* Meeting. Madison, WI. June 1999. Johnson CD, Baumeister R, Coulson AR, Toland B, Eimer S, Hughes D, Szczygielski B, Gilchrist EJ, Wiesinger B, Goebel C, Medelberg J, **Jones S**, Moerman DG, Mullen GP, Durbin RM, Ly N-S, Barstead RJ, Cook N, Rose AM, Moulder GL. A Gene Knockout Service for C. elegans.

589. 12th International *C. elegans* international meeting. Madison, WI. June 1999. Echeverri C, Gonczy P, Oegema K, Pichler S, Kirkham M, Brehm M, Coulson A, **Jones S**, Hyman A. Genome wide RNA-I based screen to identify genes required for cell division processes in *C. elegans*.

590. 12th Internation *C. elegans* international meeting. Madison, WI. June 1999. McDowall J, **Jones S**, Freeman T, Coulson A, and Kuwabara P. Whole Genome Analysis of *C. elegans* Using DNA microarrays.

591. 12th Internation *C. elegans* international meeting. Madison, WI. June 1999. Rose AM, Johnsen RC, **Jones SJM**,. Genetic amenability of Chromosome I left.

592. 12th International *C. elegans* international meeting. Madison, WI. June 1999. Coulson AR, McDowall JS, Freeman T, Jones S, Kuwabara PE. Whole Genome Analysis of C. elegans Using DNA Microarrays.

593. European Worm Meeting. Cambridge, UK. July 1998. Guiliano D, Daub J, **Jones SJ**, and Blaxter ML. Towards a physical map of *Brugia malayi*. New insights into the Biology of Filarial Nematodes.

594. European Worm Meeting. Cambridge, UK. July 1998. Hughes D, **Jones SJ**, Durbin RM, and Coulson AR. Systematic gene inactivation in *C. elegans*.

595. Genome Sequencing and Mapping: Cold Spring Harbor, NY. May 1997. **Jones SJM**, Brinkman FSL, Wan I, Av-Gay Y, Baillie DL, Brunham R, Butland S, Fernandez RC, Finlay BB, Hancock REW, Haywood-Farmer C, Keeling P, de Koning A, Moerman DG, Otto SP, Ouellette BF, Taylor IEP, Rose AM. Pathogenomics: Bioinformatic approaches to determine host and pathogen molecular interactions.

596. Genome Sequencing and Mapping: Cold Spring Harbor, NY. May 1997. Fuhrmann DR, Marra MA, Chinwalla A, **Jones S**, Waterston R. Automated image analysis for DNA restriction mapping.

597. 11th C. elegans international meeting. Madison, WI. May 1997. **Jones S** and Durbin R. Sequence Analysis in the *C. elegans* genome project.

598. 11th C. elegans international meeting. Madison, WI. May 1997. Blaxter M, Scott A, Slatko B, Jayaram K, Ramzy R, **Jones S**, Baron L, and Daub J. Waterfall and the WHO filarial genome project.

599. 11th C. elegans international meeting. Madison, WI. May 1997. Blaxter ML, Williams SA, Scott AL, Slatko B, Jayaraman K, Ramzy R, **Jones SJ**, Baron L, Daub J, Waterfall M. The Brugia Malayo Genome Project.

600. International C. elegans Meeting. Madison, WI. June, 1993. **Jones S**, Baillie D. The molecular analysis of the let-653 gene.

601. *Worm Breeder's Gazette* 12: 45. **Jones SJM**, Clark DV, Baillie DL. 1992. The Characterization of the let-653 Gene in the NematodeCaenorhabditis elegans.