

# GAVIN HA

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[GavinHaLab.org](http://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

- 2022 NIH Director's New Innovator Award (DP2)
- 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

- 9/13/2022 – 8/31/2027 Sponsor: NIH National Cancer Institute, Office of the Director, Common Fund  
NIH Director's New Innovator Award  
DP2 CA280624  
Title: Translating the tumor regulome from cell-free DNA for precision oncology  
Total Direct Costs: \$1,500,000  
Role: PI
- 09/01/2022 – 08/31/2023 Sponsor: NIH National Cancer Institute  
Pacific Northwest Prostate Cancer SPORE Core C: Biostatistics Core  
P50 CA097186  
Principal Investigator: Peter Nelson (Fred Hutch), Core Director: Ruth Etzioni (Fred Hutch)  
Role: Core Co-I
- 10/01/2022 – 09/30/2025 Sponsor: CDMRP Department of Defense (DoD)  
DoD Prostate Cancer, Data Science Award  
PC210181  
Title: Identifying driver non-coding alterations in metastatic prostate cancer from tumor and cell-free DNA  
Total Direct Costs: \$1,000,000  
Principal Investigators: Michael Haffner (Fred Hutch), Stephanie Harmon (NIH)  
Role: Co-Investigator
- 01/01/2022 – 12/31/2024 Sponsor: Kuni Foundation  
Discovery Grants for Cancer Research: Advancing Innovation  
Title: Detecting & subtyping lung cancer through analysis of gene expression from circulating tumor DNA  
Total Direct Costs: \$675,000  
Principal Investigators: Gavin Ha, David MacPherson (Fred Hutch)  
Role: Co-PI
- 01/01/2022 – 12/31/2022 Sponsor: Fred Hutch  
STTR Cancer Granting Program  
Title: Characterizing tumor heterogeneity in advanced bladder cancer from rapid autopsies  
Total Direct Costs: \$100,000  
Principal Investigators: Andrew Hsieh (Fred Hutch), Gavin Ha  
Role: Co-PI
- 09/10/2021 – 08/31/2023 Sponsor: NIH National Cancer Institute  
Development of Innovative Informatics Methods and Algorithms for Cancer Research and Management (R21, RFA-CA-20-007)  
R21 CA264383  
Title: Predicting transcriptional signatures and tumor subtypes from circulating tumor DNA  
Total Direct Costs: \$275,000  
Role: PI
- 07/01/2021 – 06/30/2024 Sponsor: CDMRP Department of Defense (DoD)  
DoD Prostate Cancer, Idea Development Award (W81XWH-20-PCRP-IDA)  
PC200608  
Title: Defining and targeting the DNA hypomethylation phenotype in advanced prostate cancer  
Principal Investigator: Michael Haffner (Fred Hutch)  
Role: Co-Investigator
- 07/01/2021 – 06/30/2024 Sponsor: CDMRP Department of Defense (DoD)  
DoD Prostate Cancer, Idea Development Award (W81XWH-20-PCRP-IDA)  
W81XWH-21-1-0513  
Title: Accurate molecular classification of mCRPC for precision treatment through multi-omic analysis of circulating tumor DNA

Total Direct Costs: \$600,000  
Role: PI

02/01/2021 –  
01/31/2023  
(NCE)

Sponsor: Brotman Baty Institute for Precision Medicine  
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 –  
07/31/2022  
(NCE)

Sponsor: Fred Hutch  
Cascadia Data Alliance Pilot Grant  
Title: Monitoring Breast Cancer: Bringing single-cell and liquid biopsy analysis to the cloud  
Total Direct Costs: \$201,194  
Principal Investigators: Gavin Ha, Andrew Roth (BCCRC), Samuel Aparicio (BCCRC), Natasha Hunter (UW)  
Role: Co-PI

08/01/2020 –  
07/31/2022

Sponsor: NIH National Cancer Institute  
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 –  
03/31/2023

Sponsor: NIH National Cancer Institute  
NCI Transition Career Development Award (K22)  
NCI 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

11/01/2019 –  
10/31/2022  
(NCE)

Sponsor: The V Foundation  
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 –  
09/30/2022

Sponsor: Prostate Cancer Foundation  
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

## PENDING

Submitted  
06/2022

Sponsor: NIH National Cancer Institute  
R01 CA280056  
Title: Evaluating prostate cancer phenotype and genotype classification from circulating tumor DNA as biomarkers for predicting treatment outcomes  
Total Direct Costs: \$1,896,389  
Role: MPI  
Status: Under review, initial submission (June 2022)

## PAST

Gavin Ha, PhD

*Curriculum Vitae*

- 12/01/2019 – 11/30/2021 Sponsor: Fred Hutch  
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
- 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)
- 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

- 2021 – Pushpa Itagi, Ph.D. (University of Kansas)  
Primary Mentor, also co-mentored by Dr. Andrew Hsieh  
2022 Translational Data Science Integrated Research Center Fellowship Grant
- 2021 – Anat Zimmer, Ph.D. (Weizmann Institute, Israel)  
Primary Mentor  
Brotman Baty Institute 2022 Catalytic Collaborations Trainee Grant
- 2020 – Robert Patton, Ph.D. (The Ohio State University)  
Primary Mentor, also co-mentored by Dr. Peter Nelson  
Brotman Baty Institute 2021 Catalytic Collaborations Trainee Grant
- 2019 – Sitapriya Moorthi, Ph.D. (Stony Brook University)  
Co-mentor, Primary PI Dr. Alice Berger  
2019 Translational Data Science Integrated Research Center Fellowship Grant

### STAFF

- 2022 – Adam Kreitzman, B.Sc., Graduate Research Assistant, Fred Hutch
- 2021 – Patricia Galipeau, B.Sc., Research Project Manager, Fred Hutch
- 2020 – 2021 Matt Neel, M.Sc., Bioinformatics Analyst, Fred Hutch (part-time)
- 2020 – 2022 Minjeong Ko, M.Sc., Bioinformatics Analyst, Fred Hutch
- 2019 – 2021 Anna Hoge, Bioinformatics Analyst, Fred Hutch
- 2019 – Jonathan Reichel, Ph.D., Research Scientist, Brotman-Baty Institute

**GRADUATE STUDENTS**

- 2022 – Present Mohamed Adil, Molecular Medicine and Mechanisms of Disease PhD Program, University of Washington (Co-advised with Dr. Michael Haffner)
- 2022 – Present A Eden Cruikshank, Molecular and Cellular Biology Program, University of Washington
- 2021 – Present Abigail Thorpe, Genome Sciences, University of Washington
- 2021 Mohamed Adil, Master of Science in Laboratory Medicine, Department of Laboratory Medicine & Pathology, University of Washington
- 2019 – 2022 Anna-Lisa Doebley, Molecular and Cellular Biology Program, Medical Scientist Training Program, University of Washington

**GRADUATE ROTATION STUDENTS**

- 2022 Summer David Chen, University of Washington Medical School
- 2022 Summer Bhargav Vermuri, Biomedical and Health Informatics, University of Washington
- 2022 Winter Hunter Colegrove, Genome Sciences, University of Washington
- 2021 Summer Abigail Thorpe, Genome Sciences, University of Washington
- 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**

- 2022 – Gerardo Javier, Molecular Medicine and Mechanisms of Disease PhD Program, University of Washington (PI: John Lee)
- 2021 – William Hannon, Molecular and Cellular Biology Program, University of Washington (PI: Jesse Bloom)
- 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**

- 2022 – Kim Thi Ha, Undergraduate Research Assistant, University of Washington, McNair Scholar
- 2021 – 2022 Adam Kreitzman, Undergraduate Research Assistant, University of San Diego
- 2021 Aditya Sriram, Masters in Genetic Epidemiology, University of Washington
- 2020 – 2021 Kelsey Luu, Bioinformatics Intern, Masters Biomedical Informatics Program, Harvard Medical School
- 2019 – 2021 Samuel Ahuno, Visiting Masters student  
Icahn School of Medicine, Mount Sinai, New York (PI: Dr. Paz Polak)

**COURSES**

- Spring 2022 GENOME 541: Introduction to Computational Molecular Biology (4 lectures)
- Fall 2021 MCB 536: Tools for Computational Biology (2 lectures)
- 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 11<sup>th</sup> Annual Asia Pacific Bioinformatics Conference (APBC), Vancouver, Canada (Jan. 21)  
Tutorial: “Profiling genome architecture for copy number alterations and loss of heterozygosity”

Gavin Ha, PhD

### *Curriculum Vitae*

- 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 Jacqueline Xu, sophomore, Massachusetts Institute of Technology
- 2011 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)

- 2021 Reviewer, Pacific Northwest Prostate Cancer SPORE Pilot Awards, Fred Hutch
- 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, Genome Research, 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](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

1. De Sarkar N<sup>^</sup>, Patton RD<sup>^</sup>, Doebley AL, Hanratty B, Kreitzman AJ, Sarthy JF, Ko M, Adil M, Brahma S, Meers MP, Janssens DH, Ang LS, Coleman I, Bose A, Dumpit RF, Lucas JM, Nunez TA, Nguyen HM, McClure HM, Pritchard CC, Schweizer MT, Morrissey C, Choudhury AD, Baca SC, Berchuck JE, Freedman ML, Ahmad K, Haffner MC, Montgomery B, Corey E, Henikoff S, Nelson PS\*, **Ha G\***. Nucleosome patterns in circulating tumor DNA reveal transcriptional regulation of advanced prostate cancer phenotypes. *bioRxiv*. June 25, 2022. doi:[10.1101/2022.06.21.496879](https://doi.org/10.1101/2022.06.21.496879)  
\* joint corresponding authors  
*In revisions at Cancer Discovery.*
2. Doebley A-L, Ko M, Liao H, Cruikshank AE, Kikawa C, Santos K, Hiatt J, Patton RD, De Sarkar N, Hoge ACH, Chen K, Weber ZT, Adil M, Reichel J, Polak Paz, Adalsteinsson VA, Nelson PS, Parsons HA, Stover DG, MacPherson D, **Ha G**. [Griffin: Framework for clinical cancer subtyping from nucleosome profiling of cell-free DNA](#). *medRxiv*, Sep 3, 2021. doi:[10.1101/2021.08.31.21262867](https://doi.org/10.1101/2021.08.31.21262867)  
*Accepted in principle at Nature Communications.*

### SUBMITTED ARTICLES

## PEER-REVIEWED ARTICLES

1. Zhou M<sup>^</sup>, Ko M<sup>^</sup>, Hoge ACH, Luu K, Liu Y, Russell ML, Hannon WW, Zhang Z, Carrot-Zhang J, Beroukhir R, Allen EMV, Choudhury AD, Nelson PS, Freedman ML, Taplin ME\*, Meyerson M\*, Viswanathan SR\*, **Ha G\*** Patterns of structural variation define prostate cancer across disease states. *JCI Insight*. 2022;7(17). doi:[10.1172/jci.insight.161370](https://doi.org/10.1172/jci.insight.161370)  
\* joint corresponding authors
2. Hoge A<sup>^</sup>, Getz M<sup>^</sup>, Zimmer A, Ko M, Raz Linoy, Beroukhir R, Golub T, **Ha G\***, Ben-David U\*. [DNA-based copy number analysis confirms genomic evolution of PDX models](#). *npj Precision Oncology*, 2022 Apr 28;6(30). doi:10.1038/s416898-022-00268-6 [PMID: 335484194]  
\* joint corresponding authors
3. Freeman SS, Sade-Feldman M, Kim J, Stewart C, Gonye ALK, Ravi A, Arniella MB, Gushterova I, LaSalle TJ, Blaum EM, Yizhak K, Frederick DT, Sharova T, Leshchiner I, Elagina L, Spiro OG, Livitz D, Rosebrock D, Aguet F, Carrot-Zhang J, **Ha G**, Lin Z, Chen JH, Barzily-Rokni M, Hammond MR, Vitzthum von Eckstaedt HC, Blackmon SM, Jiao YJ, Gabriel S, Lawrence DP, Duncan LM, Stemmer-Rachamimov AO, Wargo JA, Flaherty KT, Sullivan RJ, Boland GM, Meyerson M, Getz G, Hacoheh N. [Combined tumor and immune signals from genomes or transcriptomes predict outcomes of checkpoint inhibition in melanoma](#). *Cell Rep Med*. 2022 Feb 15;3(2):100500. doi:10.1016/j.xcrm.2021.100500.
4. Pagès M, Rotem D, Gydush G, Reed S, Rhoades J, **Ha G**, Lo C, Flaherty M, Duran M, Jones R, Becker S, Haller M, Sinai CE, Goumnerova L, Golub TR, Love JC, Ligon KL, Wright K, Adalsteinsson VA, Beroukhir R, Bandopadhyay P. Liquid biopsy detection of genomic alterations in pediatric brain tumors from cell-free DNA in peripheral blood, CSF, and urine. *Neuro-Oncol*. January 4, 2022:noab299.
5. Stover EH, Oh C, Keskula P, Choudhury AD, Tseng YY, Adalsteinsson VA, Lohr JG, Thorner AR, Ducar M, Kryukov GV, **Ha G**, Rosenberg M, Freeman SS, Zhang Z, Wu X, Van Allen EM, Takeda DY, Loda M, Wu CL, Taplin ME, Garraway LA, Boehm JS, Huang FW. Implementation of a prostate cancer-specific targeted sequencing panel for credentialing of patient-derived cell lines and genomic characterization of patient samples. *The Prostate*. 2022;82(5):584-597. doi:10.1002/pros.24305.
6. Sarkar ND, Dasgupta S, Chatterjee P, Coleman I, **Ha G**, Ang LS, Kohlbrenner EA, Frank SB, Nunez TA, Salipante SJ, Corey E, Morrissey C, Allen EV, Schweizer MT, Haffner MC, Patel R, Hanratty B, Lucas JM, Dumpit RF, Pritchard CC, Montgomery RB, Nelson PS. [Genomic attributes of homology-directed DNA repair deficiency in metastatic prostate cancer](#). *JCI Insight*. 2021;6(23). doi:10.1172/jci.insight.152789. [PMCID: PMC8675196]
7. Collier KA, Asad S, Tallman D, Jenison J, Rajkovic A, Mardis ER, Parsons HA, Tolaney SM, Winer EP, Lin NU, **Ha G**, Adalsteinsson VA, Stover DG. Association of 17q22 Amplicon Via Cell-Free DNA With Platinum Chemotherapy Response in Metastatic Triple-Negative Breast Cancer. *JCO Precis Oncol*. 2021;5. doi:10.1200/PO.21.00104.
8. Ahuno ST, Doebley A-L, Ahearn TU, Yarney J, Titiloye N, Hamel N, Adjei E, Clegg-Lampsey 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](#). *npj Precision Oncology*. 2021 Sep 17;5(1):83. doi: 10.1038/s41698-021-00219-7. [PMID: 34535742]  
\* joint corresponding authors
9. Francini E, Ou FS, Rhoades J, Wolfe EG, O'Connor EP, **Ha G**, Gydush G, Kelleher KM, Bhatt RS, Balk SP, Sweeney CJ, Adalsteinsson VA, Taplin ME, Choudhury AD. [Circulating Cell-Free DNA as Biomarker of Taxane Resistance in Metastatic Castration-Resistant Prostate Cancer](#). *Cancers (Basel)*. 2021 Aug 12;13(16).
10. Tan K-T, Kim H, Carrot-Zhang J, Zhang Y, Kim WJ, Kugener G, Wala JA, Howard TP, Chi Y-Y, Beroukhir R, Alt FW, Li H, **Ha G**, Alper SL, Perlman EJ, Mullen EA, Hahn WC, Meyerson M, Hong AL. [Haplotype-resolved germline and somatic alterations in renal medullary carcinoma](#). *Genome Medicine*. 2021 Jul 14;13(1):114. [PMCID: PMC8281718]

11. Lim Y, Arora S, Schuster S, Corey L, Fitzgibbon M, Wladyka CL, Wu X, Coleman IM, Delrow JJ, Corey E, True LD, Nelson PS, **Ha G**, Hsieh AC. [Multiplexed functional genomic analysis of 5' untranslated region mutations across the spectrum of prostate cancer](#). **Nature Communications**. 2021 Jul;12:4217. [PMCID: PMC8270899]
12. Weber ZT, Collier KA, Tallman D, Forman J, Shukla S, Asad S, Rhoades J, Freeman S, Parsons HA, Williams NO, Barros-Sousa R, Stover EH, Mahdi H, Cibulskis C, Lennon NJ, **Ha G**, Adalsteinsson VA, Tolaney SM, Stover DG. [Modeling clonal structure over narrow time frames via circulating tumor DNA in metastatic breast cancer](#). **Genome Medicine**. 2021 May;13(1):89. [PMCID: PMC8136103]
13. 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**. 2021 Mar;11(3):591-598. [PMCID: PMC7933062]
14. 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.
15. 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. [PMCID: PMC8108131]
16. 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. [PMCID: PMC7363399]  
\* equal contribution
17. 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. [PMCID: PMC7654718]
18. Nyquist MD, Corella A, Coleman I, De Sarkar N, Kaipainen A, Ha G, Gulati R, Ang L, Chatterjee P, Lucas J, Pritchard C, Risbridger G, Isaacs J, Montgomery B, Morrissey C, Corey E, Nelson PS. [Combined TP53 and RB1 Loss Promotes Prostate Cancer Resistance to a Spectrum of Therapeutics and Confers Vulnerability to Replication Stress](#). **Cell Reports** 2020 May 26;31(8):107669. doi:10.1016/j.celrep.2020.107669. [PMCID: PMC7453577]
19. 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. [PMCID: PMC6884501]
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21. 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](#)



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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

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## PRESENTATIONS

### 2022

1. **NIH/NCI Informatics Technology for Cancer Research (ITCR) 2022 Annual Meeting**  
Date: September 12-15, 2022  
Title: "Predicting transcriptional signatures and tumor subtypes from circulating tumor DNA"
2. **Prostate Cancer Foundation Working Group Seminar (Genomes/Genetics/Epigenetics)**  
Date: August 10, 2022  
Title: "Transcriptional regulation in CRPC tumor phenotypes revealed by circulating tumor DNA"
3. **GU Oncology Seminar Series**, Fred Hutch, Seattle WA  
Date: February 24, 2022  
Title: "Transcriptional regulation in CRPC tumor phenotypes revealed by circulating tumor DNA"

### 2021

4. **Combi Seminar Series**, Department of Genome Sciences, University of Washington, Seattle, WA (Virtual Seminar)  
Date: December 8, 2021  
Title: "Predicting tumor subtypes from cell-free DNA"
5. **UCSF Computational Cancer Community Seminar**, San Francisco, CA  
Date: December 3, 2021 (Virtual Seminar)  
Title: "Tumor subtype and phenotype prediction from cell-free DNA"
6. **Prostate Cancer Foundation 28th Annual Retreat** (Virtual Conference)  
Date: October 28-30, 2021  
Poster Title: "Tumor subtyping in prostate and breast cancers using circulating tumor DNA"
7. **V Foundation Scholar Summit (Virtual Conference)**  
Date: April 27-28, 2021  
Poster Title: "Characterizing molecular signatures in advanced prostate cancer using circulating tumor DNA"
8. **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

9. **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"
10. **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"
11. **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"
12. **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

13. **Cancer Consortium – Cancer Basic Biology Retreat**, Seattle, WA  
Date: December 2, 2019  
Title: Analysis of cell-free DNA in patients with advanced cancer
14. **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”
15. **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
16. **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”
17. **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.”
18. **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.”
19. **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

20. **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.”
21. **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

22. **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”
23. **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” (Abstract LB-136)
24. **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”
25. **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”

26. **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"
27. **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: <https://github.com/shahcompbio/HMMcopy>  
 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: <https://github.com/shahcompbio/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)

## INTELLECTUAL PROPERTY

- Priority 2021-04-08      CELL-FREE DNA SEQUENCE DATA ANALYSIS METHOD TO EXAMINE NUCLEOSOME  
 Filed 2022-04-08      PROTECTION AND CHROMATIN ACCESSIBILITY  
 Inventors: Gavin Ha, Anna-Lisa Doebley  
 Assignee: Fred Hutchinson Cancer Research Center
- Priority 2016-03-16      Methods for genome characterization  
 Filed 2017-03-16      WO EP US [US20190078232A1](#)  
 Published 2019-03-14      Status: Pending  
 Inventors: Gavin Ha, Viktor Adalsteinsson, Samuel Freeman  
 Assignee: Dana-Farber Cancer Institute, Inc., Broad Institute, Inc., Harvard College  
 The invention provides methods of using low coverage sequencing to assess the relative fraction of tumor versus normal DNA in a sample, and to assess copy number alterations present in the sample