THE UNIVERSITY OF BRITISH COLUMBIA

Curriculum Vitae for Faculty Members

Date: August 2017 **Initials**:SPS

1. SURNAME: Shah **FIRST NAME**: Sohrab
MIDDLE NAME(S): Prakash

2. DEPARTMENT/SCHOOL: Pathology & Laboratory Medicine

3. FACULTY: Medicine

4. PRESENT RANK: Associate Professor (Grant Tenure Track) **SINCE**: Sep 1, 2010

5. POST-SECONDARY EDUCATION

Queen's University, BSc (Hons) in Biology, 1996
University of British Columbia, BSc in Computer Science, 2001
University of British Columbia, MSc in Computer Science (Bioinformatics), 2005
- Title of Dissertation: "Detecting common secondary structure elements in RNA sequences"
- Research Supervisor: Dr. Anne Condon

University of British Columbia, PhD in Computer Science (Bioinformatics), 2008
- Title of Dissertation: "Model based approaches to array CGH data analysis"
- Research Supervisors: Drs. Raymond Ng and Kevin Murphy

Special Professional Qualifications

6. EMPLOYMENT RECORD

(a) Prior to coming to UBC

(b) At UBC

University, Company or Organization	Rank or Title	Dates
Centre for Molecular Medicine and Therapeutics	Bioinformatics Software Developer	2000/05 - 2002/05
UBC - High Throughput Bioinformatics	Chief	2002/05 - 2004/08

Canadian Bioinformatics Workshops Series, Canadian Genetic Diseases Network / Ontario Institute for Cancer Research	Instructor	2002 - Present
UBC - Department of Computer Science	Research Assistant	2005/05 - 2008/05
UBC - Interprofessional Health and Human Services	Instructor	2006/07 - 2009/08
BC Cancer Agency	Postdoctoral Research Fellow (Advisors: Drs Sam Aparicio and David Huntsman)	2008 - 2010
BC Cancer Agency	Scientist	2010 - Present
CIHR/MSFHR Bioinformatics Program	Faculty Member	2010 - Present
UBC - Department of Computer Science	Associate Member	2010 – Present
UBC - Genome Science and Technology Graduate Program	Faculty Member	2013/03 – Present
Genome Sciences Centre	Associate Member	2013/03 – Present
SFU - School of Computing Science	Adjunct Professor	2013/06 – 2019/05
UBC - Department of Pathology and Laboratory Medicine	Assistant Professor	2010 - 2014
UBC - Department of Pathology and Laboratory Medicine	Associate Professor	2015 - Present

(c) Date of granting of tenure at U.B.C.:

7. LEAVES OF ABSENCE

8. TEACHING

(a) Areas of special interest and accomplishments

As part of the steering committee for the development of a cross-disciplinary course in health informatics: IHHS302: "Topics in Health Informatics for Health/Life Science Students", I helped to develop the curriculum and led the delivery of its content in 2007 and 2008. I have given lectures in the following UBC numbered courses: STAT 540, MEDG 421, STAT 547M. From 2001 until present I have been consistently involved in the development and delivery of content for the Canadian Bioinformatics Workshops (CBW) series (http://bioinformatics.ca) which has trained more than 1000 people since its inception in 2000. My role began as a teaching assistant, but I was recently the lead faculty in a new offering titled: "Clinical genomics and biomarker discovery", which was offered in July 2009 and 2010 (teaching evaluation attached). This course was designed to fill an unmet need in bioinformatics training and had an initial cohort of 30 participants, including pathologists, graduate students and computer scientists. In summer of 2011, I was a core faculty member in another new course entitled Bioinformatics for Cancer Genomics where I introduced 2 new topics: "Copy number analysis using genotype microarrays" and "Somatic mutation detection in next generation sequencing data". This course was offered to ~30 participants in Toronto in 2011, 2012 and is scheduled for May, 2013. Lastly, I am currently preparing a graduate course for the Dept of Pathology and Lab Medicine to cover the salient topics in cancer genome sequencing and bioinformatics analysis.

(b) Courses Taught

Year	Course #	Sched. Hrs	Class Size	Contact Hrs	Hours Taught			
					Lectures	Tutorials	Labs	Other
2005S (08/22/05-09/02/05)	IHHS 302				1.5			
2006S (08/21/06-09/01/06)	IHHS 302				1.5			
2007S (09/15/07)	IHHS 302				3			
2009S (08/26/09)	IHHS 302				1.5			
2009W (01/14/10)	STAT 547M				1.5			
2009W (03/16/10)	MEDG 421				1.5			
2010W (03/10/11)	MEDG 421				1.5			
2010W (03/09/11)	STAT 540				1.5			
2011W (03/07/12)	STAT 540				1.5			
2012W	MBB 505		12		4			

Year	Course #	Sched	Class	Contact	Hours Taught			
(03/13/13-03/18/13)	/ BIOF 520							
2012W (03/27/13)	STAT 540				1.5			
2013W (10/16/13-11/08/13	PRINb[1]		8			22		
2013W (01/29/14-02/03/14)	MBB 505 / BIOF 520				4			
2013W (03/03/14-03/10/14)	PATH 500B				2.5			
2013W (04/02/14)	STAT 540				1.5			
2014W (01/19/15; 01/21/15; 01/23/15)	UBC Pathology Genomics Course				3.5			
2014W (02/23/15; 03/02/15)	PATH 502				2			
2014W (04/01/15)	STAT540				1.5			
2015W (01/26/16)	MEDG 421				1.5			
2015W (02/22/16; 02/29/16)	PATH 502		19;4		2.5			
2015W (03/09/16; 03/14/16)	BIOF 520		12		4.0			
2015W (04/04/16)	STAT 540		50		2.0			
2016W (02/20/17; 02/27/17)	PATH 502		15		2.0			
2016W (03/08/17; 03/13/17)	BIOF 520		11		4.0			
2016W (03/04/17)	STAT 540		23		1.5			

[1] PBL Tutor

(c) Other Teaching of Undergraduates, Graduates and Postgraduates

1.	Lecturer, “Evolution in human cancer”; SFU MADD-GEN Workshop on Cancer

	Genomics, May 1, 2015.
2.	Lead Instructor, UBC Department of Pathology and Laboratory Medicine, Genomics Core Teaching. Jan 19-23, 2014
3.	Lead Instructor, UBC Department of Pathology and Laboratory Medicine, Residency Training, Genomics Course for Pathology Trainees. Jan 6-10, 2014 (http://pathology.ubc.ca/educational-programs/residency-training/new-genomics-course-for-pathology-trainees/)
4.	Panel Member, UBC Department of Pathology and Laboratory Medicine, Professional Advancement Learning Series. Dec 12, 2014 // "Interview Skills: How to be a truly hot commodity"
5.	Panel Member, UBC Departments of Microbiology & Immunology and Computer Science (Combined Degree Career Panel). Jan 20, 2016

(d) Students Supervised

Undergraduate Students

BSc Total = 8; 1 current; 7 completed

Student Name	**Program Type**	**Program Details**	**Year**		**Supervisory Role**	**Current Position/ Awards**
			Start	**Finish**		
Directed Studies						
Khushboo Chachcha	BSc	Computer Science	2013/01	2013/04	Primary Supervisor	
Kenneth Wing Cheung Lui	BSc	Computer Science	2011/09	2011/12	Primary Supervisor	Chinese University of Hong Kong Graduate Program
Co-op						
Minh (Alan) Le	BSc	Computer Science & Microbiology and Immunology	2012/05	2012/12	Primary Supervisor	
Jeffrey Knaggs	BSc	Computational Linguistics (SFU)	2012/05	2013/04	Primary Supervisor	
Kevin Wagner	BASc	Computer Engineering	2014/01	2014/08	Primary Supervisor	

Yu Wang	Msc (co-op)	Mathematics and Statistics (UVIC)	2014/09	2014/12	Primary Supervisor	
Boyang (Tom) Jin	BSc	Computer Science and Microbiology	2014/09	2014/12	Primary Supervisor	
Lovedeep Malik	BSc	Computer Science	2015/01	2015/08	Primary Supervisor	
Claire Barretto	BSc	Computer Science	2015/05	2015/08	Primary Supervisor	
Jill (Yajie) Zhou	BSc	Computer Science (SFU)	2015/05	2015/08	Primary Supervisor	
Jamie Xu	BSc	Computer Science (SFU)	2016/01	2016/08	Primary Supervisor	
Curtis Huebner	BASc	Engineering Physics (UBC)	2017/05	2017/12	Primary Supervisor	
Jessica Ngo	BSc	Biotechnology	2017/05	2017/12	Primary Supervisor	

Graduate Students Supervised

MSc Total = 12; 1 current; 11 completed

PhD Total = 12; 5 current; 7 completed

Student Name	Degree	Start	Finish	Supervisory Role	Program	Awards
MSc Students						
Rodrigo Goya	MSc (Thesis)	2009/01	2009/05	Co-supervisor with David Huntsman	CIHR Bioinformatics Program 2nd rotation	
Andrew Roth	MSc (Thesis)	2010/05	2010/08	Primary Supervisor (SFU)	CIHR Bioinformatics Program 3rd rotation	
Michael Peabody	MSc (Thesis)	2011/01	2011/04	Primary Supervisor (SFU)	CIHR Bioinformatics Program 2nd rotation	
Ryan Giuliany	MSc (Thesis)	2010/09	2012/08	Primary Supervisor	CIHR Bioinformatics Graduate Program	
Calvin Lefebvre	MSc	2012/05	2015/05	Primary Supervisor	Graduate	

	(Thesis)				Program in Bioinformatics	
Tyler Funnell	MSc (Thesis)	2012/09	2014/12	Primary Supervisor	Graduate Program in Bioinformatics	
Xin Ren	MSS (Thesis)	2013/09	2013/12	Primary Supervisor (Co-op Student)	College for Interdisciplinary Studies Software Systems	
Diljot Singh Grewal	MSc (Thesis)	2014/01	2014/08	Primary Supervisor (SFU; Co-op Student)	Computer Science	
Emily Hindalong	MSc (Thesis)	2014/05	2015/08	Primary Supervisor	CIHR Bioinformatics Program	
Santina Lin	MSc (Rotation Student)	2014/09	2014/12	Primary Supervisor	CIHR Bioinformatics Program	
Maia Smith	MSc (Thesis)	2015/09	2016/09	Primary Supervisor	Bioinformatics	
Rebecca Asiimwe	MSc	2016/09		Primary Supervisor	Bioinformatics	
PhD. Students						
Andrew McPherson	PhD	2008/09	2015/07	Primary Supervisor Co-supervisor: Cenk Sahinalp	SFU Graduate Program in Bioinformatics	NSERC CGS PhD scholarship
Jiarui Ding	PhD	2009/09	2016/05	Primary Supervisor	Graduate Program Computer Science	
Gavin Ha	PhD	2009/09	2014/07	Primary Supervisor Co-supervisor: Sam Aparicio	Graduate Program in Bioinformatics	2012 Lloyd Skarsgaard Research Excellence Prize (top graduating student at the BCCA) 2010 NSERC Postgraduate Scholarships-Doctoral
Andrew Roth	PhD	2011/01	2015/11	Primary Supervisor	Graduate Program in Bioinformatics	CIHR Doctoral Award-

						Frederick Banting & Charles Best Canada Graduate Scholarship
Fong Chun Chan	PhD	2012/05	2017/03	Co-supervisor with Christian Steidl	CIHR Bioinformatics Graduate Program	
Adi Steif	PhD	2013/05		Co-supervisor with Sam Aparicio	Genome Science and Technology Graduate Program	CIHR Doctoral Research Award: Vanier Canada Graduate Scholarship
Fatemeh Dorri	PhD	2013/09		Primary Supervisor	Graduate Program Computer Science	
Allen Zhang	MD/PhD	2014/08		Co-supervisor with Wyeth Wasserman	Bioinformatics	Frederick Banting and Charles Best Canada Graduate Scholarships Masters Award (CGS-M); CIHR Doctoral Research Award: Vanier Canada Graduate Scholarship
Alborz Mazloomian	PhD	2014/10	2017/03	Primary Supervisor	Bioinformatics	
Tyler Funnell	PhD	2015/01		Primary Supervisor	Bioinformatics	
Emily Hindalong	PhD	2015/09	2016/04 (Transfered to Dr. Carenini's lab in Comp	Primary Supervisor	Bioinformatics	

			Sci)			
Sohrab Salehi	PhD	2016/01		Co-supervisor (with Alex Bouchard Cote)	Bioinformatics	

Graduate Student Supervisory Committees

Ph. D. Students	Program Type	Start	Finish	Supervisor	Department or Program
Eloi Mercier	PhD	2010	Withdrawn (2013/03)	Paul Pavlidis	CIHR/MSFHR Training Program in Bioinformatics
Melissa McConechy	PhD	2010	2015/03/31	David Huntsman	Pathology & Laboratory Medicine
Robert Kridel	PhD	2010	2016/03/29	Randy Gascoyne	Pathology & Laboratory Medicine
Katayayoon Kasaian	PhD	2010	2015/09/02	Steven Jones	CIHR/MSFHR Training Program in Bioinformatics
Julie Chih-yu Chen	PhD	2011		Wyeth Wasserman	CIHR/MSFHR Training Program in Bioinformatics
Shing Hei Zhan	PhD	2011	Withdrawn (2016/03)	Steven Jones	CIHR/MSFHR Training Program in Bioinformatics
Alborz Mazloomian	PhD	2011	Transfer to Shah Lab (2014/10)	Irmtraud Meyer	CIHR/MSFHR Training Program in Bioinformatics
Casper Shyr	PhD	2011	2016/04/21	Wyeth Wasserman	CIHR/MSFHR Training Program in Bioinformatics
Wenqiang Shi	PhD	2012		Wyeth Wasserman	Graduate Program in Bioinformatics
Charles Soong	PhD	2012		Sam Aparicio	Pathology & Laboratory Medicine
Trace (Yue) Sun	PhD	2012		Martin Hirst	Bioinformatics
Rod Docking	PhD	2013		Aly Karsan	Experimental Medicine
Bruno Grande	PhD	2013		Ryan Morin	SFU Molecular Biology and Biochemistry
Josh Scurll	PhD	2013		Daniel Coombs	Mathematics
Jake Lever	PhD	2013		Steven Jones	Bioinformatics
Jasleen Grewal	PhD	2015		Steven Jones	Bioinformatics
M.Sc. Students		**Start**	**Finish**	**Supervisor**	**Program**

Fong Chun Chan	MSc	2010	2011 (Moved to PhD program)	Randy Gascoyne	CIHR/MSFHR Training Program in Bioinformatics
Patrick Tan	MSc	2010	2012	Paul Pavlidis	Bioinformatics
Adrin Jalali	MSc	2012	Inactive	Ryan Brinkman	Bioinformatics
Raewyn Billings	MSc	2012	2014	Sam Aparicio	Medical Genetics
Thuy Nguyen	MSc	2013	06/2016	Art Poon	Bioinformatics
Sohrab Salehi	MSc	2013	12/2015	Alex Bouchard-Cote	Bioinformatics
Celia Siu	MSc	2014		Steven Jones	Bioinformatics
Emma Laks	MSc	2015		Sam Aparicio	Genome Science and Technology Graduate Program
Farhia Kabeer	MSc	2015		Sam Aparicio	Pathology and Lab Medicine
Michael Yuen	MSc	2015		Peter Lansdorp / Peter Stirling	Medical Genetics

Postgraduate Students Supervised

Student Name	**Program Type**	**Program Details**	**Year**		**Supervisory Role**	**Current Position/Awards**
			Start	**Finish**		
Gholamreza Haffari	Fellowship	Post-doc Fellow, PhD	2010/ 04	2011/ 06	Primary Supervisor	Lecturer, Monash University
Ali Bashashati	Fellowship	Post-doc Fellow, Research Assoc.	2010/ 09	2013/ 09	Primary Supervisor	Eli Lilly Fellowship, Staff Scientist
Yikan Wang	Fellowship	Post-doc Fellow	2013/ 06		Primary Supervisor	Michael Smith Foundation for Health Research /BC Cancer Foundation Post-Doctoral Fellowship Award
Cydney Nielsen	Fellowship	Research Associate	2013/ 07		Primary Supervisor	
Camila deSouza	Fellowship	Post-doc Fellow	2013/ 10	2014/ 09	Co-Supervisor with Jennifer Bryan and Nancy	

					Heckman	
Hossein Shahrabi Farahani	Fellowship	Post-doc Fellow	2013/ 12		Primary Supervisor	
Yifei Huang	Fellowship	Post-doc Fellow	2014/ 05	2015/ 05	Primary Supervisor	
Camila deSouza	Fellowship	Post-doc Fellow	2014/ 10		Primary Supervisor	
Andrew McPherson	Fellowship	Post-doc Fellow	2015/ 09		Primary Supervisor	
Andrew Roth	Fellowship	Post-doc Fellow	2015/ 12		Primary Supervisor	

(e) Continuing Education Activities

1) Activities as presenter/facilitator at CME Courses (UBC and non-UBC)

1.	"Needles from Haystacks: Computational Biology and Distillation of Knowledge from Cancer Genomic Data": Canadian Association of Pathologists, Vancouver, BC, June 4-6, 2011
2.	"Genomic architecture of novel breast cancer subtypes" 11th International Congress on the Future of Breast Cancer, Coronado CA, July 28, 2012
3.	"Interpreting the mutational landscapes of breast cancer through two in-silico lenses: models of evolution and gene expression impact" Triple Negative Breast Cancer Conference, London UK, Jun 26, 2013
4.	"Evolutionary dynamics of high-grade serous ovarian cancer genomes across anatomic space and time". American Association of Cancer Research: Advances in Ovarian Cancer Research: From Concept to Clinic. Miami, Fl. Sep 20, 2013
5.	Lead Instructor, UBC Department of Pathology and Laboratory Medicine, Residency Training, Genomics Course for Pathology Trainees. Jan 6-10, 2014 (http://pathology.ubc.ca/educational-programs/residency-training/new-genomics-course-for-pathology-trainees/)
6.	"Studying the evolution of ovarian cancers" Next Generation Sequencing Rounds, Child and Family Research Institute, BC Children's Hospital, Vancouver, BC, May 16, 2014
7.	"Phylogenetic portraits of high grade serous ovarian cancers" Canadian Conference of Ovarian Cancer Research (CCOCR), Victoria BC, May 25-27, 2014
8.	"Phylogenetic portraits of high grade serous ovarian cancers" AACR Ovarian Cancer Research Symposium, Seattle WA, Sep 8-9, 2014
9.	"Advances in analytical mehods for clonal evolution inference at single-cell and bulk

	resolution" AACR Annual Meeting, Washington DC, April 1-5 2017

2) CME activities as an attendee

1.	Problem Based Learning Tutor Training Workshop, University of British Columbia, Faculty of Medicine, Vancouver, BC, Sep 24 and 26, 2013

(f) Visiting Lecturer (indicate university/organization and dates)

1.	"Measuring and modeling evolutionary dynamics in breast and ovarian cancer" MD Anderson Cancer Center, Houston TX; October 3, 2012
2.	"Computational Interpretation of Cancer Genomes"; Distinguished Speakers Lecture Series, Roswell Park Cancer Institute, Buffalo NY; Nov 14, 2012
3.	"Phylogenetic portraits of high grade serous cancers of the ovary" WIP Seminar, University of Pittsburgh,Pittsburgh, PA; Apr 3, 2014

(g) Educational Leadership

1.	UBC Department of Pathology and Laboratory Medicine, Genomics and Bioinformatics Program (for residents). Development and implementation/leadership. 2013 - present

(h) Curriculum Development & Innovation

1.	Canadian Bioinformatics Workshops Series. Curriculum delivery and development. 2001 - present
2.	IHHS302: "Topics in Health Informatics for Health/Life Science Students, Curriculum delivery and development. 2007, 2008

(i) Other Teaching & Learning Activities

1.	Instructor: "Bioinformatics: Developing the Tools", Canadian Bioinformatics Workshops Series, Montreal, PQ; 2005
2.	Instructor: "Introduction to Programming for Bioinformatics", Canadian Bioinformatics Workshops Series, Vancouver, BC; February 18, 2005
3.	Instructor: "Analysis of array CGH data", Canadian Bioinformatics Workshops Series. Vancouver, BC; July 2007
4.	Lead faculty: "Clinical genomics and biomarker discovery". Canadian Bioinformatics Workshops Series. Toronto, ON; July 16-17, 2009. Developed and delivered curriculum.
5.	Faculty: "Exploratory Data Analysis and Essential Statistics using R". Canadian Bioinformatics Workshops Series. Vancouver, BC; May 2010 (www.bioinformatics.ca)
6.	Lead faculty: "Clinical genomics and biomarker discovery", Canadian Bioinformatics Workshops Series. Toronto, ON; September 2010 (www.bioinformatics.ca)

7.	Lead faculty:"Bioinformatics for Cancer Genomics", Canadian Bioinformatics Workshop (BiCG) Toronto, ON; August 2011 (www.bioinformatics.ca)
8.	Core Faculty: Canadian Bioinformatics Workshop, Ontario Institute of Cancer Research, Toronto, ON; May 29-30, 2012
9.	Invited Speaker: "Evolutionary dynamics of high grade serous ovarian cancer genomes across anatomic space and time", Department of Molecular Biology & Biochemistry, Simon Fraser University, Vancouver, BC; Nov 2, 2012
10.	Tutorial Lead and Speaker: "Overview of mutation discovery in cancer genome sequencing" in Tutorial Session 2 (Identifying and interpreting somatic mutations in cancer genomes), Asia Pacific Bioinformatics Conference (APBC), Vancouver, BC; Jan 20, 2013
11.	Invited Speaker: "Uncovering the impact of somatic mutations on transcriptional networks in cancer", Invited Speaker, Canadian Institute for Advanced Research Genetic Networks workshop, Banff, AB; Apr 6, 2013
12.	Invited Speaker: "Towards identification of clonal populations in tumours through deep mutational profiling" Evolution of Cancer Symposium, Alpert Medical School, Brown University, Providence, RI; May 3, 2013
13.	Lead Faculty and Speaker: Canadian Bioinformatics Workshop, Ontario Institute of Cancer Research, Toronto, ON; May 29, 2013
14.	Attendee: Problem based learning tutor training. UBC Division of Continuing Professional Development. Vancouver, BC; Sep 24-26, 2013
15.	"Studying the evolution of ovarian cancers" Next Generation Sequencing Rounds, Child and Family Research Institute, BC Children's Hospital, Vancouver, BC; May 16, 2014
16.	Lead Faculty: Canadian Bioinformatics Workshop, Ontario Institute of Cancer Research, Toronto, ON; May 26-30, 2014
17.	"Cancer as an example of where the field is headed". Presentation at the Best Brains Exchange<http://www.cihr-irsc.gc.ca/e/43978.html> on "Canada as a Leader in the Development and Deployment of Precision/Personalized Medicine" being hosted in collaboration by the Canadian Institutes of Health Research (CIHR) and the Healthcare Innovation Secretariat to inform the work of the Advisory Panel on Healthcare Innovation<http://www.hc-sc.gc.ca/hcs-sss/innovation/index-eng.php>. Ottawa, ON; March 23, 2015
18.	Lead Faculty: Canadian Bioinformatics Workshop, Ontario Institute of Cancer Research, Toronto, ON; May 26-28, 2015
19.	"Clonal dynamics in space and time: inference of evolutionary properties of cancer", AACR Annual Meeting Educational Session, New Orleans, LA, Apr 16, 2016
20.	Lead Faculty: Cancer Genomics - Canadian Bioinformatics Workshop, Ontario Institute of Cancer Research, Toronto, May 30-Jun 3, 2016 (teaching on Jun 1, 2016)
21.	Invited Speaker: "Do clonal dynamics in human cancers reflect fitness properties? A spatio-temporal exploration." The Institute of Cancer Research, and Barts Cancer Institute, London,UK; May 18-19, 2017

9. SCHOLARLY AND PROFESSIONAL ACTIVITIES

(a) Areas of special interest and accomplishments

Cancer Genomics My research program has driven discovery and computational model development in cancer genomics and tumour evolution with significant progress in breast, ovary and lymphoid cancers. This has led to recognition locally, nationally and internationally. My program of research focuses on evolutionary dynamics of cancers using a combination of genomics and statistical modeling of tumour progression. Since 2010, I have raised more than $8.4M (my portion) in competitive grant funding to support this work, and my papers have been cited 7469 times (Google Scholar, h-index: 35, i-index: 52). My work has produced 7 first/senior/corresponding author contributions in NEJM, Nature, and Nature Methods.

Clonal Evolution in Solid Cancers My research as resulted in several world firsts including the determination of tumour evolution demonstrated at nucleotide resolution in a lobular breast cancer (Shah et al., Nature 2009#), the first description of the mutational landscape and clonal evolution in a population of triple negative breast cancers (**Shah et al., Nature 2012#),** establishing reproducible patterns of clonal dynamics in patient derived xenografts (**Eirew et al., Nature 2014*)** and quantifying the degree of clonal diversity in primary untreated HGS ovarian cancers (**Bashashati et al., J Path 2013*).** My lab led the data analysis of the METABRIC project, leading to the most precise characterization of prognostically significant molecular subtypes of breast cancer, establishing a new standard in the field of breast cancer patient stratification (**Curtis et al., Nature 2012#**). Studying evolution in cancer has exploded in recent years in the field. The lobular breast cancer paper has been cited 718 times since 2009 and the triple negative breast cancer work has been cited 655 times since 2012.

Discovery of New Cancer Genes My work has identified 3 new cancer genes: FOXL2 (**Shah et al., NEJM 2009#**), ARID1A (**Wiegand et al., NEJM 2010**) and CIITA (**Steidl et al., Nature 2011#).** This series of papers describes discoveries of novel, somatic, recurrent alterations in ovarian cancers and lymphomas. These studies represent single gene discoveries associated with cancer subtypes that had not previously been implicated in disease progression. FOXL2 has led to new class of diagnostics for granulosa cells of the ovary, while ARID1A has opened up the study of chromatin remodeling as a disrupted process in cancer biology. Additional collaborative efforts with Drs. Marra, Gascoyne, Jones have led to the discovery of EZH2 mutations in follicular and diffuse large B cell lymphomas, and PTPN1 mutations in B cell lymphomas.

Computational methods for cancer genome interpretation My lab has developed several statistical and computational approaches for analysis and interpretation of cancer genomes. These include PyClone (**Roth et al., Nature Methods 2014***) for inference of clonal population structures in tumours, TITAN (**Ha et al., Genome Research 2014***) for identification of clonal diversity in the genome architecture of tumours, defuse (**McPherson et al., PLoS Computational Biology 2011***) for identification of gene fusions from RNASeq and mutationSeq (**Ding et al., Bioinformatics 2012***), SNVMix (**Goya et al., Bioinformatics 2011**), and JointSNVMix (**Roth et al., Bioinformatics 2012**) for point mutation detection**.**
We have also developed a conceptual advance in modeling the impact of somatic mutations on gene expression. This work has been published in Genome Biology (**Bashashati et al., 2012**). A very recent advance in this field will appear in Nature Communications (**Ding et al., 2015**) where we have determined a systematic landscape of mutations impacting gene expression across twelve major tumour types. In summary, our computational methods have been in continual application

to NGS datasets in my and collaborator labs as described above, driving discovery. I have released numerous software tools that have been downloaded >4000 times and are in use in laboratories worldwide.

Selected Publications (trainees underlined bold):

Clonal Evolution in Solid Cancers

Eirew P*, **Steif A***, Khattra J*, **Ha G**, Yap D, Farahani H, Gelmon K, Chia S, Mar C, Wan A, Laks E, Biele J, Shumansky K, Rosner J, **McPherson A**, Nielsen C, **Roth AJ, Lefebvre C, Bashashati A, de Souza C, Siu C, Aniba R**, Brimhall J, Oloumi A, Osako T, Bruna A, Sandoval JL, Algara T, Greenwood W, Leung K, Cheng H, Xue H, Wang Y, Lin D, Mungall AJ, Moore R, Zhao Y, Lorette J, Nguyen L, Huntsman D, Eaves CJ, Hansen C, Marra MA, Caldas C, **Shah SP**#, Aparicio S#.
Dynamics of genomic clones in breast cancer patient xenografts at single-cell resolution.
Nature. 2015 Feb 19;518(7539):422-6. doi: 10.1038/nature13952. Epub 2014 Nov 26. PubMed PMID: 25470049. * - equal contribution, # corresponding author

Ha G, Roth A, Khattra J, Ho J, Yap D, Prentice LM, Melnyk N, McPherson A, Bashashati A, Laks E, Biele J, Ding J, Le A, Rosner J, Shumansky K, Marra MA, Gilks CB, Huntsman DG, McAlpine JN, Aparicio S, **Shah SP**.
TITAN: inference of copy number architectures in clonal cell populations from tumor whole-genome sequence data.
Genome Res. 2014 Nov;24(11):1881-93. doi: 10.1101/gr.180281.114. Epub 2014 Jul 24. PubMed PMID: 25060187;

Roth A, Khattra J, Yap D, Wan A, Laks E, Biele J, Ha G, Aparicio S, Bouchard-Côté A, **Shah SP**.
PyClone: statistical inference of clonal population structure in cancer.
Nat Methods. 2014 Apr;11(4):396-8. doi: 10.1038/nmeth.2883. Epub 2014 Mar 16. PubMed PMID: 24633410.

Curtis C*, **Shah SP***, Chin SF, Turashvili G, Rueda OM, Dunning MJ, Speed D, Lynch AG, Samarajiwa S, Yuan Y, Gräf S, **Ha G**, **Haffari G**, Bashashati A, Russell R, McKinney S; METABRIC Group, Langerød A, Green A, Provenzano E, Wishart G, Pinder S, Watson P, Markowetz F, Murphy L, Ellis I, Purushotham A, Børresen-Dale AL, Brenton JD, Tavaré S, Caldas C, Aparicio S.
The genomic and transcriptomic architecture of 2,000 breast tumours reveals novel subgroups.
Nature. 2012 Apr 18;486(7403):346-52. doi: 10.1038/nature10983. PubMed PMID: 22522925;
*- equal contribution

Bashashati A, Ha G, Tone A, Ding J, Prentice LM, Roth A, Rosner J, Shumansky K, Kalloger S, Senz J, Yang W, McConechy M, Melnyk N, Anglesio M, Luk MT, Tse K, Zeng T, Moore R, Zhao Y, Marra MA, Gilks B, Yip S, Huntsman DG, McAlpine JN, **Shah SP**.
Distinct evolutionary trajectories of primary high-grade serous ovarian cancers revealed through spatial mutational profiling.
J Pathol. 2013 Sep;231(1):21-34. doi: 10.1002/path.4230. PubMed PMID: 23780408

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. doi: 10.1038/nature10933. PubMed PMID: 22495314

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(b) Research or equivalent grants (indicate under COMP whether grants were obtained competitively (C) or non-competitively (NC)). ***BOLD = current funding***

Granting agency	Title	COMP Or Non-COMP	$ per year	Duration mo/yy to mo/yy	Principal Investigator	Co-PI(s)
	OPERATING GRANTS					
Canadian Institutes of Health Research (CIHR)	Improving computational inference of single nucleotide variants from next generation sequencing of cancer genomes	C	$99,078	Oct/09-Sept/10	S Aparicio	**S Shah**
Canadian Institutes of Health Research (CIHR)	Mutations in the SWI/SNF chromatin remodelling complex genes: an alternative mechanism for ovarian carcinogenesis	C	$135,410	Oct/10-Sept/14	D Huntsman	**S Shah**, S Aparicio,
Canadian Breast Cancer Research Alliance	Genome heterogeneity in predictive models of drug action in triple negative breast cancer	C	$288,488	Apr/11-Mar/15	S Aparicio	S Shah, S Chia, K Gelmon, M Martin, T Mak, M Marra
Canadian Institutes of Health Research (CIHR)	Genomic disruption in high-grade serous ovarian carcinomas: Steady state or continuous drift?	C	$131,428	Oct/11-Sept/15	S Shah	J McAlpine, B Gilks, D Huntsman
Canadian Cancer Society Research Institute (CCSRI)	Finding driver mutations in cancer through integrative profiling of mutational landscapes and transcriptional networks	C	$99,803	Apr/12-Mar/14	S Shah	
Canadian Institutes of Health Research (CIHR)	**The Genetics of Hereditary Upper Gastrointestinal Cancers: Beyond CDH1 Germline Mutations**	**C**	**$186,467**	**Oct/12 – Sept/17**	**D Huntsman**	**D Schaeffer, G Zogopoulos, K Schrader, S Shah, S Gallinger**

Granting agency	Title	COMP Or Non-COMP	$ per year	Duration mo/yy to mo/yy	Principal Investigator	Co-PI(s)
Canadian Institutes of Health Research (CIHR)	Prognostic markers and biology of relapsed Hodgkin lymphoma	C	$167,386	Oct/12-Sept/15	C Steidl	S Shah, R Gascoyne
TFRI	Are genomic instability and clonal diversity prognostic indicators of high grade serous ovarian cancer?	C	$149,834	Nov/12-Nov/15	S Shah	
Canadian Cancer Society Research Institute (CCSRI) / BC Cancer Foundation / VGH Foundation	**Contextual Genomics: the Foundation for Subtype Specific Approaches to Ovarian Cancer Control**	**C**	**$250,000 / 75,000 / 75,000**	**Feb/13-Jan/18**	**D Huntsman, S Shah**	**B Gilks, M Anglesio, M Hirst, A Tone, J McAlpine**
Canadian Cancer Society Research Institute (CCSRI)	**Defining the role of clonal genomes in the evolution and treatment of cancers**	**C**	**$248,002**	**Feb/13-Jan/18**	**S Aparicio**	**S Shah, C Hansen**
Canadian Institutes of Health Research (CIHR)	Linking clonal genomes to tumour evolution and therapeutics	C	$208,088	Apr/13-Mar/16	S Aparicio	S Shah, C Hansen
Genome Canada	Measuring and modeling tumour evolution from next generation sequencing data: enabling clinical study of clonal diversity in cancer patients	C	$124,842	Jul/13-Jun/15	S Shah	

Granting agency	Title	COMP Or Non-COMP	$ per year	Duration mo/yy to mo/yy	Principal Investigator	Co-PI(s)
Genome Canada	Computational interpretation of cancer genomes: defining mutational landscapes for translational genomics	C	$345,253	Jul/13-Jun/16	S Shah	R Morin, P Boutros
Genome Canada	Applied Bioinformatics of Cis-regulation for Disease Exploration (ABC4DE)	C	$250,000	Jul/13-Jul/16	W Wasserman	S Shah, A Lehman, C Van Karnebeek
BC Cancer Foundation	Cancer Genomics Research Fund / High grade serous ovarian cancer genome sequencing	Non-COMP	$333,333	Oct/13 – Sept/16	S Shah	
Canadian Cancer Society Research Institute (CCSRI)	Building a Bridge from the Cancer Genome to the Cancer Clinic with Visual Analytics	C	$99,831	Feb/14 – Jan/16	S Shah	S Aparicio, D Huntsman, J Laskin, M Marra
Canadian Cancer Society Research Institute (CCSRI)	How does the immune system contend with intratumoral heterogeneity?	C	$99,969	Feb/14 – Jan/16	B Nelson	S Shah, R Holt
Canadian Institutes of Health Research (CIHR)	**Integrating Quantitative Imaging Methods and Genomic Biomarkers to Assess the Therapeutic Response of Cancers**	**C**	**$398,605**	**Dec 2014 – Nov 2019 (5 y)**	**F Benard**	**Morin RD, Aparicio S, Celler A, Laskin J, Shah SP, Gelmon K, Connors J, Chia S, Hamarneh G**

Granting agency	Title	COMP Or Non-COMP	$ per year	Duration mo/yy to mo/yy	Principal Investigator	Co-PI(s)
Canadian Cancer Society Research Institute (CCSRI)	REAL-PDX: Resistance modeling in EGFR and ALK Lung cancer Patient-derived xenografts for personalized post-progression therapy	C	$250,000	Feb/15 – Jan/20	G Liu (Toronto)	S Shah, Tsao M, Shepherd FA, Leighl N, Yasufuku K, Pintille M, Lupien M, Haibe-Kains B, Bradbury P,
Canadian Institutes of Health Research (CIHR) – Foundation Grant	The clonal dynamics of ovarian cancers: phylogenetic models of chemosensitivity and resistance	C	$182,126	July/15-June/20	S Shah	S Aparicio, P Hieter, J McAlpine, A Bouchard-Cote, D Huntsman, C Hansen, M Marra
CDMRP / US DOD	Mechanistic Investigation of Breast Cancer Synthetic Lethality Through Inhibition of CDK12	C	$1,032,242 USD TOTAL	May/2016-Apr/2019	G Morin, S Aparicio	S Shah
Genome Canada	Reimagining genome browsing for the era of single cell genomics – *Under Embargo*	C	$125,000	July/2016-Jun/2018	S Shah, C Nielsen	
Canadian Cancer Society Research Institute (CCSRI)	Deciphering the cellular crosstalk in the tumour microenvironment of classical Hodgkin lymphoma	C	$98,000	Feb/17 - Jan/19	C Steidl, S Shah	A Weng, S Aparicio, K Savage
BC Cancer Foundation	Cancer Genomics Research	Non-Comp	$300,000	Apr/17-Mar/19	S Shah	
CANARIE	Montage: a software platform to drive the revolution in single cell cancer genomics	C	$121,950	July/17-Sept/20	S Shah	

Granting agency	Title	COMP Or Non-COMP	$ per year	Duration mo/yy to mo/yy	Principal Investigator	Co-PI(s)
	TEAM GRANT					
Canadian Institutes of Health Research (CIHR)	CIHR Team in genomics of forme fruste tumours: new vistas on cancer biology and management.	C	$1,042,122	Jul/10-Jun/13	D Huntsman	S Shah, S Aparicio, C Hansen, P Sorensen
Canadian Institutes of Health Research (CIHR)	Forme fruste tumours Sub-project of the above. Sub-Project 1: Sequencing of Forme Fruste Tumours	C	$436,605	Jul/10-Jun/13	D Huntsman	S Shah
Terry Fox Research Institute (TFRI)	**The Terry Fox New Frontiers Program Project Grant, The Genomics of Forme Fruste tumours: New vistas on cancer biology and treatment**	**C**	**$1,500,000**	**Jul/13 – Jun/18**	**D Huntsman (Nominated PI)** **S Aparicio, G Morin, R Morin, S Shah, C Hansen, M Hirst, C Lee, M Marra, T Nielsen, P Sorensen, TM Underhill, S Yip**	
Terry Fox Research Institute (TFRI)	**Data Analysis Core. Sub-project of the above**	**C**	**$296,036**	**Jul/13 – Jun/18**	**S Shah**	**M Hirst, R Morin**
Terry Fox Research Institute (TFRI)	**Sub-project 2: Models for Clonal Diversity & Tumour Evolution in Forme Fruste Tumours. Sub-project of the above**	**C**	**$252,520**	**Jul/13 – Jun/18**	**S Aparicio**	**C Hansen, T Nielsen, S Shah**

Granting agency	Title	COMP Or Non-COMP	$ per year	Duration mo/yy to mo/yy	Principal Investigator	Co-PI(s)
Terry Fox Research Institute (TFRI)	The Terry Fox New Frontiers Program Project Grant, Molecular Correlates of Treatment Failure in Lymphoid Cancers	C	$1,295,209	Jul/13 – Jun/16	R Gascoyne (Nominated PI) J Connors, M Marra, C Steidl, S Shah, S Jones	
Terry Fox Research Institute (TFRI)	Sub-project 1: Evolutionary dynamics and driver mutations underlying histological transformation and treatment resistance in follicular lymphoma. Sub-project of the above	C	$210,261	Jul/13 – Jun/16	M Marra, S Shah	
Natural Sciences and Engineering Research Council of Canada (NSERC)	**The Cancer Genome Collaboratory**	**C**	**$1,499,965**	**Mar/14 – Mar/18**	**L Stein**	**P Boutros, S Sahinalp, Ferretti, K EL Emam, BK Shoichet, BM Knoppers, BFFO Ouellette, G Bourque, GD Bader, S Shah, A Bouchard-Cote**
Natural Sciences and Engineering Research Council of Canada (NSERC)	**Research Module 3: Modeling tumour evolution. Sub-project of the above**	**C**	**$115,750**	**Mar/14 – Mar/18**	**S Shah**	

Granting agency	Title	COMP Or Non-COMP	$ per year	Duration mo/yy to mo/yy	Principal Investigator	Co-PI(s)
Terry Fox Research Institute (TFRI)	**The Terry Fox New Frontiers Program Project Grant, Overcoming treatment failure in lymphoid cancers**	**C**	**$1,500,000**	**Jul/16 – Jun/21**	**J Connors (Nominated PI)** **M Marra, C Steidl, S Shah, D Scott, A Weng, G Morin, A Mungall, G Slack**	
Terry Fox Research Institute (TFRI)	**Sub-project 1: Co-evolution of malignant cell populations and infiltrating immune cells in B-cell lymphomas. Sub-project of the above**	**C**	**$255,760**	**Jul/16 – Jun/21**	**S Shah, A Weng**	**C Hansen**
Cancer Research UK Grand Challenge	**IMAXT, Imaging and Molecular Annotation of Xenografts and Tumours**	**C**	**$183,333 GBP**	**May/17 - Apr/23**	**G Hannon**	**S Aparicio, B Bodenmiller, E Boyden, J Joyce, X Zhuang**
	INFRASTRUCTURE GRANTS					
CFI Leaders Opportunity Fund / BC Knowledge Development Funds (matching CFI funds) / Other eligible partners	[1]Computational infrastructure for defining genomic landscapes and resolving the clinical impact of somatic mutations in cancer	C	$265,681 / $265,680 / $214,380 Total $745,741	Apr/13 – Mar/16	S Shah	

Granting agency	Title	COMP Or Non-COMP	$ per year	Duration mo/yy to mo/yy	Principal Investigator	Co-PI(s)
CFI Leaders Opportunity Fund / BC Knowledge Development Funds (matching CFI funds) / Other eligible partners	**A surgical-genomic tissue bank for endometriosis**	**C**	**$125,000 / $125,000 / $62,500** **Total $312,500**	**May/14 – Apr/17**	**P Yong**	**S Shah**
	TRAINING GRANTS					
Natural Sciences and Engineering Research Council of Canada (NSERC)	**Create Program for Computational Methods for the Analysis of the Diversity and Dynamics of Genomes**	**C**	**$300,000**	**Apr/13 – Mar/18**	**C Sahinalp**	**S Shah, F Brinkman, T Moller, C Chauve, P Unrau, J Chen, C Collins, M Ester, R Morin, A Shiraman**
	OTHER GRANTS					
Department of Defense (USA) *(Consortium Development Grant)*	Multidisciplinary Ovarian Cancer Outcomes Group	C	$328,625	Jan/13-Jan/15	M Pike	S Shah

[1] This equipment is high performance computing equipment to be used in various cancer genome sequencing projects and in the development of new computational methods for analysis.

(c) Research or equivalent contracts, including funding for clinical trials (indicate under COMP whether grants were obtained competitively (C) or non-competitively (NC). ***BOLD = current funding.***

(d) Invited Presentations

1.	"Pegasys: Workflow management for genome annotation." Network Tools and Applications in Biology (NETTAB2005), Naples, Italy "Workflows management: new abilities for the biological information overflow", Naples, Italy; Oct 7, 2005
2.	"Integrating copy number polymorphisms into array CGH analysis using a robust HMM." International Conference on Intelligent Systems for Molecular Biology (ISMB) 2006, Fortaleza, Brazil; August 2006
3.	"Modeling recurrent DNA copy number alterations in array CGH data." International Conference on Intelligent Systems for Molecular Biology (ISMB) 2007, Vienna, Austria; August 2007
4.	"Computational inference of copy number changes from next generation sequencing of cancer genomes." AGBT 2009, Marco Island, USA; February 2009
5.	"Model-based clustering of array CGH data". International Conference on Intelligent Systems for Molecular Biology (ISMB) 2009, Stockholm, Sweden; August 2009
6.	"Probabilistic models for detecting SNVs from next gen sequencing of tumours". International Conference on Intelligent Systems for Molecular Biology (ISMB) 2009, Stockholm, Sweden; August 2009
7.	"Mutation discovery in cancer using next generation sequencing and probabilistic models". Centre for Cellular and Biomolecular Research, University of Toronto. Toronto, ON; Nov 3, 2009. Host: Michael Brudno.
8.	"Mutation discovery in cancer using next generation sequencing and probabilistic models". Stanford University. Nov 13, 2009. Host: Matt van de Rijn.
9.	"Mutation discovery in cancer using next generation sequencing and probabilistic models". Vancouver Bioinformatics Users Group Seminar Series, Vancouver, BC; Nov 26, 2009.
10.	"Mutation discovery in cancer using next generation sequencing and probabilistic models". Memorial Sloan Kettering Cancer Center, New York, NY; Apr 2010
11.	Invited Speaker: "Integrative genomic and transcriptomic profiling of 1000 breast cancers". 10th Annual McGill Workshop on Bioinformatics, Holetown, Barbados; January 2011
12.	"Mutation discovery in cancer using next generation sequencing and probabilistic models". The Hospital for Sick Children, Toronto, ON; May 2010
13.	"Beyond Sequencing". San Francisco, CA; June 2010
14.	"Statistical models for inference of SNVs in cancer genomes". Isaac Newton Institute, Cambridge, UK; July 2010
15.	"Defining mutational landscapes of tumors with sequencing and statistical models". University of Washington COMBI Seminar series, Seattle, WA; Nov 2010
16.	"Defining mutational landscapes of tumors with sequencing and statistical models". Aarhus University, Denmark; November 2010
17.	"Integrative genomic and transcriptomic profiling of 1000 breast cancers" 10th Annual McGill Workshop on Bioinformatics, Holetown, Barbados; January 2011
18.	"The cancer genome and probabilistic models" UBC Comp Science Faculty Lecture Series, Vancouver, BC; March 2011
19.	"The somatic mutational landscapes of breast cancer subtypes" 6th Annual Canadian

	Genetic Epidemiology & Statistical Genetics Meeting, King City, ON; May 2011
20.	"The mutational landscapes of breast cancer subtypes". Keynote address: Bioinformatics Training Program (BTP) and the Interdisciplinary Oncology Program (IOP), UBC. Vancouver, BC; May 27th, 2011
21.	"Mutation discovery in cancer using next generation sequencing and probabilistic models" University of Washington COMBI Seminar series, Seattle, WA; Nov 2011
22.	"Somatic mutation discovery in cancer with NGS sequencing: From allelic counts to biologic inference" Gene Technology Access Centre (GTAC), Walter and Eliza Hall Institute of Medical Research, Parkville Australia; December 5-7, 2011
23.	"Genome-wide mutational heterogeneity in breast and ovarian cancer" Peter McCallum Cancer Centre, Melbourne Australia; December 8, 2011
24.	"Measuring patterns of tumour evolution: Computational models and biological inference" Plenary Session on Computational Genomics. Canadian Human and Statistical Genetics Meeting, Niagara on the Lake, ON; May 2, 2012
25.	Keynote Speaker: Measuring Patterns of Tumour Evolution: computational models and biological inference, U of Toronto Genome Biology and Bioinformatics, Toronto, ON; May 23, 2012
26.	Measuring patterns of tumour evolution: Computational models and biological inference" Ontario Institute for Cancer Research Informatics and Bio-Computing (Canadian Bioinformatics Workshop), Toronto, ON; May 31, 2012
27.	"Measuring patterns of tumour evolution: Computational models and biological inference" Copenhagenomics, Kobenhavn, Copenhagen; June 14, 2012
28.	"Measuring patterns of tumour evolution: Computational models and biological inference" BioC 2012; Fred Hutchinson Cancer Centre, Seattle, WA; July 24, 2012
29.	"Computational Interpretation of Cancer Genomes" Takeda Shonan Research Centre Splicing Meeting, Shonan, Japan; Oct 18, 2012
30.	"Evolutionary Dynamics of High-Grade Serous Ovarian Cancer Genomes Across Anatomic Space and Time" New Principal Investigators Meeting, Mont-Gabriel, PQ; October 26-28, 2012
31.	"Modeling tumour evolution in breast and ovarian cancer"; University of British Columbia Department of Anesthesiology, Pharmacology and Therapeutics Seminar Series, Vancouver, BC; Nov 20, 2012
32.	"Evolutionary dynamics of high grade serous ovarian cancer genomes across anatomic space and time"; BC Cancer Agency Annual Conference, Vancouver, BC; Nov 30, 2012
33.	"Measuring and modeling evolutionary dynamics of breast and ovarian cancer", Princess Margaret Hospital, Ontario Cancer Institute, Toronto, ON; Dec 4, 2012
34.	"Evolutionary dynamics of high grade serous ovarian cancer genomes across anatomic space and time", Pacific Symposium on Biocomputing (PSB) 2013, Big Island of Hawaii; January 5, 2013
35.	"Evolutionary dynamics in breast and ovarian cancer: implications for personalized therapy", Invited Speaker, Ottawa Illumina Seminar 2013: The Age of Personalized Medicine, Ottawa, ON; Feb 19, 2013
36.	"Evolutionary dynamics of primary high-grade serous ovarian cancers revealed through

	spatial and temporal mutational profiling", Invited Speaker, Quebec TFRI Node Research Day, Montreal, PQ; Apr 18, 2013
37.	"Forme Fruste Tumors"; Terry Fox Research Institute Annual Scientific Meeting, Ottawa, ON; May 10, 2013
38.	"Evolutionary dynamics of high-grade serous ovarian cancers: implications for personalized medicine", Invited Speaker, Personalized Medicine and Individualized Drug Delivery Conference, 2013 Canadian Society for Pharmaceutical Sciences Annual Symposium. Vancouver, BC; Jun 12, 2013
39.	"Statistical models for evolutionary dynamics of tumour cell populations profiled with deep digital sequencing" Bertinoro Computational Biology Meeting 2013, Bertinoro, Italy; Sep 9, 2013
40.	"Are Genomic Instability and Clonal Diversity Prognostic Indicators of High Grade Serous Ovarian Cancer?"TFRI BC Node Research Day, Vancouver, BC; Oct 31, 2013
41.	"Modeling Tumour Evolution in the "Big Data" Era of Cancer Genome Sequencing" Plenary session at Canadian Cancer Research Conference, Toronto, ON; Nov 4, 2013
42.	"Modeling evolution of the structural genome in cancer cell populations" New York Bioinformatics Symposium, New York, NY; Nov 15, 2013
43.	"Inferring clonal population structure in human cancer" SFU MADD-GEN/DiDy Annual Joint Workshop, Burnaby, BC; Mar 5, 2014
44.	"Phylogenetic portraits of high grade serous ovarian cancers" Genome Sciences Centre All Staff Meeting, Vancouver, BC; Mar 14, 2014
45.	"Phylogenetic portraits of high grade serous ovarian cancers" Defeating Ovarian Cancer, Long Island, NY; Apr 21-23, 2014
46.	"The evolutionary dynamics of follicular lymphoma revealed through whole genome sequencing" TFRI Conference, Montreal, PQ; May 8, 2014
47.	"Clonal dynamics in space and time in human cancer" Evolution of Drug Resistance, the Kavli Institute for Theoretical Physics – University of California, Santa Barbara, CA; Sept 18, 2014
48.	"DNA and the hidden faces of cancer" Interface 2014, Vancouver, BC; Sept 29, 2014
49.	"Genomics + cancer + big data = Startup" Interface 2014, Vancouver, BC; Sept 30, 2014
50.	"Clonal Dynamics of Human Cancers Measured in Space and Time at Single Cell Resolution" CIFAR Genetic Networks Workshop, University of Washington, Seattle, WA; Nov 9, 2014
51.	"Clonal dynamics in space and time in human cancers" 12th Annual Symposium of the Dept. of Genome Sciences, University of Washington, Seattle, WA; Nov 10, 2014
52.	"Comparing the genomic landscapes of poor responders and long-term survivors of high grade serous ovarian cancer" Seventh AACR Conference on the Science of Cancer Health Disparities in Racial/Ethnic Minorities and the Medically Underserved, San Antonio, TX; Nov 11, 2014
53.	"Clonal dynamics in space and time in human cancers", Precursors to breast cancer and tumor evolution, 14th Annual BCI-McGill Workshop, Bellairs Research Institute, Holetown, Barbados; January 24, 2015
54.	"Characterization of Cancer Genomes", Cambridge Healthtech Institute's Third Annual Clinical Sequencing - Translating NGS to Practice; part of the 22nd Annual Molecular

	Medicine Tri-Conference, San Francisco, CA; Feb 18, 2015
55.	"Cancer as an example of where the field is headed". Presentation at the Best Brains Exchange http://www.cihr-irsc.gc.ca/e/43978.html on "Canada as a Leader in the Development and Deployment of Precision/Personalized Medicine" being hosted in collaboration by the Canadian Institutes of Health Research (CIHR) and the Healthcare Innovation Secretariat to inform the work of the Advisory Panel on Healthcare Innovation http://www.hc-sc.gc.ca/hcs-sss/innovation/index-eng.php. Ottawa, ON; March 23, 2015
56.	"Evolution in human cancer", SFU MADD-GEN Workshop on Cancer Genomics, Burnaby, BC; May 1, 2015
57.	"Clonal dynamics in human cancers measured across time and space", Canadian Cancer Immunotherapy Conference Genomics, Vancouver, BC; May 20, 2015
58.	"Comprehensive approaches to mutation interpretation: tumour evolution and gene expression integration." Genetics and Genomics for the Practicing Clinician, Session 1: Overview of Available Technologies and Pathology, ASCO Pre-annual meeting seminar, Chicago, IL; May 28, 2015
59.	"Tracking clonal dynamics in human cancers across space and time." Oxford University. London, UK; June 10, 2015
60.	"Tracking clonal dynamics in human cancers in space and time at single cell resolution". BACR/CRUK Evolution and Intratumoural Heterogeneity Meeting. Royal Society of Medicine. London, UK; June 11, 2015
61.	"Tracking clonal dynamics in human cancers in space and time at single cell resolution". Plenary Session 2: Molecular Genomics. BCCA Translational Retreat, Vancouver, BC; June 19, 2015. Plenary speaker and session chair.
62.	"Tracking clonal dynamics in human cancers in space and time at single cell resolution". Forecasting Evolution, Lisbon, Portugal; July 6, 2015
63.	"Somatic mutations in two cancer contexts: evolutionary dynamics and gene expression impact". Statistical and Computational Challenges In Bridging Functional Genomics, Epigenomics, Molecular QTLs, and Disease Genetics meeting (15w5142), Banff, AB; August 7, 2015
64.	"Tracking Clonal Dynamics in Human Cancers". 2015 Gordon Research Conference (GRC) on Hormone-Dependent Cancers: mechanisms to tailored therapeutics. Sunday River Resort, Newry, ME, USA; August 17, 2015
65.	"Somatic Mutations in Context: Toward Modeling Cancer Ecosystems". Workshop "Systems Genetics of Cancer 2015"- Lucy Cavendish College, Cambridge, UK; Sept 21, 2015
66.	"Inferring fitness landscapes in cancers". International Workshop on Computational Precision Medicine, Montpelier, FR; Sept 24, 2015
67.	"Somatic mutations in two cancer contexts: evolutionary dynamics and gene expression impact". Stanford Cancer Systems Biology Symposium, Stanford, CA; Oct 22, 2015
68.	"Towards modeling clonal fitness in human cancers", Invited Seminar, Ontario Institute for Cancer Research, Toronto, ON; Oct 26, 2015
69.	"Phylogenetic analysis reveals divergent modes of clonal spread and intraperitoneal mixing in high grade serous ovarian cancer". NCRI Cancer Conference 2015, Liverpool UK; Nov 3, 2015
70.	"Towards modelling fitness in human cancers", Genomics Seminar Series, Imperial College Hammersmith, London, UK; Nov 4, 2015
71.	"Towards modelling fitness in human cancers", The Institute of Cancer Research, London,

	UK; Nov 5, 2015
72.	"Tumour Complexity – Overview of Tumour Heterogeneity", 41st Annual D.A. Boyes Society Meeting & Obstetrics and Gynaecology Clinical Review, Vancouver, BC; Nov 6, 2015
73.	"Towards modeling fitness of clonal populations in human cancers", Mayo Clinic, Rochester, MN; Nov 19, 2015Delete
74.	"Towards inference of fitness landscapes in human cancer", University of Toronto, Toronto, ON; Jan 18, 2016
75.	"Towards inference of fitness landscapes in human cancer", Simons Institute Computational Cancer Biology Workshop, Berkeley, CA, Feb 1-5, 2016
76.	"Towards inference of evolutionary fitness landscapes in human cancer", Tucson Symposium, Tucson, AZ, Mar 8, 2016
77.	"Clonal dynamics in space and time: inference of evolutionary properties of cancer", AACR Annual Meeting Educational Session, New Orleans, LA, Apr 16, 2016
78.	"Clonal evolution in high grade serous ovarian cancer: implications for intraperitoneal spread", National Invited Speaker: Canadian Conference on Ovarian Cancer Research, Niagara Falls, ON, May 15, 2016
79.	"Clonal dynamics in space and time: inference of evolutionary properties of cancer", Latsis Symposium on "Personalized Medicine – Challenges and Opportunities", Zurich, Switzerland, Jun 28, 2016
80.	"Evolutionary dynamics of cancer: a spatio-temporal analysis". Keynote speaker, 14th RECOMB Comparative Genomics Satellite Workshop. Montréal, Canada, October 11-14, 2016.
81.	"Cancer Evolution Using Bulk and Single Cell Analysis", American Association for Cancer Research Annual Meeting 2017. Washington, DC, Apr 1-5, 2017.
82.	"Machine learning for cancer evolution", Microsoft Research, Redmond, USA, May 15, 2017
83.	"Clonal fitness in human cancers: a spatio-temporal exploration", Institute for Cancer Research, Royal Marsden Hospital, London UK, May 18, 2017
84.	"Clonal fitness in human cancers: a spatio-temporal exploration", Barts Cancer Institute, London UK, May 18, 2017
85.	"Cancer evolution: a spatio-temporal exploration", Arnie Charbonneau Cancer Institute, Calgary, Canada, Jun 10, 2017
86.	"Machine learning for cancer evolution", Google Research, MountainView, CA, Jun 20, 2017 (scheduled)
87.	"Cancer evolution: a spatio-temporal exploration", Memorial Sloan Kettering Cancer Center, NY, USA, Aug 23, 2017 (scheduled)

(e) Invited Participation

1.	Peter Wall Theme Development Workshop on "Public engagement around a new model for access to research resources", Vancouver, BC, May 25, 2016

(f) Conference Participation (Organizer, Chair, Moderator, etc.)

1.	Scientific committee for the Network Tools and Applications in Biology (NETTAB2005) workshop entitled: "Workflows management: new abilities for the biological information overflow", Naples, Italy Subject: workflows in bioinformatics. Oct 5-7, 2005
2.	Chair, International Conference on Research in Computational Molecular Biology (RECOMB) Satellite Workshop on Computational Cancer Biology (RECOMB-CCB), Vancouver, BC, March 2011
3.	Organizer, Speaker, Bioinformatics in Cancer Genomics (BiCG), Toronto, ON, August 28 - September 2, 2011
4.	Program Committee Member: International Conference on Intelligent Systems for Molecular Biology (ISMB) 2012 Satellite Meeting on High Throughput Sequencing (HitSeq), Los Angeles, CA, July 2012
5.	Organizing Committee Member: International Conference on Intelligent Systems for Molecular Biology (ISMB) 2013 Satellite Meeting on High Throughput Sequencing, Berlin, Germany, July 2013
6.	Organizing Committee Member and Plenary One Chair: 2014 Terry Fox Research Institute Annual Scientific Meeting, Montreal, PQ, May 8-10, 2014
7.	Plenary speaker and Session Chair. Plenary Session 2: Molecular Genomics. BCCA Translational Retreat, Vancouver, BC, June 19, 2015.
8.	Co-organizer / Plenary Session Chair, 2016 Keystone Symposium, The Cancer Genome. Banff, AB. Feb 7-12, 2016
9.	Committee Member, AACR Scientific Program Committee, Apr 16-20, 2016
10.	Scientific Committee Member, The European Society for Medical Oncology (ESMO) Congress in partnership with EACR, Madrid, Spain. Sept 8-12, 2017

(g) Other Presentations

1.	Invited Speaker: "Molecular investigations of breast cancer: What's in the genome?" Canadian Breast Cancer Foundation Speaker Series , West Vancouver Community Centre, March, 2011.

(h) Other Scholarship of Education Activities

(i) Other Professional Contributions

10. SERVICE TO THE UNIVERSITY

(a) Areas of special interest and accomplishments

1.	Associate member: Peter Wall Institute of Advanced Studies. 2012-2013
2.	Ad hoc data sciences working group. UBC Faculty of Medicine. 2015-
3.	FoM IT Governance Committee. UBC Faculty of Medicine. Jan/2016-Dec/2018

(b) Memberships on committees, including offices held and dates

	Department of Pathology and Laboratory Medicine Committees
1.	Committee Member, Tier 2 Canada Research Chair (CRC) Search Committee, Dec 2012 – present.

(c) Faculty mentoring

(d) Other service, including dates

11. SERVICE TO THE HEALTH PROFESSIONS/HEALTH AUTHORITIES

(a) Areas of special interest and accomplishments

(b) Memberships on committees, including offices held and dates

(c) Other service, including dates

12. SERVICE TO THE COMMUNITY

(a) Areas of special interest and accomplishments

(b) Memberships on scholarly societies, including offices held and dates

(c) Memberships on other societies, including offices held and dates

(d) Memberships on scholarly committees, including offices held and dates

1.	Scientific officer and reviewer. Canadian Cancer Society Research Institute, Panel J2 competition, 2009 – 2011
2.	Member, CIHR Doctoral Awards A Committee, 2011 -
3.	Reviewer, Aarhus University Interdisciplinary Research Centre competition, 2011
4.	Reviewer, Strategic Grants competition of Quebec Breast Cancer Foundation, 2011
5.	Committee Member, Michael Smith Foundation for Health Research. Research Advisory Council, Jun 2011 - present
6.	Scientific Reviewer, National Grants Competition, Canadian Breast Cancer Foundation,

	2012 -
7.	Reviewer. Canadian Cancer Society Research Institute, Innovation Grants Panel Biomarkers and Genomics (Panel I1a), 2012 – present (2012, 2013, 2014)
8.	Referee, Health Innovation Challenge Fund, Wellcome Trust, Jan – Feb 2013
9.	Committee Member, TFRI COEUR Study Committee, Jul 2013 - present
10.	Member, Canadian Institute for Advanced Research (CIFAR) Genetic Networks Program, Jul 2013 - present
11.	Committee Member, TFRI PPG Competition Peer Review Committee, 2014
12.	Reviewer, NSERC Discovery Grant, 2014
13.	Committee Member, NSERC-Create Steering Committee, 2015
14.	Reviewer, CIHR GMX Peer Review Committee, 2015
15.	Reviewer, CFI John R Evans Fund, 2015
16.	Reviewer, Prostate Cancer Canada Movember Discovery Grant Competition (**Panel B –** Early Detection and Biomarkers), 2016
17.	Reviewer. CIHR Foundation Scheme (Stage 2), 2016
18.	Steering Committee Member. High Dimensional Bioinformatics (NSERC CREATE grant), 2015-
19.	Reviewer, Canada Research Chairs Program 2016

(e) Memberships on other committees, including offices held and dates

(f) Editorships (list journal and dates)

1.	Associate Editor, BMC Cancer, Jan 2010 - present

(g) Reviewer (journal, agency, etc. including dates)

1.	Ad hoc Evaluation of Articles. Referee for Biometrika, Bioinformatics (3 manuscripts Aug 23, 2013) NAR, Pacific Symposium on Biocomputing, Journal of Statistical Methodology, BMC Bioinformatics, BMC Genomics, PLoS Computational Biology, Genome Research, Genome Biology, Molecular Cancer Research, Nature Communications, Nature Biotechnology, Nature, BioMedCentral Cancer, Journal of Pathology, Nature Genetics

(h) External examiner (indicate universities and dates)

1.	University of British Columbia, Department of Pathology and Laboratory Medicine; Vincent Montoya, M.Sc., Thesis title "A Metagenomic Analysis of Female Genital Tract Diseases", Apr 9, 2013
2.	University of Toronto, Institute of Medical Science; Zaheer S Kanji, M.Sc., Thesis title

	"Somatic Copy Number Aberrations In Familial Pancreatic Cancer: Integrative Genomics And Gene Discovery", Sep 11, 2013
3.	Chair. University of British Columbia, Department of Bioinformatics; Adriana Sedeno, Oct 9, 2014
4.	Research Proficiency Evaluation (RPE) Committee. University of British Columbia, Department of Computer Science. Mohamed Ahmed, April 15, 2015
5.	University of Toronto, Dept of Molecular Genetics; Gavin Wilson, Thesis title "Accurate identification of adenosine deamination with RNA-seq", Jan 18, 2016
6.	University of British Columbia, Department of Pathology and Laboratory Medicine; Robert Kridel, PhD., Thesis Title "The genetic basis of transformation and progression in follicular lymphoma", Mar 29, 2016
7.	University of British Columbia, Department of Computer Science; Jiarui Ding, PhD, Thesis Title "Computational methods for systems biology data of cancer", May 4, 2016
8.	University of British Columbia, Department of Bioinformatics; Thuy Nguyen, M.Sc., Thesis Title "Overcoming missing data in phylogenetic analysis of shotgun sequencing to detect HIV adaptation to immune response", June 6, 2016
9.	University of British Columbia, Department of Bioinformatics; Maia A. Smith, M.Sc., Thesis Title "E-scape: interactive visualization of single cell phylogenetics and spatio-temporal evolution in cancer", Aug 29, 2016
10.	University of British Columbia, Department of Bioinformatics; Celia Siu, M.Sc., Thesis Title "Characterization of the human thyroid epigenome", Feb 28, 2017
11.	University of British Columbia, Department of Bioinformatics; Fong Chun Chan, PhD, Thesis Title "Clinical Implications of inter-tumour, intra-tumour, and tumour microenvironment heterogeneity in B-cell lymphomas", Mar 10,2017
12.	University of British Columbia, Department of Bioinformatics; Seyed Alborz Mazloomian, PhD, Thesis Title "A systems biology study of alternative splicing regulations and functions", Apr 27, 2017

(i) Consultant (indicate organization and dates)

(j) Other service to the community

1.	Guest Blogger, BC Cancer Foundation, May – Jun 2012.

13. AWARDS AND DISTINCTIONS

(a) Awards for Teaching (indicate name of award, awarding organizations, date)

(b) Awards for Scholarship (indicate name of award, awarding organizations, date)

1.	Lap-Chee Tsui Publication Award from the Canadian Institutes for Health Research Institute of Genetics, In recognition of outstanding published health research carried out by trainees, For the discovery of the mutation in FOXL2 in granulosa cell tumors of the

	ovary (published in NEJM). $1000
2.	Senior Graduate Trainee Award, Michael Smith Foundation For Health Research, Canada, 04/2006-04/2008, $45,000
3.	University Graduate Fellowship (declined), University of British Columbia, Effective: 05/2006-05/2009, $48,000
4.	ISCB travel award, International Society for Computational Biology, United States, 07/2007-08/2007, Travel fellowship to ISMB 2007 conference, $1,100
5.	Postdoctoral Fellowship, Michael Smith Foundation For Health Research, Canada ($120,000 over 3yrs), 10/2008-10/2011
6.	ISCB travel award, International Society for Computational Biology, United States,, 07/2009-08/2009, Travel fellowship to ISMB 2009 conference, $1,100
7.	Canadian Breast Cancer Foundation Bioinformatics Fellowship. (part of $500,000 over 5yrs to Dr. Sam Aparicio), 2008-2013
8.	Research Fellowship, Eli Lilly. ($130,000 over 2yrs), 09/2009-09/2011
9.	Career Investigator Award, Michael Smith Foundation for Health Research ($635,000 over 8yrs). 07/2011-06/2019
10.	Associate, Peter Wall Institute for Advanced Studies, $1000. 09/2012-09/2013
11.	Terry Fox New Investigator Award, Terry Fox Research Institute ($450,000 over 3 yrs) 10/2012-10/2015
12.	Distinguished Achievement Award for Overall Excellence – Early Career. Faculty of Medicine, UBC, 2013
13.	Canada Research Chair Tier 2 in Computational Cancer Genomics ($500,000 over 5 years), 04/2013-03/2018
14.	Award for Early Career Excellence in Research and Discovery. UBC Department of Pathology and Laboratory Medicine, 05/2015
15.	UBC Killam Research Prize. Applied Science, Junior Category 01/2016

(c) Awards for Service (indicate name of award, awarding organizations, date)

1.	Student service award. Department of Computer Science, UBC, 2008

(d) Other Awards

14. <u>OTHER RELEVANT INFORMATION</u> (Maximum One Page)

THE UNIVERSITY OF BRITISH COLUMBIA
Publications Record

SURNAME: Shah

FIRST NAME: Sohrab
Initials:SPS
MIDDLE NAME(S): Prakash
Date: August 2, 2017

Authorship Statement

Underline – trainees under my direct supervision

1. REFEREED PUBLICATIONS

(a) Journals

MANUSCRIPTS SUBMITTED FOR PUBLICATION

De Souza CPE, Faharani H, Billings R, Yap D, Shumansky K, Aniba MR, Wan A, Mes-Masson AM, Aparicio S, and **Shah SP**. Engineered in-vitro cell line mixtures and robust evaluation of computation methods for clonal decomposition and longitudinal dynamics in cancer. *Scientific Reports.* Submitted (2017)

MANUSCRIPTS ACCEPTED FOR PUBLICATION

PUBLISHED REFEREED PUBLICATIONS

1.	**Shah SP**, McVicker GP, Mackworth AK, Rogic S, Ouellette BF. GeneComber: combining outputs of gene prediction programs for improved results. *Bioinformatics*. 2003 Jul 1;19(10):1296-7. Contribution: designed, implemented and tested the software; wrote the manuscript.
2.	**Shah SP**, He DY, Sawkins JN, Druce JC, Quon G, Lett D, Zheng GX, Xu T, Ouellette BF. Pegasys: software for executing and integrating analyses of biological sequences. *BMC Bioinformatics*. 2004 Apr 19;5:40. Contribution: designed, implemented and tested the software; wrote the manuscript.
3.	Kemmer D, Huang Y, **Shah SP**, Lim J, Brumm J, Yuen MM, Ling J, Xu T, Wasserman WW, Ouellette BF. Ulysses - an application for the projection of molecular interactions across species. *Genome Biol*. 2005 Dec;6(12):R106. Contribution:developed the Atlas data warehouse, enabled this analysis
4.	**Shah SP**, Huang Y, Xu T, Yuen MM, Ling J, Ouellette BF. Atlas - a data warehouse for integrative bioinformatics. *BMC Bioinformatics*. 2005 Feb 21;6:34. Contribution: designed, implemented and tested the software; wrote the manuscript.
5.	**Shah SP**, Xuan X, DeLeeuw RJ, Khojasteh M, Lam WL, Ng R, Murphy KP. Integrating copy number polymorphisms into array CGH analysis using a robust

	HMM. *Bioinformatics.* 2006 Jul 15;22(14):e431-9. Contribution: derived implemented and evaluated the algorithm; wrote the manuscript.
6.	**Shah SP**, Lam WL, Ng RT, Murphy KP. Modeling recurrent DNA copy number alterations in array CGH data. *Bioinformatics*. 2007 Jul 1;23(13):i450-8. Contribution: derived, implemented and evaluated the algorithm; wrote the manuscript.
7.	**Shah SP**. Computational methods for identification of recurrent copy number alteration patterns by array CGH. *Cytogenet Genome Res*. 2008;123(1-4):343-51. Contribution: sole author, solicited review article
8.	Cheung KJ*, **Shah SP***, Steidl C, Johnson N, Relander T, Telenius A, Lai B, Murphy KP, Lam W, Al-Tourah AJ, Connors JM, Ng RT, Gascoyne RD, Horsman DE. Genome-wide profiling of follicular lymphoma by array comparative genomic hybridization reveals prognostically significant DNA copy number imbalances. *Blood*. 2009 Jan 1;113(1):137-48. doi: 10.1182/blood-2008-02-140616 (*equal contribution) Contribution: led and performed data analysis
9.	**Shah SP**, Cheung KJ Jr, Johnson NA, Alain G, Gascoyne RD, Horsman DE, Ng RT, Murphy KP. Model-based clustering of array CGH data. *Bioinformatics*. 2009 Jun 15;25(12):i30-8. doi: 10.1093/bioinformatics/btp205 Contribution: derived, implemented and evaluated the algorithm; wrote the manuscript.
10.	**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 FOXL2 in granulosa-cell tumors of the ovary. *N Engl J Med*. 2009 Jun 25;360(26):2719-29. **This paper was the first clinically useful discovery from next generation sequencing of tumours. It has now been implemented as a diagnostic test in several non-Canadian jurisdictions.**
11.	**Shah SP**, Morin RD, Khattra J, Prentice L, Pugh T, Burleigh A, Delaney A, Gelmon K, Giuliany R, Senz J, Steidl C, Holt RA, Jones S, Sun M, Leung G, Moore R, Severson T, Taylor GA, Teschendorff AE, Tse K, Turashvili G, Varhol R, Warren RL, Watson P, Zhao Y, Caldas C, Huntsman D, Hirst M, Marra MA, Aparicio S. Mutational evolution in a lobular breast tumour profiled at single nucleotide resolution. *Nature*. 2009 Oct 8;461(7265):809-13. Contribution: project lead; developed algorithms, performed data analysis **This paper reported the world's first fully sequenced epithelial cancer genome and was the first study to compare the complete set of mutations across temporal samples to measure tumour evolution. The announcement of this work led the Globe and Mail, CBC and CTV news.**
12.	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. *Nat Genet*. 2010 Feb;42(2):181-5.
13.	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. Contribution: supervised data analysis and bioinformatics component of the study
14.	Goya R, Sun MG, Morin RD, Leung G, Ha G, Wiegand KC, Senz J, Crisan A, Marra MA, Hirst M, Huntsman D, Murphy KP, Aparicio S, **Shah SP**. SNVMix: predicting single nucleotide variants from next-generation sequencing of tumors. *Bioinformatics*. 2010 Mar 15;26(6):730-6. Contribution: project conception and oversight; wrote the manuscript.
15.	Steidl C, Telenius A, **Shah SP**, Farinha P, Barclay L, Boyle M, Connors JM, Horsman DE, Gascoyne RD. Genome-wide copy number analysis of Hodgkin Reed-Sternberg cells identifies recurrent imbalances with correlations to treatment outcome. *Blood*. 2010 Jul 22;116(3):418-27.
16.	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 Biol*. 2010 August;11(8):R82.
17.	Cheung KJ, Delaney A, Ben-Neriah S, Schein J, Lee T, **Shah SP**, Cheung D, Johnson NA, Mungall AJ, Telenius A, Lai B, Boyle M, Connors JM, Gascoyne RD, Marra MA, Horsman DE. High resolution analysis of follicular lymphoma genomes reveals somatic recurrent sites of copy-neutral loss of heterozygosity and copy number alterations that target single genes. *Genes, Chromosomes Cancer*. 2010 Aug;49(8):669-81.
18.	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):1532-43.
19.	Cheung KJ, Johnson NA, Affleck JG, Severson T, Steidl C, Ben-Neriah S, Schein J, Morin RD, Moore R, **Shah SP**, Qian H, Paul JE, Telenius A, Relander T, Lam W, Savage K, Connors JM, Brown C, Marra MA, Gascoyne RD, Horsman DE. Acquired TNFRSF14 mutations in follicular lymphoma are associated with worse prognosis. *Cancer Res*. 2010 Nov 15;70(22):9166-74.

20.	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. *Equal contribution.
21.	McConechy MK, Anglesio MS, Kalloger SE, Yang W, Senz J, Chow C, Heravi-Moussavi A, Morin GB, Mes-Masson AM; Australian Ovarian Cancer Study Group, Carey MS, McAlpine JN, Kwon JS, Prentice LM, Boyd N, **Shah SP**, Gilks CB, Huntsman DG. Subtype-specific mutation of PPP2R1A in endometrial and ovarian carcinomas. *J Pathol*. 2011 Apr;223(5):567-73.
22.	McPherson A, Hormozdiari F, Zayed A, Giuliany R, Ha G, Sun MGF, Griffith M, Moussavi AH, Senz J, Melnyk N, Pacheco M, Marra MA, Hirst M, Nielsen TO, Sahinalp SC, Huntsman D, **Shah SP**. deFuse: an algorithm for gene fusion discovery in tumor RNA-Seq data. *PLoS Comput Biol*. 2011 May: 7(5):e1001138.
23.	McPherson A, Wu C, Hajirasouliha I, Hormozdiari F, Hach F, Lapuk A, Volik S, S**hah S**, Collins C, Sahinalp SC. Comrad: a novel algorithmic framework for the integrated analysis of RNA-Seq and WGSS data. *Bioinformatics* 2011 June: 27(11):1481-8
24.	Schrader KA, Heravi-Moussavi A, Waters PJ, Senz J, Whelan J, Ha G, Eydoux P, Nielsen T, Gallagher B, Oloumi A, Boyd N, Fernandez BA, Young TL, Jones 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. *J Pathol* 2011 Sep;225(1):12-8.
25.	Ding J, Bashashati A, Roth A, Oloumi A, Tse K, Zeng T, Haffari G, Hirst M,Marra MA, Condon A, Aparicio S, **Shah SP**. Feature based classifiers for somatic mutation detection in tumour-normal paired sequencing data. *Bioinformatics*. 2012 Jan 15;28(2):167-75.
26.	Lee CH, Ou WB, Mario-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.
27.	Heravi-Moussavi A, Anglesio MS, Cheng SW, Senz J, Yang W, Prentice L, Fejes AP, Chow C, Tone A, Kalloger SE, Hamel N, Roth A, Ha G, Wan AN, Maines-Bandiera S, Salamanca C, Pasini B, Clarke BA, Lee AF, Lee CH, Zhao C, Young RH, Aparicio SA, Sorensen PH, Woo MM, Boyd N, Jones SJ, Hirst M, Marra MA, Gilks B, **Shah SP**, Foulkes WD, Morin GB, Huntsman DG. Recurrent somatic DICER1 mutations in nonepithelial ovarian cancers. *N Engl J Med* 2012 Jan 19;366(3):234-42.
28.	Roth A, Ding J, Morin R, Crisan A, Ha G, Giuliany R, Bashashati A, Hirst M, Turashvili G, Oloumi A, Marra MA, Aparicio S, **Shah SP**. JointSNVMix: a probabilistic model for accurate detection of somatic mutations in normal/tumour paired next-generation sequencing data. *Bioinformatics* 2012 Apr 1;28(7):907-13.

29.	Curtis C*, **Shah SP***, Chin SF*, Turashvili G*, Rueda OM, Dunning MJ, Speed D, Lynch AG, Samarajiwa S, Yuan Y, Gräf S, Ha G, Haffari G, Bashashati A, Russell R, McKinney S; METABRIC Group, Langerød A, Green A, Provenzano E, Wishart G, Pinder S, Watson P, Markowetz F, Murphy L, Ellis I, Purushotham A, Børresen-Dale AL, Brenton JD, Tavaré S, Caldas C, Aparicio S. The genomic and transcriptomic architecture of 2,000 breast tumours reveals novel subgroups. *Nature* 2012 Apr 18;486(7403):346-52. (* equal contribution) **This paper describes the genomic landscape of 2,000 breast cancers and reveals a novel molecular stratification of the breast cancer tumour population. This paper was featured as one of the top 10 medical breakthroughs of 2012 by the BBC: http://www.bbc.co.uk/news/health-20785638**
30.	**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. (*co-corresponding authors) **This paper was the world's first description of the distribution of clonal evolution in a population of patient tumours. It was also the first survey of the mutational landscape of triple negative breast cancers. The announcement of the paper was featured in the Globe and Mail, CBC and CTV news.**
31.	McAlpine JN, Porter H, Köbel M, Nelson BH, Prentice LM, Kalloger SE, Senz J, Milne K, Ding J, **Shah SP**, Huntsman DG, Gilks CB. BRCA1 and BRCA2 mutations correlate with TP53 abnormalities and presence of immune cell infiltrates in ovarian high-grade serous carcinoma. *Mod Pathol* 2012 May;25(5):740-50.
32.	Crisan A, Goya R, Ha G, Ding J, Prentice LM, Oloumi A, Senz J, Zeng T, Tse K, Delaney A, Marra M, Huntsman D, Hirst M, Aparicio S, **Shah SP**. Mutation discovery in regions of segmental cancer genome amplifications with CoNAn-SNV: a mixture model for next generation sequencing of tumors. *PLoS One*. 2012 August;7(8):e41551
33.	McConechy MK, Ding J, Cheang MC, Wiegand KC, Senz J, Tone AA, Yang W, Prentice LM, Tse K, Zeng T, McDonald H, Schmidt AP, Mutch DG, McAlpine JN, Hirst M, **Shah SP**, Lee CH, Goodfellow PJ, Gilks CB, Huntsman DG. Use of mutation profiles to refine the classification of endometrial carcinomas. *J Pathol* 2012 Sep;228(1):20-30. doi: 10.1002/path.4056.
34.	Steidl C, Diepstra A, Lee T, Chan FC, Farinha P, Tan K, Telenius A, Barclay L, **Shah SP**, Connors JM, van den Berg A, Gascoyne RD. Gene expression profiling of microdissected Hodgkin Reed Sternberg cells correlates with treatment outcome in classical Hodgkin lymphoma. *Blood*. 2012 Oct 25;120(17):3530-40. doi: 10.1182/blood-2012-06-439570.
35.	Ha G, Roth A, Lai D, Bashashati A, Ding J, Goya R, Giuliany R, Rosner J, Oloumi

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(b) Conference Proceedings

(c) Other

2. NON-REFEREED PUBLICATIONS

(a) Journals

(b) Conference Proceedings

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1.	McPherson A, **Shah S**. Gene fusion discovery in paired end RNA-Seq data with application to ovarian cancer. Oral presentation. ISMB 2010 (HiTSeq 2010). Boston, MA; July 11, 2010
2.	McPherson A, **Shah S**. Integrated analysis of multiple next generation sequencing datasets with application to gene fusion discovery. Oral presentation. Genome Informatics 2010. Hinxton, UK; Sept 15, 2010
3.	McPherson A, **Shah S**. deFuse: an algorithm for gene fusion discovery in tumor RNA-Seq. Oral presentation. Third Annual RECOMB Satellite Workshop on Computational Cancer Biology. Vancouver, BC; March 28, 2011
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44.	Ennishi D, Bashashati A, Saberi S, Mottok A, Meissner B, Boyle M, Ben-Neriah S, Kridel R, Dominguez-Sola D, Savage K, Sehn L, Connors JM, Morin RD, Marra MA, **Shah SP**, Steidl C, Scott DW, Gascoyne RD. Frequent Genetic Alterations of PI3K-AKT Pathway and Their Clinical Significance in Germinal Center B-Cell-like Diffuse Large B-Cell Lymphoma. American Society of Hematology 568th Annual Meeting & Exposition; Dec 3-6, 2016; San Diego, CA.

3. BOOKS

1 *(a) Authored*

(b) Edited

1.	Banerjee, D, **Shah SP** (Editors). Methods in Molecular Biology 973: Array Comparative Genomic Hybridization (Protocols and Applications). 2013. Humana Press

(c) Chapters

2.	Ha G, **Shah S**. Distinguishing somatic and germline copy number events in cancer patient DNA hybridized to whole-genome SNP genotyping arrays. *Methods Mol Biol.* 2013;973:355-72. doi: 10.1007/978-1-62703-281-0_22.

4. PATENTS

1.	**Methods and devices for analyzing particles** First named inventor: Carl Hansen Inventors: Hans Zahn, Jens Huft, Marinus Van Loenhout, Kaston Leung, Bill Lin, Anders Klaus, Samuel Aparicio, Sohrab Shah Application number: PCT/CA2016/0000031 Application Filing Date: February 4, 2016 International Publication Date: August 11, 2016

	International Publication Number: WO 2016/123692 A1
2.	**Novel biomarkers and targets for ovarian carcinoma - ABANDONED** First named inventor: David G. Huntsman Inventors: David G. Huntsman, Marco Marra, Kimberly Wiegand, Martin Hirst, Sohrab Prakash Shah Application number 13/642337 US Provisional Patent Filed on Apr 22, 2011 Publication Date Aug 01, 2013 US Patent Application 20130197056
3.	**Predicting treatment response in cancer patients - ABANDONED** First named inventor: Andrew Roth Inventors: Sohrab Shah, Samuel Aparicio, Alexandre Bouchard-Côté, Andrew Roth Application number 61734456 US Provisional Patent Filed on Dec 07, 2012
4.	**Method of Identifying Diffuse large B-cell Lymphoma patients with Poor Outcome - ABANDONED** First named inventor: Fong Chun Chan Inventors: Fong Chun Chan, Randy Gascoyne, Sohrab Shah, Christian Steidl Application number 61734755 US Provisional Patent Filed on Dec 07, 2012
5.	**Detection of granulosa-cell tumors - ABANDONED** First named inventor: David G. Huntsman Inventors: Marco Marra, Martin Hirst, Ryan D. Morin, Sohrab Prakash Shah, Janine Senz Application number US 13/123,313 Provisional Patent Filed on Oct 6, 2009 Publication Date Aug 11, 2011 PCT CA2009/001403

5. <u>SPECIAL COPYRIGHTS</u>

6. <u>ARTISTIC WORKS, PERFORMANCES, DESIGNS</u>

7. <u>OTHER WORKS</u>

8. <u>WORK IN PROGRESS</u> (including degree of completion)

Collaborations:

With Sam Aparicio (BCCA):
Modeling clonal evolution in xeno-engrafted tumour samples (50% complete)
Single cell genomics to identify somatic genotypes under evolutionary selection (10% complete)
The mutational landscape of triple negative breast cancer (30% complete)

With David Huntsman (BCCA):
The mutational landscape of ovarian clear cell carcinomas (50% complete)

With Alex Cote-Bouchard (UBC Statistics):
Statistical models for phylogenetic inference of clonal population structures in human cancers (25% complete)

With Paul Boutros (Ontario Institute for Cancer Research (OICR)):
A clinical-grade computational platform for cancer genome sequencing analysis (75% complete)

With Randy Gascoyne (BCCA):
The evolutionary dynamics of follicular lymphoma and genomic mechanisms for transformation to aggressive DLBCL (75% complete)

With Christian Steidl (BCCA):
Integrative analysis of the genomes and transcriptomes of diffuse large B-cell lymphomas (75% complete)

With Torben Falck-Ortnoft (University of Aarhus, Denmark):
Evolutionary dynamics of bladder cancer (100% complete)

With Michael Taylor (OICR):
Genomic comparisons of primary and metastatic medulloblastomas (100% complete)

With Lincoln Stein (OICR):
Analysis of >2500 tumour normal whole genome datasets from the ICGC consortium (25% complete)

With Karen Gelmon (BCCA):
Spatial heterogeneity in locally advanced breast cancers (25% complete)

With Brad Nelson (BCCA)
How the immune system contends with clonal diversity in high grade serous ovary cancers (25% complete)