BIOGRAPHICAL SKETCH

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NAME	POSITION TITLE
Shah, Sohrab	Associate Professor, Department of Pathology & Laboratory Medicine, University of British Columbia Scientist, Molecular Oncology, BC Cancer Agency

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	MM/YY	FIELD OF STUDY
Queen's University, Kingston, ON, Canada	BSc	1996	Biology
University of British Columbia, Vancouver, BC Canada	BSc	2001	Computer Science
University of British Columbia, Vancouver BC Canada	MSc	2005	Computer Science (Bioinformatics)
University of British Columbia, Vancouver BC Canada	PhD	2008	Computer Science (Bioinformatics)
University of British Columbia, Vancouver BC Canada	PDF	2008-10	

A. Personal Statement

Dr. Shah is a Canada Research Chair in Computational Cancer Genomics, and the recipient of both a Michael Smith Foundation for Health Research Career Investigator Award and a Terry Fox Research Institute New Investigator Award. His research focuses on understanding cancer genomes from the perspective of identifying pathogenic driver alterations and how tumours evolve over time. This work involves the development of statistical models, algorithms and computational approaches to analyze large, high dimensional genomics and transcriptomic data sets derived from tumours in order to describe mutational landscapes of cancer subtypes and quantify clonal diversity and intratumoural heterogeneity. Much of this work is devoted to analysis and interpretation of next generation sequencing data applied in cancer-focused experimental designs with specific focus on ovarian cancer. In particular Dr. Shah is engaged in studying the genomic properties of long term survivors of high grade serous ovarian cancer patients and methylation properties of clear cell carcinomas. Dr. Shah received a PhD in computer science from UBC in 2008. Postdoctoral work overseen by Dr. Sam Aparicio and Dr. David Huntsman at the BC Cancer Agency was devoted to analysis of cancer genome sequencing data, resulting in landmark papers on breast and ovarian cancers published in *Nature* and the *New England Journal of Medicine*. Dr. Shah was appointed as an Assistant Professor, Dept of Pathology and Lab Medicine as well as a Scientist at the BC Cancer Agency in 2008, and as an Associate Professor in 2014. His research program is well supported by independent grant funding and he currently oversees a group of bioinformatics students, PDFs and staff devoted to deciphering biological properties from cancer genome data sets using novel and state-of-the art computational analysis. Collaboration with Dr. Huntsman remains a key component of Dr. Shah's program.

B. Positions and Honors

Positions

2000 - 2002	Bioinformatics software developer, CMMT, UBC, Vancouver, BC
2002 - 2004	Chief, High throughput bioinformatics, UBC
2002 - present	Instructor, Canadian Bioinformatics Workshops Series
2005 - 2008	Research Assistant, UBC Department of Computer Science
2006 - 2009	Instructor, Interprofessional Health and Human Services, UBC
2008 - 2010	Postdoctoral Research Fellow, BC Cancer Agency
2010 - 2014	Assistant Professor, Department of Pathology and Laboratory Medicine, UBC
2010 - present	Scientist, Molecular Oncology and Breast Cancer Research Program, BC Cancer Agency
2010 - present	Associate Member, UBC Dept of Computer Science
2013 - present	Faculty Member, Genome Science and Technology Graduate Program
2013 - present	Associate Member, Genome Sciences Centre
2013 - present	Adjunct Professor, SFU School of Computing Science

2014 - present	Associate Professor, UBC Dept of Pathology and Laboratory Medicine

Honors

2006-2008	Senior Graduate Trainee Award, Michael Smith Foundation For Health Research, Canada;
2006-2009	University Graduate Fellowship (declined), UBC, Canada; $48,000
2007	International Society for Computational Biology Travel Fellowship to ISMB 2007 conference;
2008	Student Service Award, Department of Computer Science, UBC
2008-2011	Postdoctoral Fellowship, Michael Smith Foundation For Health Research, Canada; $120,000/3yrs
2008-2011	Canadian Breast Cancer Foundation Bioinformatics Fellowship; part of $500,000 over 5yrs to Dr. Sam Aparicio
2009-2011	Research Fellowship, Eli Lilly; $130,000 over 2yrs
2009	International Society for Computational Biology Travel Fellowship to ISMB 2009 conference;
2010	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);
2011-2019	MSFHR Career Investigator Award; $635,000 (over 8 years)
2012	Associate member of the Peter Wall Institute of Advanced Studies
2012-2015	Terry Fox New Investigator Award (TFRI). Are genomic instability and clonal diversity prognostic indicators of high grade serous ovarian cancer?; $449,503
2013	Distinguished Achievement Award for Overall Excellence – Early Career. Fac. of Medicine, UBC
2013-2018	Canada Research Chair (Tier 2) in Computational Cancer Genomics

C. Peer-reviewed Publications

1. Twa DDW, Mottok A, Chan FC, Ben-Neriah S, Woolcock BW, Tan KL, Mungall AJ, McDonald H, Zhao Y, Lim RS, Nelson BH, Milne K, **Shah SP**, Morin RD, Marra MA, Scott DW, Gascoyne RD, Steidl C. Recurrent genomic rearrangements in primary testicular lymphoma, Journal of Pathology, 2015 Feb 25. doi: 10.1002/path.4522. [Epub ahead of print]
2. 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 AJL, Lefebvre C, Bashashati A, de Souza C, Siu C, Aniba R, Brimhall J, Oloumi A, Osako T, Bruna A, Sandoval J, Algara T, Greenwood W, Leung K, Cheng H, Xue H, Wang Y, Lin D, Mungall A, Moore R, Zhao 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. ** - corresponding author; * denotes equal contribution
3. Anglesio MS, Bashashati A, Wang Y, Senz J, Ha G, Yang W, Aniba MR, Prentice LM, Farahani H, Chang HL, Karnezis AN, Marra MA, Yong PJ, Hirst M, Gilks B, **Shah SP***, Huntsman DG*. Multifocal endometriotic lesions associated with cancer are clonal and carry a high mutation burden, including oncogenic alterations. *Journal of Pathology*, 2015 Feb 18. doi: 10.1002/path.4516. [Epub ahead of print]
4. Hansford S, Kaurah P, Li-Chang H, Woo M, Senz J, Pinheiro H, Schrader KA, Schaeffer DF, Shumansky K, Zogopoulos G, Almeida Santos T, Claro I, Carvalho J, Nielsen C, Padilla S, Lum A, Talhouk A, Baker-Lange K, Richardson S, Lewis I, Lindor NM, Pennell E, MacMillan A, Fernandez B, Keller G, Lynch H, **Shah SP**, Guilford P, Gallinger S, Corso G, Roviello F, Caldas C, Oliveria C, Pharoah PD, Huntsman DG. Hereditary Diffuse Gastric Cancer SyndromeCDH1 Mutations and Beyond. JAMA Oncology. Published online February 12, 2015. doi:10.1001/jamaoncol.2014.168
5. Vollan HK, Rueda OM, Chin SF, Curtis C, Turashvili G, **Shah S**, Lingjærde OC, Yuan Y, Ng CK, Dunning MJ, Dicks E, Provenzano E, Sammut S, McKinney S, Ellis IO, Pinder S, Purushotham A, Murphy LC, Kristensen VN, METABRIC group, Brenton JD, Pharoah PD, Børresen-Dale A, Aparicio S, Caldas C. A tumor DNA complex aberration index is an independent predictor of survival in breast and ovarian cancer. Published in *Molecular Oncology*, 2015 Jan;9(1):115-27. doi: 10.1016/j.molonc.2014.07.019.

6. Tone AA, McConechy MK, Yang W, Ding J, Yip S, Kong E, Wong KK, Gershenson DM, Mackay H, **Shah S**, Gilks B, Tinker AV, Clarke B, McAlpine JN, Huntsman D. Intratumoral heterogeneity in a minority of ovarian low-grade serous carcinomas. *BMC Cancer.* 2014 Dec, 14:982.
7. Nguyen LV, Cox C, Eirew P, Knapp DJHF, Pellacani D, Kannan K, Carles A, Moksa M, Balani S, **Shah S**, Hirst M, Aparicio S, Eaves CJ. DNA barcoding reveals diverse growth kinetics of human breast tumour subclones in serially passaged xenografts. *Nature Communications*. 2014 Dec 23;5:5871.
8. Ha G, Roth A, Khattra J, Yap D, Melnyk N, McPherson A, Prentice L, Bashashati A, Laks E, Biele J, Ding J, Le A, Rosner J, Shumansky K, Marra M, Gilks CB, Huntsman DG, McAlpine JN, Aparicio S, **Shah SP**. TITAN: Inferring copy number architectures of clonal cell populations from tumour whole genome sequencing data. *Genome Research*. 2014 Nov;24(11):1881-93. doi: 10.1101/gr.180281.114.
9. Chan FC, Connors JM, Marra MA, Gascoyne RD, **Shah SP***, Steidl C*. An RCOR1 loss-associated gene expression signature identifies a prognostically significant DLBCL subgroup. *Blood.* 2014 Nov 13. pii: blood-2013-06-507152. [Epub ahead of print]* - senior, corresponding author
10. Nordentoft I, Lamy P, Birkenkamp-Demtröder K, Shumansky K, Vang S, Hornshøj H, Juul M, Villesen P, Hedegaard J, Roth A, Thorsen K, Høyer S, Borre M, Reinert T, Fristrup N, Dyrskjøt L, **Shah S**, Pedersen JS, Ørntoft TF. Mutational context and diverse clonal development in early and late bladder cancer. *Cell Reports* 2014 Jun 12;7(5):1649-63. http://dx.doi.org/10.1016/j.celrep.2014.04.038
11. Ramos P, Karnezis AN, Craig DW, Sekulic A, Russell ML, Hendricks WP, Corneveaux JJ, Barrett MT, Shumansky K, Yang Y, **Shah SP**, Prentice LM, Marra MA, Kiefer J, Zismann VL, McEachron TA, Salhia B, Prat J, D'Angelo E, Clarke BA, Pressey JG, Farley JH, Anthony SP, Roden RB, Cunliffe HE, Huntsman DG, Trent JM. Small cell carcinoma of the ovary, hypercalcemic type, displays frequent inactivating germline and somatic mutations in SMARCA4. *Nat Genet*. 2014 May;46(5):427-9. doi: 10.1038/ng.2928.
12. Roth A, Khattra J, Yap D, Wan A, Laks E, Biele J, Ha G, Aparicio S, Bouchard-Cote A, **Shah SP**. PyClone: statistical inference of clonal population structure in cancer. *Nature Methods* 2014 Apr;11(4):396-8. doi: 10.1038/nmeth.2883.
13. Gunawardana J, Chan FC, Telenius A, Woolcock B, Kridel R, Tan KL, Ben-Neriah S, Mottok A, Lim RS, Boyle M, Rogic S, Rimsza LM, Guiter C, Leroy K, Gaulard P, Haioun C, Marra MA, Savage KJ, Connors JM, **Shah SP**, Gascoyne RD, Steidl C. Recurrent Somatic Mutations of PTPN1 in Primary Mediastinal B cell lymphoma and Hodgkin Lymphoma. *Nat Genet*. 2014 Apr;46(4):329-35. doi: 10.1038/ng.2900.
14. Twa D, Chan FC, Ben-Neriah S, Woolcock BW, Tan KL, Slack GW, Gunawardana J, Lim RS, McPherson AW, Kridel R, Telenius A, Scott DW, Savage KJ, **Shah SP**, Gascoyne RD, Steidl C. Genomic rearrangements involving programmed death ligands are recurrent in primary mediastinal large B-cell lymphoma. *Blood* 2014 Mar 27;123(13):2062-5. doi: 10.1182/blood-2013-10-535443.
15. McConechy MK, Ding J, Senz J, Yang W, Melnyk N, Tone AA, Prentice LM, Wiegand KC, McAlpine JN, **Shah SP**, Lee CH, Goodfellow PJ, Gilks CB, Huntsman DG. Ovarian and endometrial endometrioid carcinomas have distinct CTNNB1 and PTEN mutation profiles. *Mod Pathol.* 2014 Jan;27(1):128-34. doi: 10.1038/modpathol.2013. 107.
16. Anglesio MS, Wiegand KC, Melnyk N, Chow C, Salamanca C, Prentice LM, Senz J, Yang W, Spillman MA, Cochrane DR, Shumansky K, **Shah SP**, Kalloger SE, Huntsman DG. Type-specific cell line models for type-specific ovarian cancer research.*PLoS One*. 2013 Sep 4;8(9):e72162. doi: 10.1371/journal.pone.0072162.
17. 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.
18. 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. doi: 10.1182/blood-2013-02-483727.
19. Mezlini AM, Smith EJM, Fiume M, Buske O, Savich G, **Shah S**, Aparicio S, Chiang D, Goldenberg A, and Brudno M. iReckon: Simultaneous isoform discovery and abundance estimation from RNA-seq data. *Genome Res*. 2013 Mar;23(3):519-29. doi: 10.1101/gr.142232.112.
20. Ding J, **Shah S**. A robust hidden semi-Markov model with application to aCGH data processing. *Int J Data Min Bioinform.* 2013 January;8(4):427-42.

21. 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 January;973:355-72. Bashashati A, Haffari G, Ding J, Ha G, Lui K, Rosner J, Huntsman D, Caldas C, Aparicio S, **Shah SP**. DriverNet: uncovering the impact of somatic driver mutations on transcriptional networks in cancer. *Genome Biology*. 2012 Dec 26;13(12):R124.
22. McPherson AW, Wu C, Wyatt A, **Shah SP**, Collins C, Sahinalp SC. nFuse: Discovery of complex genomic rearrangements in cancer using high-throughput sequencing. *Genome Res* 2012 Nov;22(11):2250-61.
23. Ha G, Roth A, Lai D, Bashashati A, Ding J, Goya R, Giuliany R, Rosner J, Oloumi A, Shumansky K, Chin SF, Turashvili G, Hirst M, Caldas C, Marra MA, Aparicio S, **Shah SP**. Integrative analysis of genome-wide loss of heterozygosity and mono-allelic expression at nucleotide resolution reveals disrupted pathways in triple negative breast cancer. *Genome Res* 2012 Oct;22(10):1995-2007. doi: 10.1101/gr.137570.112.
24. 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.
25. 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.
26. 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
27. 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.
28. **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)
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)
30. 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.
31. 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.
32. 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.
33. 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.