

GAVIN HA

Fred Hutchinson Cancer Research Center
1100 Fairview Ave. N.
Seattle, WA 98109
Tel: 206-667-2802
gha@fredhutch.org
GavinHaLab.org

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 analyze genomic alterations in tumor and liquid biopsies 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 Professor**, Herbold Computational Biology Program
Public Health Sciences and Human Biology Divisions
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

- 2020 Top 40 Under 40 in Cancer: Rising Stars and Emerging Leaders
- 2020 – 2023 NIH NCI Transition Career Development Award (K22)
- 2019 – The V Foundation V Scholar Award
- 2019 – 2022 Prostate Cancer Foundation Young Investigator Award
- 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**

- 02/01/2021 – Sponsor: Brotman Baty Institute for Precision Medicine
01/31/2022 Precision Medicine Clinical Laboratory Grant
Title: Development and implementation of a tumor type-specific LOH assay for the clinical determination of homology directed repair deficiency
Total Costs: \$150,000
Role: PI
- 02/01/2021 – Sponsor: Fred Hutch
01/31/2022 Cascadia Data Alliance Pilot Grant
Title: Monitoring Breast Cancer: Bringing single-cell and liquid biopsy analysis to the cloud
Total Direct Costs: \$201,194
Role: Co-PI
Principal Investigators: Gavin Ha, Andrew Roth, Samuel Aparicio, Julie Gralow
- 10/01/2020 – Sponsor: Fred Hutch
09/30/2021 Translational Data Science Pilot Grant
Title: Molecular profiling of small-cell lung cancer using circulating tumor DNA
Total Direct Costs: \$100,000
Role: Co-PI
Principal Investigators: Gavin Ha and David MacPherson
- 08/01/2020 – Sponsor: NIH National Cancer Institute
07/31/2022 UH2 CA239105-01A1 (PI: Niall Lennon, Broad Institute)
Title: Assay Validation of Cell-Free DNA Shallow Whole Genome Sequencing to Determine 'Tumor Fraction' in Advanced Cancers
Role: Co-Investigator
- 04/01/2020 – Sponsor: NIH National Cancer Institute
03/31/2023 NCI Transition Career Development Award (K22)
NCI 1 K22 CA237746
Title: Identifying driver non-coding alterations in metastatic prostate cancer from tumor and cell-free DNA
Total Direct Costs: \$526,200
Role: PI
- 12/01/2019 – Sponsor: Fred Hutch
11/30/2021 Global Oncology Pilot Award (PIs: Alice Berger, Nixon Niyonzima)
Title: Utility of a Liquid Biopsy in Patients with Lung Cancer at the Uganda Cancer Institute
Role: Co-Investigator
- 11/01/2019 – Sponsor: The V Foundation
10/31/2021 V Scholar Grant
V2019-007
Title: Characterizing molecular signatures associated with therapeutic resistance in advanced prostate cancer using liquid biopsies
Total Costs: \$200,000
Role: PI
- 10/01/2019 – Sponsor: Prostate Cancer Foundation
09/30/2022 Young Investigator Award
19YOUNG10
Title: Developing novel computational approaches to study therapeutic resistance in castration-resistant prostate cancer using circulating tumor DNA
Total Direct Costs: \$225,000
Role: PI

07/01/2019 –
06/30/2021

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

PENDING

07/01/2021 –
06/30/2024

Sponsor: CDMRP Department of Defense (DoD)
DoD Prostate Cancer, Idea Development Award (W81XWH-20-PCR-IDA)
Title: Accurate molecular classification of mCRPC for precision treatment through multi-omic analysis of circulating tumor DNA
Total Direct Costs: \$450,000
Role: PI
Status: Under review

07/01/2021 –
06/30/2023

Sponsor: NIH National Cancer Institute
Development of Innovative Informatics Methods and Algorithms for Cancer Research and Management (R21, RFA-CA-20-007)
Title: Predicting transcriptional signatures and tumor subtypes from circulating tumor DNA
Total Direct Costs: \$275,000
Role: PI
Status: Under review

PAST

12/03/2018 –
12/03/2020

Sponsor: Fund for Innovation in Cancer Informatics
Major Grant Award (PI: Ha & Pritchard)
Title: Accelerating the development and validation of liquid biopsy assays
Total Direct Costs: \$200,000
Role: PI

01/01/2019 –
08/31/2020

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

01/01/2019 –
12/31/2019

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: \$127,380
Role: PI

2015 – 2018

Sponsor: Canadian Institutes for Health Research
Postdoctoral Fellowship
MFE-140389
Title: Characterizing the clonal diversity and patterns of tumour evolution in non-small cell lung cancer
Total Costs: \$150,000 CAD
Role: PI

TEACHING AND MENTORING

POST-DOCTORAL FELLOWS

- 2020 – Robert Patton, Ph.D., Fred Hutch (Primary Supervisor; co-mentored by Dr. Peter Nelson).
Brotman Baty Institute 2021 Catalytic Collaborations Trainee Grant
- 2019 – Sitapriya Moorthi, Ph.D., Fred Hutch (Co-mentored; Primary PI Dr. Alice Berger)
Translational Data Science Integrated Research Center Fellowship Grant

STAFF

- 2021 – Matt Neel, M.Sc., Bioinformatics Analyst, Fred Hutch (part-time)
- 2020 – Minjeong Ko, M.Sc., Bioinformatics Analyst, Fred Hutch
- 2019 – Anna Hoge, Bioinformatics Analyst, Fred Hutch
- 2019 – Jonathan Reichel, Ph.D., Research Scientist, Brotman-Baty Institute (Co-supervised; Primary PI Dr. Colin Pritchard)

GRADUATE STUDENTS

- 2021 – Mohamed Adil, Master of Science in Laboratory Medicine, Department of Laboratory Medicine & Pathology, University of Washington
- 2019 – Anna-Lisa Doebley, Molecular and Cellular Biology Program, Medical Scientist Training Program, University of Washington

GRADUATE ROTATION STUDENTS

- 2021 Winter Eden Cruikshank, Molecular and Cellular Biology Program, University of Washington
- 2020 Fall Hanna Liao, Molecular and Cellular Biology Program, University of Washington
- 2020 Summer Caroline Kikawa, Medical Scientist Training Program, University of Washington
- 2020 Winter Yuzhen Liu, Molecular and Cellular Biology Program, University of Washington
- 2019 Fall Magdalena Russell, Molecular and Cellular Biology Program, University of Washington
- 2019 Fall William Hannon, Molecular and Cellular Biology Program, University of Washington
- 2019 Spring Eliza Barkan, Molecular and Cellular Biology Program, University of Washington
- 2019 Winter Katharine Chen, Molecular and Cellular Biology Program, University of Washington

STUDENT COMMITTEES

- 2021 – Yuzhen Liu, Molecular and Cellular Biology Program, University of Washington (PI: Brian Beliveau)
- 2021 – Maya Lewinsohn, Genome Sciences, Medical Scientist Training Program, University of Washington (PI: Trevor Bedford)
- 2019 – David Bacsik, Genome Sciences, Medical Scientist Training Program, University of Washington (PI: Jesse Bloom)

INTERNS AND VISITORS

- 2021 – Aditya Sriram, Masters in Genetic Epidemiology, University of Washington
- 2020 – Kelsey Luu, Bioinformatics Intern, Masters Biomedical Informatics Program, Harvard Medical School
- 2019 – Samuel Ahuno, Visiting Masters student Icahn School of Medicine, Mount Sinai, New York (PI: Dr. Paz Polak)

COURSES

- Fall 2020 MCB 536: Tools for Computational Biology (2 lectures)
- Spring 2020 GENOME 541: Introduction to Computational Molecular Biology (4 lectures)
- Fall 2019 MCB 517A: Tools for Computational Biology (2 lectures)

LECTURES AND WORKSHOPS

- 2017 – 2018 Broad Institute Cancer Program BootCamp, Cambridge, MA
Lecture: 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)
Lecture: Modules for Copy number alterations in cancer and Somatic mutations in cancer
Teaching assistant: All 9 modules
- 2007 Teaching Assistant, Computer Science Dept., University of British Columbia
Introduction to Software Development (CPSC211)

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
2011

Jacqueline Xu, sophomore, Massachusetts Institute of Technology
Daniel Lai, junior graduate student, University of British Columbia

SERVICES

FACULTY RECRUITMENT (FRED HUTCH)

2020 – 2021 PHS Subcommittee, Cluster Hire (Diversity, Equality, Inclusion)
2019 – 2020 Selection Committee, Computational Cancer Biology Position in Prostate Cancer Program

GRANT REVIEWS (LOCAL)

2020 Reviewer, Pacific Northwest Prostate Cancer SPORE Pilot Awards, Fred Hutch

SCIENTIFIC COMMITTEES (LOCAL)

2020 – Member, Cell-free DNA Working Group, Brotman Baty Institute for Precision Medicine

AD-HOC REVIEWER

Bioinformatics, Cell Discovery, EBioMedicine, Epigenetics & Chromatin, European Urology, Genome Biology, Genome Medicine, Journal of Clinical Investigation, Journal of the National Cancer Institute, Nature Communications, Nature Methods, PLoS Computational Biology, Scientific Advances, Scientific Reports

PUBLICATIONS

ORCID: <https://orcid.org/0000-0001-7578-7272>

Google Scholar: https://scholar.google.com/citations?user=dP_fqIqAAAAJ&hl=en

PubMed: <https://www.ncbi.nlm.nih.gov/myncbi/gavin.ha.1/bibliography/public/>

PRE-PRINT SERVER ARTICLES

- Hoge A, Getz M, Beroukhi R, Golub T, **Ha G***, Ben-David U*. DNA-based copy number analysis confirms genomic evolution of PDX models. *bioRxiv*, Jan 17, 2021.
* joint corresponding authors
- Ahuno ST, Doebley A-L, Ahearn TU, Yarney J, Titiloye N, Hamel N, Adjei E, Clegg-Lamprey J-N, Edusei L, Awuah B, Song X, Vanderpuye V, Abubakar M, Duggan M, Stover D, Nyarko K, Bartlett JM, Aitpillah F, Ansong D, Gardner KL, Boateng FA, Bowcock AM, Caldas C, Foulkes WD, Wiafe S, Wiafe-Addai B, Garcia-Closas M, Kwarteng A, **Ha G***, Figueroa JD*, Polak P*. Circulating tumor DNA is readily detectable among Ghanaian breast cancer patients supporting non-invasive cancer genomic studies in Africa. *medRxiv*, 2020.
* joint corresponding authors

PEER-REVIEWED ARTICLES

- Carrot-Zhang J, Soca-Chafre G, Patterson N, Thorner AR, Nag A, Watson J, Genovese G, Rodriguez J, Gelbard MK, Corrales-Rodriguez L, Mitsuishi Y, **Ha G**, Campbell JD, Oxnard GR, Arrieta O, Cardona AF, Gusev A, Meyerson M. Genetic ancestry contributes to somatic mutations in lung cancers from admixed Latin American populations. *Cancer Discovery*. 2020 Dec 2.
- Pomerantz MM, Qiu X, Zhu Y, Takeda DY, Pan W, Baca SC, Gusev A, Korthauer KD, Severson TM, **Ha G**, Viswanathan SR, Seo JH, Nguyen HM, Zhang B, Pasaniuc B, Giambartolomei C, Alaiwi SA, Bell CA, O'Connor EP, Chabot MS, Stillman DR, Lis R, Font-Tello A, Li L, Cejas P, Bergman AM, Sanders J, van der Poel HG, Gayther SA, Lawrenson K, Fonseca MAS, Reddy J, Corona RI, Martovetsky G, Egan B, Choueiri T, Ellis L, Garraway IP, Lee GM, Corey E, Long HW, Zwart W, Freedman ML. Prostate cancer reactivates developmental epigenomic programs during metastatic progression. *Nature Genetics*. 2020 Aug;52(8):790-799.
- Zviran A, Schulman R, Shah M, Kothen-Hill S, Deochand S, Maloney D, Patel K, Liao W, Widman A, Khamnei C, Wong P, Callahan M, **Ha G**, Reed S, Rotem D, Frederick D, Sharova T, Miao B, Kim T, Gydush G, Rhoades J, Huang K, Omans N, Ang C, Malbari M, Spinelli C, Runnels A, Fennessey S, Kazancioglu S, Stolte C, Gaiti F, Inghirami G, Adalsteinsson V, Houck-Loomis B, Ishii J, Wolchok JD, Boland G, Robine N, Altorki N, Landau DL. Genome-wide cell-free DNA mutational integration enables ultra-sensitive cancer monitoring. *Nature Medicine*, 2020 Jun 1;26:1114-1124.
- Schweizer MT*, **Ha G***, Gulati R, Brown L, McKay RR, Dorff T, Hoge ACH, Reichel J, Vats P, Kilari D, Patel V,

Oh WK, Chinnaiyan A, Pritchard CC, Armstrong AJ, Montgomery RB, Alva A. CDK12-Mutated Prostate Cancer: Clinical Outcomes with Standard Therapies and Immune Checkpoint Blockade. **JCO Precision Oncology** 2020 Apr 21;4:382-392.

* equal contribution

5. Parsons HA, Rhoades J, Reed S, Gydush G, Ram P, Exman P, Xiong K, Lo CC, Li T, Fleharty M, Kirkner G, Rotem D, Cohen O, Yu F, Fitarelli-Kiehl M, Leong KW, Hughes ME, Rosenberg SM, Collins LC, Miller KD, Blumenstiel B, Trippa L, Cibulskis C, Neuberger DS, DeFelice M, Freeman SS, Lennon NJ, Wagle N, **Ha G**, Stover DG, Choudhury AD, Getz G, Winer EP, Meyerson M, Lin NU, Krop I, Love JC, Makrigiorgos GM, Patridge AH, Mayer EL, Golub TR, Adalsteinsson V. Sensitive detection of minimal residual disease: methods and application to patients treated for early-stage breast cancer. **Clinical Cancer Research** 2020 Mar 13; pii:clincanres.3005.2019.
6. Chen H, 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 Y, Bao D, Huang Y, Li X, Zhang Y, Xiang J, Sun Y, Li Y, Cherniack AD, Campbell JD, Shi L, Meyerson M. Genomic and immune profiling of pre-invasive lung adenocarcinoma. **Nature Communications** 2019 Nov 29;10(1):5472.
7. 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.
8. 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 Jan 24;10.1200/PO.18.00235.
9. 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.
10. 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
11. 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, Bandopadhyay 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.
12. 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.
13. 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.
14. 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.

15. 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.
16. Guo G, Raje NS, Seifer C, Kloeber J, Isenhardt 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 Aug; 32(8):1838-1841.
17. 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
18. 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.
19. 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
20. 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
21. 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.
22. 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.
23. 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.
24. 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

25. 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.
26. 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.
27. 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.
28. 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.
29. 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.
30. 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.
31. 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.
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* equal contribution
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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.

PRESENTATIONS

2021

1. **NIH Circulating Nucleic Acids & Liquid Biopsies Special Interest Group Seminar** (Virtual Seminar)
Date: January 12, 2021
Title: Analysis of Transcriptional Regulation from Circulating Tumor DNA

2020

2. **Prostate Cancer Foundation 27th Annual Retreat** (Virtual Conference)
Date: October 20-23, 2020
Poster Title: "Multi-omic Profiling of Circulating Tumor DNA in Castration-Resistant Prostate Cancer"
3. **Combi Seminar Series**, Department of Genome Sciences, University of Washington, Seattle, WA
Date: October 21, 2020 (Virtual Seminar)
Title: "Analysis of Transcriptional Regulation from Circulating Tumor DNA"
4. **UCLA Bioinformatics Seminar**, UCLA, Los Angeles, CA
Date: January 31, 2020
Title: "Genomic alterations in advanced prostate cancer revealed by tumor and cell-free DNA sequencing"
5. **GU Oncology Seminar Series**, Fred Hutch, Seattle WA
Date: January 30, 2020
Title: "Methods for genome and nucleosome profiling of cell-free DNA in advanced prostate cancer"

2019

6. **Cancer Consortium – Cancer Basic Biology Retreat**, Seattle, WA
Date: December 2, 2019
Title: Analysis of cell-free DNA in patients with advanced cancer
7. **Prostate Cancer Foundation 26th Annual Retreat**, Carlsbad, CA
Date: October 24-26, 2019
Poster Title: "Multi-omic profiling of circulating tumor DNA in patients with CRPC"
8. **Translational Data Science Integrated Research Center Retreat**, Seattle, WA
Date: October 7, 2019
Title: Tumor and Cell-Free DNA Analysis in Cancer

* Session Chair – Computational Biology

9. **Brotman Baty Institute Cell-free DNA Symposium**, Seattle, WA
Date: April 17, 2019
Title: “Developing computational approaches for multi-omics profiling of circulating tumor DNA”
10. **Vancouver Prostate Centre Invited Speaker**, Vancouver, BC, Canada
Date: April 12, 2019
Title: “Genomic Alterations in Advanced Prostate Cancer Revealed by Tumor and Liquid Biopsies.”
11. **7th International PacRim Breast and Prostate Cancer Meeting**, Barossa Valley, South Australia
Date: March 17-20, 2019
Title: “Multi-omic profiling from circulating tumor DNA.”
12. **PPCR/SPORE Seminar Series**, Fred Hutch, Seattle, WA
Date: January 10, 2019
Title: “Genomic alterations in CRPC revealed by linked-read DNA sequencing and liquid biopsies.”

2018

13. **Translational Research Program Seminar Series**, Fred Hutch, Seattle, WA
Date: October 25, 2018
Title: “Genomic Alterations in Prostate Cancer Revealed by Linked-Read Tumor DNA Sequencing and Blood Biopsies.”
14. **Combi Seminar Series**, Department of Genome Sciences, University of Washington, Seattle, WA
Date: October 10, 2018
Title: “Genomic Alterations in Cancer Revealed by Linked-Read Tumor DNA Sequencing and Blood Biopsies”

PAST PRESENTATIONS

15. **Computational Biology Seminar**, Fred Hutch, Seattle, WA
Date: September 25, 2017
Title: “Genomic structural alterations in cancer: Application of long-range tumor DNA sequencing and blood biopsies”
16. **AACR Annual Meeting**, New Orleans, Louisiana
Date: April 16-20, 2016
Poster Title: “High concordance of whole-exome sequencing of cell-free DNA and matched biopsies enables genomic discovery in metastatic cancer” (Abstact LB-136)
17. **Seminars in Quantitative Biology**, Cancer Research UK, Cambridge, UK
Date: January 27, 2014
Title: “Profiling the Subclonal Copy Number Architecture from Whole Genome Sequencing of Heterogeneous Tumours”
18. **21st Annual International Conference on Intelligent Systems for Molecular Biology (ISMB)**, High Throughput Sequencing Analysis and Algorithms (HiTSeq) Special Interest Group, Berlin, Germany
Date: July 20, 2013
Title: “Probabilistic inference of subclonal copy number alterations and LOH in whole genome sequencing of tumours”
19. **Research Seminar Series**, BC Cancer Research Centre, Vancouver, Canada
Date: February 25, 2013
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”
20. **19th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB)**, High Throughput Sequencing Analysis and Algorithms (HiTSeq) Special Interest Group, Vienna, Austria
Date: July 16, 2011
Title: “APOLLOH: copy number aware approach to detect loss of heterozygosity in tumour genome sequence data”.

BIOINFORMATICS SOFTWARE

- ichorCNA Homepage: <https://github.com/GavinHaLab/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)