GAVIN HA

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RESEARCH SUMMARY

My laboratory is interested in studying the role of genomic alterations in cancer and expanding applications for precision medicine. We develop novel algorithms to identify genomic structural alterations in tumor and circulating cell-free DNA from patients with cancer. Our goals are to uncover the genetic and epigenetic mechanisms of treatment resistance, to identify blood-based genomic biomarkers, and to translate these findings and innovations to advance clinical research and precision medicine.

FACULTY POSITIONS

2018 – **Assistant Member,** Computational Biology Program, Public Health Sciences Division
Fred Hutchinson Cancer Research Center, Seattle, WA

2019 – **Affiliate Assistant Professor,** Department of Genome Sciences
University of Washington, Seattle, WA

RESEARCH EXPERIENCE

2014 – 2018 **Postdoctoral Research Fellow**, Dana-Farber Cancer Institute, Boston, MA and Broad Institute of Harvard and MIT, Cambridge, MA
Mentor: Dr. Matthew Meyerson

2009 – 2014 **Graduate Student**, BC Cancer Agency, University of British Columbia, Canada
Advisors: Drs. Sohrab P. Shah and Samuel Aparicio

EDUCATION

2008 – 2014 **Ph.D., Bioinformatics**
University of British Columbia, Vancouver, BC, Canada

2003 – 2008 **B.Sc., Computer Science & Microbiology/Immunology**
University of British Columbia, Vancouver, BC, Canada

HONORS AND AWARDS

2019 – Prostate Cancer Foundation Young Investigator Award

2019 – NIH NCI Transition Career Development Award (K22)

2015 – 2018 Canadian Institutes of Health Research (CIHR) Postdoctoral Fellowship

2012 Lloyd Skarsgard Graduate Research Excellence Award, BC Cancer Agency

2010 – 2013 Natural Sciences and Engineering Research Council of Canada (NSERC) Postgraduate Scholarship

2010 – 2014 Four Year Fellowships (FYF), University of British Columbia

2008 – 2010 Canadian Institutes of Health Research (CIHR) Graduate Scholarship

2008 – 2010 College for Interdisciplinary Studies Graduate Award, University of British Columbia

RESEARCH FUNDING

CURRENT

2019 – 2021 Sponsor: Fund for Innovation in Cancer Informatics
Title: Accelerating the development and validation of liquid biopsy assays
Total Costs: $173,881
Role: PI

2019 Sponsor: Brotman Baty Institute for Precision Medicine – Catalytic Pilot Grant
Title: Developing an analytical framework for clinical genome sequencing of cell-free DNA
Total Costs: $150,000
Role: PI

2019 Sponsor: Pacific Northwest Prostate Cancer SPORE Career Enhancement Program
NCI 2 P50 CA097186-16A1 (Subaward)
Title: Defining the genomic alteration signatures of advanced prostate cancer
Total Costs: $50,000
Role: PI

2019 – 2021 Sponsor: Cancer Center Support Grant (CCSG) New Investigator Support
NCI 5 P30 CA015704-44 (Subaward)
Title: Characterizing molecular signatures in advanced prostate cancer using liquid biopsies
Total Costs: $80,000
Role: PI

PENDING

2019 – 2022 Sponsor: Prostate Cancer Foundation (PCF) Young Investigator Award (YIA)
Title: Developing novel computational approaches to study therapeutic resistance in castration-resistant prostate cancer using circulating tumor DNA
Total Costs: $225,000
Role: PI
Status: Awarded

2019 Sponsor: NIH/NCI Transition Career Development Award (K22)
NCI 1 K22 CA237746-01
Title: Identifying driver non-coding alterations in metastatic prostate cancer from tumor and cell-free DNA
Total Costs: $450,000
Role: PI
Status: Selected for funding

2019 Sponsor: The V Foundation Scholar Award
Title: Characterizing molecular signatures associated with therapeutic resistance in advanced prostate cancer using liquid biopsies
Role: PI
Status: Under review

PAST

2015 – 2018 Sponsor: Canadian Institutes for Health Research
Title: Characterizing the clonal diversity and patterns of tumour evolution in non-small cell lung cancer
Total Costs: $150,000 CAD
Role: PI

TEACHING RESPONSIBILITIES

GRADUATE STUDENTS

2019 – Anna-Lisa Doebley, Molecular and Cellular Biology Program, Medical Scientist Training Program, University of Washington

2019 Eliza Barkan, Rotation student, Molecular and Cellular Biology Program, University of Washington (Apr – Jun)

2019 Katharine Chen, Rotation student, Molecular and Cellular Biology Program, University of Washington (Jan – Mar)

STUDENT COMMITTEES

2019 – David Bacsik, Molecular and Cellular Biology Program, Medical Scientist Training Program, University of Washington

PAST MENTORSHIP

2018 Kar-Tong Tan, graduate student, Biological and Biomedical Sciences, Harvard Medical School
2017 – 2018 Christopher Lo, computational biologist, Broad Institute of Harvard & MIT
2017 – 2018 Justin Rhoades, MSc., Broad Institute of Harvard & MIT
2015 – 2018 Samuel Freeman, graduate student, Bioinformatics and Integrated Genomics, Harvard Medical School
2015 Jacqueline Xu, sophomore, Massachusetts Institute of Technology
2011 Daniel Lai, junior graduate student, University of British Columbia

LECTURES AND WORKSHOPS

2017 – 2018 Broad Institute Cancer Program BootCamp, Cambridge, MA
Lecturer: Introduction to data analysis of cell-free DNA and applications for studying metastatic cancer.
2016 Broad Institute Cancer Program BootCamp, Cambridge, MA
Coach: Teaching, mentoring, supervising 3 experimental biologists (postdocs) on a cancer genomics project.
2013 11th Annual Asia Pacific Bioinformatics Conference (APBC), Vancouver, Canada (Jan. 21)
Tutorial: "Profiling genome architecture for copy number alterations and loss of heterozygosity"
2012 Canadian Bioinformatics Workshop, Cancer Genomics, Toronto, Canada (May 30)
Lecturer: Copy number alterations in cancer (Module 4) and Somatic mutations in cancer (Module 5)
Teaching assistant: All 9 modules
2007 Teaching Assistant, Computer Science Dept., University of British Columbia
Introduction to Software Development (CPSC211)

PUBLICATIONS

PEER-REVIEWED ARTICLES

1. Winters BR, De Sarkar N, Arora S, Bolouri H, Jana S, Vakar-Lopez F, Cheng HH, Schweizer M, Yu E, Grivas P, Lee JK, Kollath L, Holt SK, McFerrin L, **Ha G**, Nelson PS, Montgomery RB, Wright J, Lam HM, Hsieh AC. Genomic Distinctions between metastatic lower and upper tract urothelial carcinoma revealed through rapid autopsy. *JCI Insight* 2019 May 30;4(13):e128728.

2. Hemming ML, Klega K, Rhoades J, **Ha G**, Acker KE, Andersen JL, Thai E, Nag A, Thorner AR, Raut CP, George S, Crompton BD. Detection of Circulating Tumor DNA in Patients With Leiomyosarcoma With Progressive Disease. JCO Precision Oncology 2019 Epub Jan 24.

3. Choudhury AD, Werner L, Francini E, Wei XX, **Ha G**, Freeman SS, Rhoades J, Reed SC, Gydush G, Rotem D, Lo C, Taplin ME, Harshman LC, Zhang Z, O'Connor EP, Stover DG, Parsons HA, Getz G, Meyerson M, Love JC, Hahn WC, Adalsteinsson VA. Tumor fraction in cell-free DNA as a biomarker in prostate cancer. ***JCI Insight*** 2018 Nov 2; 3(21):e122109.

4. Viswanathan SR*, **Ha G***, Hoff AM*, Wala JA, Carrot-Zhang J, Whelan CW, Haradhvala NJ, Freeman SS, Reed SC, Rhoades J, Polak P, Cipicchio M, Wankowicz SA, Wong A, Kamath T, Zhang Z, Gydush G, Rotem D, International PCF/SU2C Prostate Cancer Dream Team, Love JC, Getz G, Gabriel S, Zhang C-Z, Dehm SM, Nelson PS, Van Allen EM, Choudhury AD, Adalsteinsson VA, Beroukhim R, Taplin M-E, Meyerson M. Structural alterations driving castration-resistant prostate cancer revealed by linked-read genome sequencing. ***Cell*** 2018 Jul 12;174(2):433-447.e19. *equal contribution

5. Ben-David U, Siranosian B, **Ha G**, Tang H, Oren Y, Hinohara K, Strathdee C, Dempster J, Lyons NJ, Burns R, Nag A, Kugener G, Gimini B, Tsvetkov P, Maruvka Y, O'Rourke R, Garriti A, Tubelli AA, Feldman D, Bandopadhayay P, Tsherniak A, Vasquez F, Wong B, Birger C, Ghandi M, Thorner AR, Bittker J, Meyerson M, Getz G, Beroukhim R, Golub TR. Genetic and transcriptional evolution alters cancer cell line drug response. ***Nature*** 2018 Aug 15;560(7718):325-330.

6. Klega K, Imamovic-Tuco A, **Ha G**, Clapp AN, Meyer S, Ward A, Clinton C, Nag A, Van Allen E, Mullen E, DuBois

SG, Janeway K, Meyerson M, Thorner AR, Crompton BD. Detection of Somatic Structural Variants Enables Quantification and Characterization of Circulating Tumor DNA in Children With Solid Tumors. ***JCO Precision Oncology*** 2018 Jul 5 Epub.

7. Shulman DS, Klega K, Imamovic-Tuco A, Clapp A, Nag A, Thorner AR, Van Allen E, **Ha G**, Lessnick SL, Gorlick R, Janeway KA, Leavey PJ, Mascarenhas L, London WB, Vo KT, Stegmaier K, Hall D, Krailo MD, Barkauskas DA, DuBois SG, Crompton BD. Detection of circulating tumour DNA is associated with inferior outcomes in Ewing sarcoma and osteosarcoma: a report from the Children's Oncology Group. ***British Journal of Cancer*** 2018 Aug 21 Epub.

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

9. Manier S, Park J, Capelletti M, Bustoros M, Freeman SS, **Ha G**, Rhoades J, Liu CJ, Huynh D, Reed SC, Gydush G, Salem KZ, Rotem D, Freymond C, Yosef A, Perilla-Glen A, Garderet L, Van Allen EM, Kumar S, Love JC, Getz G, Adalsteinsson VA, Ghobrial IM. Whole-exome sequencing of cell-free DNA and circulating tumor cells in multiple myeloma. ***Nature Communications*** 2018 Apr 27;9(1):1691.

10. Guo G, Raje NS, Seifer C, Kloeber J, Isenhart R, **Ha G**, Yee AJ, O'Donnell EK, Tai YT, Richardson PG, Bianchi G, Laubach JP, Warren D, Gemme E, Voisine J, Frede J, Kokkalis A, Yun H, Dimitrova V, Vijaykumar T, Meyerson M, Munshi NC, Anderson KC, Knoechel B, Lohr JG. Genomic discovery and clonal tracking in multiple myeloma by cell-free DNA sequencing. ***Leukemia*** 2018 Mar 27.

11. Stover DG*, Parsons HA*, **Ha G***, Freeman S, Barry WT, Guo H, Choudhury AD, Gydush G, Reed SC, Rhoades J, Rotem D, Hughes ME, Dillon DA, Partridge AH, Wagle N, Krop IE, Getz G, Golub TR, Love JC, Winer EP, Tolaney SM, Lin NU, Adalsteinsson VA. Association of cell-free DNA tumor fraction and somatic copy number alterations with survival in metastatic triple-negative breast cancer. ***Journal of Clinical Oncology*** 2018 Feb 20;36(6):543-553. *equal contribution

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

13. Adalsteinsson, VA *, **Ha G***, Freeman SS*, Choudhury AD, Stover DG, Parsons HA, Gydush G, Reed SC, Rotem D, Rhoades J, Loginov D, Livitz D, Rosebrock D, Leshchiner I, Kim J, Stewart C, Rosenberg M, Francis JM, Zhang CZ, Cohen O, Oh C, Ding H, Polak Paz, Lloyd M, Mahmud S, Helvie S, Merrill MS, Santiago RA, O'Connor EP, Jeong SH, Leeson R, Barry RM, Kramkowski JF, Zhang Z, Polacek L, Lohr J, Schleicher M, Lipscomb E, Saltzman A, Oliver NM, Marini L, Waks AG, Harshman LC, Tolaney SM, Van Allen EM, Winer EP, Lin NU, Nakabayashi M, Taplin ME, Johannessen CM, Garraway LA, Golub RE, Boehm JS, Wagle N, Getz G*, Love JC*, Meyerson M*. Scalable whole-exome sequencing of cell-free DNA reveals high concordance with metastatic tumors. ***Nature Communications*** 2017 8:1324. *equal contribution

14. Ben-David U, **Ha G**, Tseng YY, Greenwald NF, Oh C, Shih J, McFarland JM, Wong B, Boehm JS, Beroukhim R, Golub TR. Patient-derived xenografts undergo mouse-specific tumor evolution. ***Nature Genetics*** 2017 Nov;49(11):1567-1575

15. Pectasides E, Stachler MD, Derks S, Liu Y, Maron S, Islam M, Alpert L, Kwak H, Kindler H, Polite B, Sharma MR, Allen K, O'Day E, Lomnicki S, Maranto M, Kanteti R, Fitzpatrick C, Weber C, Setia N, Xiao SY, Hart J, Nagy R, Kim KM, Choi MG, Min BH, Nason KS, O'Keefe L, Watanabe M, Baba H, Lanman R, Agoston AT, Oh DJ, Dunford A, Thorner AR, Ducar MD, Wollison BM, Coleman HA, Ji Y, Posner MC, Roggin KK, Turaga K, Chang P, Hogarth K, Siddiqui U, Gelrud A, **Ha G**, Freeman SS, Rhoades J, Reed S, Gydush G, Rotem D, Davison J, Imamura Y, Adalsteinsson V, Lee J, Bass AJ, Catenacci DV. Genomic Heterogeneity as a Barrier to Precision Medicine in Gastroesophageal Adenocarcinoma. ***Cancer Discovery*** 2018 Jan;8(1):37-48.

16. Zhang X, Choi PS, Francis JM, Gao GF, Campbell JD, Ramachandran A, Mitsuishi Y, **Ha G**, Shih J, Vazquez F, Tsherniak A, Taylor AM, Zhou J, Wu Z, Berger AC, Giannakis M, Hahn WC, Cherniack AD, Meyerson M. Somatic super-enhancer duplications and hotspot mutations lead to oncogenic activation of the KLF5

transcription factor. ***Cancer Discovery*** 2017 Jan;8(1):108-125.

17. McPherson AW, Roth A, **Ha G**, Chauve C, Steif A, de Souza CPE, Eirew P, Bouchard-Côté A, Aparicio S, Sahinalp SC, Shah SP. ReMixT: clone-specific genomic structure estimation in cancer. ***Genome Biology*** 2017 Jul 27;18(1):140.

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

19. Mishima Y, Paiva B, Shi J, Park J, Manier S, Takagi S, Massoud M, Perilla-Glen A, Aljawai Y, Huynh D, Roccaro AM, Sacco A, Capelletti M, Detappe A, Alignani D, Anderson KC, Munshi NC, Prosper F, Lohr JG, **Ha G**, Freeman SS, Van Allen EM, Adalsteinsson VA, Michor F, San Miguel JF, Ghobrial IM. The Mutational Landscape of Circulating Tumor Cells in Multiple Myeloma. ***Cell Reports*** 2017 Apr 4;19(1):218-224.

20. Lohr JG, Kim S, Gould J, Knoechel B, Drier Y, Cotton MJ, Gray D, Birrer N, Wong B, **Ha G**, Zhang CZ, Guo G, Meyerson M, Yee AJ, Boehm JS, Raje N, Golub TR. Genetic interrogation of circulating multiple myeloma cells at single-cell resolution. ***Science Translational Medicine*** 2016 Nov 2;8(363):363ra147.

21. Aguirre AJ, Meyers RM, Weir BA, Vazquez F, Zhang CZ, Ben-David U, Cook A, **Ha G**, Harrington WF, Doshi MB, Kost-Alimova M, Gill S, Xu H, Ali LD, Jiang G, Pantel S, Lee Y, Goodale A, Cherniack AD, Oh C, Kryukov G, Cowley GS, Garraway LA, Stegmaier K, Roberts CW, Golub TR, Meyerson M, Root DE, Tsherniak A, Hahn WC. Genomic Copy Number Dictates a Gene-Independent Cell Response to CRISPR/Cas9 Targeting. ***Cancer Discovery*** 2016 Aug;6(8):914-29.

22. Ben-David U, **Ha G**, Khadka P, Jin X, Wong B, Franke L, Golub TR. The landscape of chromosomal aberrations in breast cancer mouse models reveals driver-specific routes to tumorigenesis. ***Nature Communications*** 2016 Jul 4;7:12160.

23. McPherson A, Roth A, Laks E, Masud T, Bashashati A, Zhang AW, **Ha G**, Biele J, Yap D, Wan A, Prentice LM, Khattra J, Smith MA, Nielsen CB, Mullaly SC, Kalloger S, Karnezis A, Shumansky K, Siu C, Rosner J, Chan HL, Ho J, Melnyk N, Senz J, Yang W, Moore R, Mungall AJ, Marra MA, Bouchard-Côté A, Gilks CB, Huntsman DG, McAlpine JN, Aparicio S, Shah SP. Divergent modes of clonal spread and intraperitoneal mixing in high-grade serous ovarian cancer. ***Nature Genetics*** 2016 Jul;48(7):758-67.

24. Ding J, McConechy M, Horlings H, **Ha G**, Chan FC, Funnell T, Mullaly S, Bashashati A, Huntsman D, Aparicio S, Condon A, Shah SP Systematic analysis of somatic mutations impacting gene expression in 12 tumour types. ***Nature Communications*** 2015 6:8554.

25. Anglesio MS, Bashashati A, Wang YK, Senz J, **Ha G**, Yang W, Lefebvre C, Aniba MR, Prentice LM, Chang HL, Kazernis A, Sharabi-Farahani H, Hirst M, Marra MA, Shah SP, Huntsman DG. Multifocal endometriotic lesions associated with cancer are clonal and carry a high mutation burden. ***The Journal of Pathology*** 2015 Jun;236(2):201-9.

26. 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 Feb19; 518(7539):422-26. *equal contribution

27. Chan FC, Telenius A, Healy S, Ben-Neriah S, Mottok A, Lim R, Drake M, Hu S, Ding J, **Ha G**, Scott DW, Kridel R, Bashashati A, Rogic S, Johnson N, Morin RD, Rimsza LM, Sehn L, Connors JM, Marra MA, Gascoyne RD, Shah SP, Steidl C. An RCOR1 loss-associated gene expression signature identifies a prognostically significant DLBCL subgroup. ***Blood*** 2015; 125(6):959-66.

28. **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 Research*** 2014; 24(11):1881-93.

29. 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. ***Nature Methods*** 2014; 11(4):396-8.

30. 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. ***The Journal of Pathology*** 2013; 231(1):21-34. * equal contribution

31. Bashashati A*, Haffari G*, Ding J*, **Ha G**, Lui K, Rosner J, Huntsman DG, Caldas C, Aparicio SA, Shah SP. DriverNet: uncovering the impact of somatic driver mutations on transcriptional networks in cancer. ***Genome Biology*** 2012; 13(12):R124. *equal contribution

32. **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 monoallelic expression at nucleotide resolution reveals disrupted pathways in triple-negative breast cancer. ***Genome Research*** 2012; 22(10):1995-2007.

33. 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; 486(7403):346-52.

34. 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; 486(7403):395-9. *equal contribution

35. 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; 28(7):907-13.

36. 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. ***The New England Journal of Medicine*** 2012; 366(3):234-42.

37. Crisan A, Goya R, **Ha G**, Ding J, Prentice LM, Oloumi A, Senz J, Zeng T, Tse K, Delaney A, Marra MA, Huntsman DG, Hirst M, Aparicio S, Shah S. Mutation discovery in regions of segmental cancer genome amplifications with CoNAn-SNV: a mixture model for next generation sequencing of tumors. ***PLoS One*** 2012; 7(8):e41551.

38. Schrader KA, Heravi-Moussavi A, Waters PJ, Senz J, Whelan J, **Ha G**, Eydoux P, Nielsen T, Gallagher B, Oloumi A, Boyd N, Fernandez BA, Young TL, Jones SJ, Hirst M, Shah SP, Marra MA, Green J, Huntsman DG. Using next-generation sequencing for the diagnosis of rare disorders: a family with retinitis pigmentosa and skeletal abnormalities. ***The Journal of Pathology*** 2011; 225(1):12-8.

39. McPherson A, Hormozdiari F, Zayed A, Giuliany R, **Ha G**, Sun MG, Griffith M, Heravi Moussavi A, 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 Computational Biology*** 2011; 7(5):e1001138.

40. Kortmann U, McAlpine JN, Xue H, Guan J, **Ha G**, Tully S, Shafait S, Lau A, Cranston AN, O'Connor MJ, Huntsman DG, Wang Y, Gilks CB. Tumor growth inhibition by olaparib in BRCA2 germline-mutated patient-derived ovarian cancer tissue xenografts. ***Clinical Cancer Research*** 2011; 17(4):783-91.

41. 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. ***The New England Journal of Medicine*** 2010; 363(16):1532-43.

42. 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; 26(6):730-6.

SUBMITTED MANUSCRIPTS

1. Carrot-Zhang J , Zhao Y, Hu H, Freeman SS , Yu S, **Ha G** , Taylor AM, Berger AC, Westlake L, Zheng Y, Zhang J, Ramachandran A, Zheng Q, Pan Y, Zheng D, Zheng S, Cheng C, Kuang M, Zhou X, Zhang Y, Li H, Ye T, Ma Y, Gao Z, Tao X, Han H, Shang J, Yu J , Bao D, Huang Y, Li X, Zhang Y, Xiang J, Sun Y, Li Y, Cherniack AD, Campbell JD, Shi L, Meyerson M, Chen H. Genomic and immune profiling of pre-invasive lung adenocarcinoma. Submitted to *Nature Communications*, November 30, 2018.

BOOK CHAPTERS

1. **G. Ha**, S. P. Shah, Distinguishing Somatic and Germline Copy Number Events in Cancer Patient DNA Hybridized to Whole-Genome SNP Genotyping Arrays, Vol. 973 of *Array Comparative Genomic Hybridization: Protocols and Applications*, *Methods in Molecular Biology*, D. Banerjee, S. P. Shah (Eds.), Springer Science and Business Media, LLC, 2013, chapter 22, pg 355-372. (PMID: 23412801)

ABSTRACTS

1. Adalsteinsson VA*, **Ha G***, Freeman SS*, Choudhury AD, Stover DG, Heather PA, Gydush G, Reed S, Loginov D, Livitz D, Rosebrock D, Leshchiner I, Cohen O, Oh C, Kim J, Stewart C, Rosenberg M, Ding H, Lloyd MR, Mahmud S, Helvie KE, Merrill MS, Santiago RA, O'Connor EP, Jeong SH, Kramkowski JF, Lohr JG, Polacek L, Oliver N, Marini L, Francis J, Harshman LC, Van Allen EM, Winer EP, Lin NU, Nakabayashi N, Taplin ME, Garraway LA, Golub TR, Boehm JS, Wagle N, Getz G, Meyerson M and Love CJ. High Concordance of whole-exome sequencing of cell-free DNA and matched biopsies enables genomic discovery in metastatic cancer. Cancer Research 2016; 76 (14 Supplement), Abstract LB-136.
2. DG Stover, HA Parsons, **G Ha**, S Freeman, B Barry, H Guo, A Choudhury, G Gydush, S Reed, J Rhoades, D Rotem, ME Hughes, DA Dillon, AH Partridge, N Wagle, IE Krop, G Getz, TA Golub, JC Love, EP Winer, SM Tolaney, NU Lin, VA Adalsteinsson. Genome-wide copy number analysis of chemotherapy-resistant metastatic triple-negative breast cancer from cell-free DNA. Cancer Research 2018; 78 (4 Supplement), Abstract GS3-07.
3. SS Freeman, ZLin, **G Ha**, I Leshchiner, J Rhoades, D Livitz, D Rosebrock, SC Reed, G Gydush, C Lo, D Rotem, AD Choudhury, DG Stover, HA Parsons, JS Boehm, JC Love, M Meyerson, P Grandgenett, MA Hollingsworth, VA Adalsteinsson, G Getz. Liquid biopsies identify trunk mutations and reflect multiple tumors in a patient. Cancer Research 2018; 78 (13 Supplement), Abstract LB-225.

BIOINFORMATICS SOFTWARE

ichorCNA Homepage: https://github.com/broadinstitute/ichorCNA/
Description: Cell-free DNA analysis tool for estimating the tumor fraction and predicting large-scale copy number alterations in ultra-low-pass whole genome sequencing (0.1x coverage) from metastatic cancer patients (Adalsteinsson*, Ha*, Freeman*, et al. *Nature Commun.* 2017)

TitanCNA Homepage: https://github.com/gavinha/TitanCNA/
Bioconductor: http://www.bioconductor.org/packages/release/bioc/html/TitanCNA.html
Description: Cancer genomics software for inferring clonal structure and detecting subclonal copy number alterations and loss of heterozygosity from genome sequencing data of tumors (Ha et al. *Genome Res*. 2014)

HMMcopy
Homepage: http://shahlab.ca/projects/hmmcopy_utils/
Bioconductor: http://bioconductor.org/packages/release/bioc/html/HMMcopy.html
Description: Copy number prediction with correction for GC and mappability bias for HTS data (Ha et al. *Genome Res*. 2012)
Co-authors: Daniel Lai and Sohrab Shah

APOLLOH
Homepage: http://shahlab.ca/projects/apolloh/
Description: Cancer genomics software for detecting loss of heterozygosity from whole genome sequencing data of tumors (Ha et al. *Genome Res*. 2012)

HMM-Dosage
Homepage: http://compbio.bccrc.ca/software/hmm-dosage/
Description: Prediction of both somatic and germline copy number changes in SNP-genotyping data of tumours (Ha et al. *Methods Mol Biol.* 2013)

PRESENTATIONS

2019 **Vancouver Prostate Centre Invited Speaker**, Vancouver, BC, Canada (April 12)
Title: "Genomic Alterations in Advanced Prostate Cancer Revealed by Tumor and Liquid Biopsies."

2019 **7th International PacRim Breast and Prostate Cancer Meeting**, Barossa Valley, South Australia (March 17-20)
Title: "Multi-omics profiling from circulating tumor DNA."

2019 **PPCR/SPORE Seminar Series,** Fred Hutchinson Cancer Research Center, Seattle, WA (January 10)
Title: "Genomic alterations in CRPC revealed by linked-read DNA sequencing and liquid biopsies."

2018 **Translational Research Program Seminar Series**, Fred Hutchinson Cancer Research Center, Seattle, WA (October 25)
Title: "Genomic Alterations in Prostate Cancer Revealed by LinkedRerad Tumor DNA Sequencing and Blood Biopsies."

2018 **Combi Seminar Series,** Department of Genome Sciences, University of Washington, Seattle, WA (October 10)

2016 **AACR Annual Meeting,** New Orleans, Louisiana (April 16-20)
Poster Title: "High concordance of whole-exome sequencing of cell-free DNA and matched biopsies enables genomic discovery in metastatic cancer" (Abstact LB-136)

2014 **Seminars in Quantitative Biology**, Cancer Research UK, Cambridge, UK (January 27)
Title: "Profiling the Subclonal Copy Number Architecture from Whole Genome Sequencing of Heterogeneous Tumours"

2013 **21st Annual International Conference on Intelligent Systems for Molecular Biology (ISMB)**, High Throughput Sequencing Analysis and Algorithms (HiTSeq) Special Interest Group, Berlin, Germany (July 20)
Title: "Probabilistic inference of subclonal copy number alterations and LOH in whole genome sequencing of tumours"

2013 **Research Seminar Series**, BC Cancer Research Centre, Vancouver, Canada (February 25)
Invited as recipient of the Lloyd Skarsgard Graduate Research Excellence Award
Title: "Profiling copy number aberrations and loss of heterozygosity mutational landscapes in cancer genomes"

2011 **19th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB),** High Throughput Sequencing Analysis and Algorithms (HiTSeq) Special Interest Group, Vienna, Austria (July 16)
Title: "APOLLOH: copy number aware approach to detect loss of heterozygosity in tumour genome sequence data".