

## GAVIN HA

Fred Hutchinson Cancer Center  
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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

- 2023 – Present **Associate Professor**, Herbold Computational Biology Program  
Divisions Public Health Sciences and Human Biology  
Fred Hutchinson Cancer Center, Seattle, WA
- 2024 – Present **Affiliate Associate Professor**, Department of Genome Sciences  
University of Washington, Seattle, WA
- 2018 – 2023 **Assistant Professor**, Herbold Computational Biology Program  
Divisions Public Health Sciences and Human Biology  
Fred Hutchinson Cancer Center, Seattle, WA
- 2018 – 2024 **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 – 2027 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 – 2021 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)<br>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

|                            |  |   |
|----------------------------|--|---|
| 02/01/2024 –<br>01/31/2025 | <u>Sponsor:</u> Klorfine Foundation<br><u>Grant Name:</u> Pilot Award<br><u>PI's:</u> Gavin Ha, Viswam Nair (Fred Hutch)   | <u>Title:</u> Mapping genomic alterations in bronchoalveolar lavage to detect lung cancer<br><u>Total Direct Costs:</u> \$71,105<br><u>Role:</u> PI   |
| 02/01/2024 –<br>01/31/2028 | <u>Sponsor:</u> NIH National Cancer Institute<br><u>Grant #:</u> R01 CA286450<br><u>MPI:</u> Michael Haffner (Fred Hutch), Michael Schweizer (UW)  | <u>Title:</u> Augmenting PSMA expression to enhance PSMA directed therapeutic efficacy<br><u>Role:</u> Co-Investigator  |
| 01/01/2024 –<br>12/31/2024 | <u>Sponsor:</u> Fred Hutch<br><u>Grant Name:</u> Human Biology Pilot Project Award<br><u>PI's:</u> Michael Haffner, Gavin Ha   | <u>Title:</u> Epigenetic ctDNA biomarkers of treatment response in prostate cancer<br><u>Total Direct Costs:</u> \$80,000<br><u>Role:</u> Co-PI   |
| 06/01/2023 –<br>05/31/2024 | <u>Sponsor:</u> Lopker Family Foundation<br><u>Donation</u><br><u>PI's:</u> Gavin Ha, Colin Pritchard (UW)   | <u>Title:</u> Development of clinical assays for tumor subtype classification to guide cancer management<br><u>Total Direct Costs:</u> \$178,125 (Ha Lab only)<br><u>Role:</u> PI                                       |
| 09/15/2023 –<br>08/30/2028 | <u>Sponsor:</u> NIH National Cancer Institute<br><u>Grant #:</u> R01 CA280056-01A1<br><u>MPI:</u> Gavin Ha, Peter Nelson (Fred Hutch)  | <u>Title:</u> Evaluating prostate cancer phenotype and genotype classification from circulating tumor DNA as biomarkers for predicting treatment outcomes<br><u>Total Direct Costs:</u> \$1,698,882<br><u>Role:</u> MPI |
| 09/13/2022 –<br>08/31/2027 | <u>Sponsor:</u> NIH National Cancer Institute, Office of the Director, Common Fund<br><u>Grant Name:</u> NIH Director's New Innovator Award<br><u>Grant #:</u> DP2 CA280624<br><u>PI:</u> Gavin Ha   | <u>Title:</u> Translating the tumor regulome from cell-free DNA for precision oncology<br><u>Total Direct Costs:</u> \$1,500,000<br><u>Role:</u> PI   |
| 09/08/2023 –<br>08/31/2028 | <u>Sponsor:</u> NIH National Cancer Institute<br><u>Grant name:</u> Pacific Northwest Prostate Cancer SPORE<br><u>Grant #:</u> P50 CA097186-22<br><u>PI:</u> Peter Nelson (Fred Hutch)<br><u>Core Co-Directors:</u> Ruth Etzioni, Gavin Ha | <u>Title:</u> Pacific Northwest (PNW) Prostate Cancer Sponsored Program of Research Excellence (SPORE)<br>Core C: Data Science and Integration Core<br><u>Role:</u> Core Co-Director                                    |
| 09/01/2023 –<br>08/31/2028 | <u>Sponsor:</u> NIH National Cancer Institute<br><u>Grant #:</u> U24 CA288185<br><u>PI's:</u> Yingye Zhen, Wei Sun (Fred Hutch)  | <u>Title:</u> Precompetitive Collaboration on Liquid Biopsy for Early Cancer Assessment: Data Management and Coordinating Unit<br><u>Role:</u> Co-Investigator  |
| 08/23/2023 –<br>07/31/2028 | <u>Sponsor:</u> NIH National Cancer Institute<br><u>Grant #:</u> R01 CA277045<br><u>PI:</u> Kevin Cheung (Fred Hutch)  | <u>Title:</u> Role of necrosis in the evolution of highly metastatic and chemo-resistant breast cancers<br><u>Role:</u> Co-Investigator   |

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| 07/01/2023 – 08/31/2025 | <u>Sponsor:</u> NIH National Cancer Institute<br><u>Grant Name:</u> NIH Diversity Supplement<br><u>Grant #:</u> DP2 CA280624-01S1<br><u>PI:</u> Gavin Ha   | <u>Title:</u> Translating the tumor regulome from cell-free DNA for precision oncology<br><u>Total Direct Costs:</u> \$142,599<br><u>Trainee:</u> Eden Cruikshank  |
| 07/01/2023 – 06/30/2026 | <u>Sponsor:</u> CDMRP Department of Defense (DoD)<br><u>Grant Name:</u> Prostate Cancer Research Program Data Science Award (W81XWH-22-PCRP-DSA)<br><u>Grant #:</u> PC220617<br><u>PI's:</u> Gavin Ha, Jian Carrot-Zhang (MSKCC) | <u>Title:</u> Exploiting real-world clinical genomic data to discover biomarkers and address outcome disparity for prostate cancer<br><u>Total Direct Costs:</u> \$1,000,000<br><u>Role:</u> Co-PI                           |
| 07/01/2023 – 06/30/2026 | <u>Sponsor:</u> CDMRP Department of Defense (DoD)<br><u>Grant Name:</u> DoD Prostate Cancer, Idea Development Award (W81XWH-22-PCRP-IDA)<br><u>Grant #:</u> PC220173<br><u>PI:</u> Jacob Berchuck (Dana-Farber)                  | <u>Title:</u> Defining clinically actionable subtypes of castration-resistant prostate cancer through epigenetic cell-free DNA analysis<br><u>Total Direct Costs:</u> \$77,307 (Ha Lab only)<br><u>Role:</u> Co-Investigator |
| 02/01/2023 – 01/31/2025 | <u>Sponsor:</u> NIH National Cancer Institute<br><u>Grant #:</u> R21 CA277368<br><u>PI:</u> Peter Nelson   | <u>Title:</u> A prostate cancer dependency map to identify tumor subtype-specific vulnerabilities<br><u>Role:</u> Co-Investigator  |
| 10/01/2022 – 09/30/2025 | <u>Sponsor:</u> CDMRP Department of Defense (DoD)<br><u>Grant Name:</u> DoD Prostate Cancer, Data Science Award<br><u>Grant #:</u> PC210181<br><u>PI's:</u> Michael Haffner (Fred Hutch), Stephanie Harmon (NIH)                 | <u>Title:</u> Identifying driver non-coding alterations in metastatic prostate cancer from tumor and cell-free DNA<br><u>Total Direct Costs:</u> \$1,000,000<br><u>Role:</u> Co-Investigator                                 |
| 09/19/2022 – 08/31/2025 | <u>Sponsor:</u> NIH National Cancer Institute<br><u>Grant #:</u> UH3 CA239105<br><u>PI:</u> Niall Lennon (Broad Institute)   | <u>Title:</u> Assay validation of cell-free DNA shallow whole genome sequencing to determine 'Tumor Fraction' in advanced cancers<br><u>Total Direct Costs:</u> \$31,257 (Ha Lab only)<br><u>Role:</u> Co-Investigator       |
| 01/01/2022 – 12/31/2024 | <u>Sponsor:</u> Kuni Foundation<br><u>Grant Name:</u> Discovery Grants for Cancer Research: Advancing Innovation<br><u>PI's:</u> Gavin Ha, David MacPherson (Fred Hutch)   | <u>Title:</u> Detecting & subtyping lung cancer through analysis of gene expression from circulating tumor DNA<br><u>Total Direct Costs:</u> \$675,000<br><u>Role:</u> Co-PI   |
| 07/01/2021 – 06/30/2024 | <u>Sponsor:</u> CDMRP Department of Defense (DoD)<br><u>Grant Name:</u> DoD Prostate Cancer, Idea Development Award (W81XWH-20-PCRP-IDA)<br><u>Grant #:</u> PC200608<br><u>PI:</u> Michael Haffner (Fred Hutch)                  | <u>Title:</u> Defining and targeting the DNA hypomethylation phenotype in advanced prostate cancer<br><u>Role:</u> Co-Investigator   |
| 07/01/2021 – 06/30/2024 | <u>Sponsor:</u> CDMRP Department of Defense (DoD)<br><u>Grant Name:</u> DoD Prostate Cancer, Idea Development Award (W81XWH-20-PCRP-IDA)<br><u>Grant #:</u> W81XWH-21-1-0513<br><u>PI:</u> Gavin Ha                              | <u>Title:</u> Accurate molecular classification of mCRPC for precision treatment through multi-omic analysis of circulating tumor DNA<br><u>Total Direct Costs:</u> \$600,000<br><u>Role:</u> PI                             |
| 10/01/2022 – 09/30/2024 | <u>Sponsor:</u> Breast Cancer Research Foundation<br><u>Grant #:</u> BCRF-22-193<br><u>PI:</u> Christopher Li (Fred Hutch)   | <u>Title:</u> Discovery and validation of molecular predictors of recurrence among patients with luminal B breast cancer<br><u>Total Direct Costs:</u> \$88,022 (Ha Lab only)<br><u>Role:</u> Co-Investigator                |

## PAST

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| 09/01/2022 – 08/31/2023       | <u>Sponsor:</u> NIH National Cancer Institute<br><u>Grant name:</u> Pacific Northwest Prostate Cancer SPORE Core C: Biostatistics Core<br><u>Grant #:</u> P50 CA097186<br><u>PI:</u> Peter Nelson (Fred Hutch)                         | <u>Core Director:</u> Ruth Etzioni (Fred Hutch)<br><u>Role:</u> Core Co-Investigator   |
| 09/10/2021 – 08/31/2023       | <u>Sponsor:</u> NIH National Cancer Institute<br>Development of Innovative Informatics Methods and Algorithms for Cancer Research and Management<br><u>Grant #:</u> R21 CA264383<br><u>PI:</u> Gavin Ha                                | <u>Title:</u> Predicting transcriptional signatures and tumor subtypes from circulating tumor DNA<br><u>Total Direct Costs:</u> \$275,000<br><u>Role:</u> PI   |
| 02/01/2021 – 09/30/2023       | <u>Sponsor:</u> Fred Hutchinson Cancer Center<br><u>Grant Name:</u> Cascadia Data Alliance Pilot Grant<br><u>PI's:</u> Gavin Ha, Andrew Roth (BCCRC), Samuel Aparicio (BCCRC), Natasha Hunter (UW)                                     | <u>Title:</u> Monitoring Breast Cancer: Bringing single-cell and liquid biopsy analysis to the cloud<br><u>Total Direct Costs:</u> \$311,194<br><u>Role:</u> Co-PI   |
| 01/01/2022 – 12/31/2023 (NCE) | <u>Sponsor:</u> Fred Hutch<br><u>Grant Name:</u> STTR Cancer Granting Program<br><u>PI's:</u> Andrew Hsieh (Fred Hutch), Gavin Ha  | <u>Title:</u> Characterizing tumor heterogeneity in advanced bladder cancer from rapid autopsies<br><u>Total Direct Costs:</u> \$100,000<br><u>Role:</u> Co-PI   |
| 02/01/2023 – 08/31/2023       | <u>Sponsor:</u> NIH National Cancer Institute<br><u>Grant name:</u> Pacific Northwest Prostate Cancer SPORE Developmental Research Program (DRP)<br><u>Grant #:</u> P50 CA097186<br><u>Project PIs:</u> Gavin Ha, Michael Haffner (FH) | <u>Title:</u> Integrated epigenetic profiling of clinically relevant prostate tumor characteristics from ctDNA<br><u>Total Direct Costs:</u> \$50,000<br><u>Role:</u> Co-PI  |
| 04/01/2020 – 03/31/2023       | <u>Sponsor:</u> NIH National Cancer Institute<br><u>Grant Name:</u> NCI Transition Career Development Award (K22)<br><u>Grant #:</u> NCI K22 CA237746<br><u>PI:</u> Gavin Ha   | <u>Title:</u> Identifying driver non-coding alterations in metastatic prostate cancer from tumor and cell-free DNA<br><u>Total Direct Costs:</u> \$526,200<br><u>Role:</u> PI  |
| 02/01/2021 – 01/31/2023 (NCE) | <u>Sponsor:</u> Brotman Baty Institute for Precision Medicine<br><u>Grant Name:</u> Precision Medicine Clinical Laboratory Grant<br><u>PI:</u> Gavin Ha  | <u>Title:</u> Development and implementation of a tumor type-specific LOH assay for the clinical determination of homology directed repair deficiency<br><u>Total Direct Costs:</u> \$150,000<br><u>Role:</u> PI       |
| 11/01/2019 – 10/31/2022 (NCE) | <u>Sponsor:</u> The V Foundation<br><u>Grant Name:</u> V Scholar Grant<br><u>Grant #:</u> V2019-007<br><u>PI:</u> Gavin Ha   | <u>Title:</u> Characterizing molecular signatures associated with therapeutic resistance in advanced prostate cancer using liquid biopsies<br><u>Total Costs:</u> \$200,000<br><u>Role:</u> PI                         |
| 10/01/2019 – 09/30/2022       | <u>Sponsor:</u> Prostate Cancer Foundation<br><u>Grant Name:</u> Young Investigator Award<br><u>Grant #:</u> 19YOUNG10<br><u>PI:</u> Gavin Ha  | <u>Title:</u> Developing novel computational approaches to study therapeutic resistance in castration-resistant prostate cancer using circulating tumor DNA<br><u>Total Direct Costs:</u> \$225,000<br><u>Role:</u> PI |
| 12/01/2019 – 11/30/2021       | <u>Sponsor:</u> Fred Hutchinson Cancer Center<br><u>Grant Name:</u> Global Oncology Pilot Award<br><u>PI's:</u> Alice Berger, Nixon Niyonzima  | <u>Title:</u> Utility of a Liquid Biopsy in Patients with Lung Cancer at the Uganda Cancer Institute<br><u>Role:</u> Co-Investigator   |
| 10/01/2020 – 09/30/2021       | <u>Sponsor:</u> Fred Hutchinson Cancer Center<br><u>Grant Name:</u> Translational Data Science Pilot Grant<br><u>PI's:</u> Gavin Ha, David MacPherson (Fred Hutch)   | <u>Title:</u> Molecular profiling of small-cell lung cancer using circulating tumor DNA<br><u>Total Direct Costs:</u> \$99,999.79<br><u>Role:</u> PI   |
| 08/01/2020 – 07/31/2022       | <u>Sponsor:</u> NIH National Cancer Institute<br><u>Grant #:</u> UH2 CA239105  | <u>Title:</u> Assay Validation of Cell-Free DNA Shallow Whole Genome Sequencing to   |

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|                         | <u>PI</u> : Niall Lennon (Broad Institute)  | Determine Tumor Fraction' in Advanced Cancers<br><u>Role</u> : Co-Investigator  |
| 07/01/2019 – 06/30/2021 | <u>Sponsor</u> : Cancer Center Support Grant (CCSG)<br><u>Grant Name</u> : New Investigator Support<br><u>Grant #</u> : NCI 5 P30 CA015704-44<br><u>PI</u> : Thomas Lynch                     | <u>Title</u> : Characterizing molecular signatures in advanced prostate cancer using liquid biopsies<br><u>Total Direct Costs</u> : \$80,000<br><u>Role</u> : Project PI (Subaward) |
| 12/03/2018 – 12/02/2020 | <u>Sponsor</u> : Fund for Innovation in Cancer Informatics<br><u>Grant Name</u> : Major Grant Award<br><u>PI's</u> : Gavin Ha, Colin Pritchard (UW)   | <u>Title</u> : Accelerating the development and validation of liquid biopsy assays<br><u>Total Direct Costs</u> : \$200,000<br><u>Role</u> : PI                                     |
| 01/01/2019 – 08/31/2020 | <u>Sponsor</u> : Pacific Northwest Prostate Cancer SPORE<br><u>Grant Name</u> : Career Enhancement Program<br><u>Grant #</u> : NCI P50 CA097186-16A1<br><u>PI</u> : Peter Nelson (Fred Hutch) | <u>Title</u> : Defining the genomic alteration signatures of advanced prostate cancer<br><u>Total Direct Costs</u> : \$75,200<br><u>Role</u> : Project PI (Subaward)                |
| 01/01/2019 – 12/31/2019 | <u>Sponsor</u> : Brotman Baty Institute for Precision Medicine<br><u>Grant Name</u> : Catalytic Collaboration Grant<br><u>PI</u> : Gavin Ha   | <u>Title</u> : Developing an analytical framework for clinical genome sequencing of cell-free DNA<br><u>Total Direct Costs</u> : \$127,380<br><u>Role</u> : PI                      |
| 2015 – 2018             | <u>Sponsor</u> : Canadian Institutes for Health Research<br><u>Grant Name</u> : Postdoctoral Fellowship<br><u>Grant #</u> : MFE-140389<br><u>PI</u> : Gavin Ha                                | <u>Title</u> : Characterizing the clonal diversity and patterns of tumour evolution in non-small cell lung cancer<br><u>Total Costs</u> : \$150,000 CAD<br><u>Role</u> : PI         |

## TEACHING AND MENTORING

### POST-DOCTORAL FELLOWS

- 2024 – Present Samantha Schuster (Ph.D., University of Washington)  
Co-mentored by Dr. Andrew Hsieh
- 2023 – Present Manasvita Vashisth (Ph.D., University of Pennsylvania)  
Primary Mentor
- 2022 – 2023 Anna-Lisa Doebley (Ph.D., University of Washington)  
Primary Mentor  
Current position: Returned to UW to complete medical school training
- 2021 – Present Pushpa Itagi, Ph.D. (Ph.D., University of Kansas)  
Primary Mentor, also co-mentored by Dr. Andrew Hsieh  
2022 Translational Data Science Integrated Research Center Fellowship Grant
- 2021 – Present Anat Zimmer (Ph.D., Weizmann Institute, Israel)  
Primary Mentor  
Brotman-Baty Institute 2022 Catalytic Collaborations Trainee Grant
- 2020 – Present 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 – 2023 Sitapriya Moorthi (Ph.D., Stony Brook University)  
Co-mentored, Primary PI Dr. Alice Berger  
2019 Translational Data Science Integrated Research Center Fellowship Grant  
Current position: Staff Scientist at Fred Hutch

### STAFF

- 2024 – Present Pooja Chandra, M.Sc., Bioinformatics Analyst II, Fred Hutch
- 2023 – Present Armand Bankhead, Ph.D., Senior Staff Scientist, Fred Hutch  
Co-supervised with Peter Nelson
- 2023 – Present Thomas Persse, M.Sc., Bioinformatics Analyst I, Fred Hutch
- 2022 – Present Michael Yang, M.Sc., Bioinformatics Analyst I, Fred Hutch
- 2023 – 2023 Lucas Occhiena, Research Technician II, Fred Hutch
- 2022 – 2023 Erin Kawelo, B.Sc., Research Technician I, Fred Hutch  
Current position: Technician at Alpha-Bio
- 2022 – 2023 Adam Kreitzman, B.Sc., Graduate Research Assistant, Fred Hutch  
Current position: Master of Information & Data Science, UC Berkeley

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- 2021 – Present 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  
Current position: Engineer at Quest Diagnostics  
2019 – 2021 Anna Hoge, Bioinformatics Analyst, Fred Hutch  
Current position: Medical student at Mayo Clinic, Arizona  
2019 – 2022 Jonathan Reichel, Ph.D., Research Scientist, Brotman-Baty Institute  
Co-supervisor; Primary PI Dr. Colin Pritchard  
Current position: Co-founder of cell-free DNA startup company

GRADUATE STUDENTS

- 2023 – Present Sarah Nguyen, Genomics Research Training for Data Science Program, University of Washington (master's program)  
2023 – Present Alexander Netzley, Genomics Research Training for Data Science Program, University of Washington (master's program)  
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 – 2022 Abigail Thorpe, MA, Genome Sciences, University of Washington  
Current position: Computational biologist at The Tisch Cancer Institute, Mount Sinai  
2021 Mohamed Adil, Master of Science in Laboratory Medicine, Department of Laboratory Medicine & Pathology, University of Washington (Primary advisor, co-advised with Dr. Colin Pritchard)  
MSc Thesis: *Accurate quantification of placental fraction by tissue-specific cell-free DNA analysis (defended June 4, 2021)*  
2019 – 2022 Anna-Lisa Doebley, Molecular and Cellular Biology Program, Medical Scientist Training Program, University of Washington  
PhD Thesis: *Predicting cancer subtypes from nucleosome profiling of cell-free DNA (defended September 27, 2022)*

GRADUATE ROTATION STUDENTS

- 2024 Summer Allie Kreitman, Medical Scientist Training Program, University of Washington  
2024 Summer Alan Min, University of Washington Medical School  
2023 Spring Sarah Huang, Molecular and Cellular Biology Program, University of Washington  
2023 Winter Katherine Feldman, Molecular and Cellular Biology Program, University of Washington  
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  
2021 Winter Aditya Sriram, Genetic Epidemiology 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

- 2023 – Alex Reers, Molecular Medicine and Mechanisms of Disease PhD Program, University of Washington (PI: Kevin Cheung)  
2023 – Hunter Colgrove, Genome Sciences University of Washington (PI: Alison Feder)  
2023 – Coohleen Coombes, Molecular and Cellular Biology Program, University of Washington (PI: Rosanna Risques)  
2022 – Gerardo Javier, Molecular Medicine and Mechanisms of Disease PhD Program, University of Washington (PI: John Lee)  
2021 – 2023 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 – 2023 Maya Lewinsohn, Genome Sciences, Medical Scientist Training Program,

University of Washington (PI: Trevor Bedford)  
 2019 – 2023 David Bacsik, Genome Sciences, Medical Scientist Training Program,  
 University of Washington (PI: Jesse Bloom)

**INTERNS AND VISITORS**

2024 Alan Min, Ph.D., Graduate research assistant, University of Washington Medical School  
 2023 Yixin Lin (Aarhus University, Denmark), Visiting Graduate Student (6 months)  
 2023 Akira Nair (Brown University), Summer Undergrad Research Program (SURP)  
 2023 Addison Gage (Willamette University), Summer Undergrad Intern  
 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 2023 GENOME 541: Introduction to Computational Molecular Biology (4 lectures)  
 Fall 2022 MCB 536: Tools for Computational Biology (2 lectures)  
 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"  
 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)**

2023 Selection Committee, Prostate Cancer Program  
 2022 – 2023 Selection Committee, Translational Data Science Integrated Research Center  
 2020 – 2021 PHS Subcommittee, Cluster Faculty Hire (Diversity, Equality, Inclusion)  
 2019 – 2020 Selection Committee, Computational Cancer Biology Position, Prostate Cancer Program

**GRANT REVIEWS (LOCAL)**

2024 Committee Member, Chen Hu Endowed Travel Awards, PHS, Fred Hutch  
 2023 Committee Member, Chen Hu Endowed Travel Awards, PHS, Fred Hutch  
 2023 Reviewer, Pacific Northwest Prostate Cancer SPORE Pilot Awards, Fred Hutch  
 2021 Reviewer, Pacific Northwest Prostate Cancer SPORE Pilot Awards, Fred Hutch

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2020

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

SCIENTIFIC COMMITTEES (LOCAL)

2020 – 2023

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

SCIENTIFIC COMMITTEES (EXTERNAL)

2022 –

Scientific Expert Committee Member, Liquid Biopsies, AURORA Program, Breast International Group (voluntary; no compensation received)

AD-HOC REVIEWER

2018 (6)

Bioinformatics, Cell Discovery, Epigenetics & Chromatin, Nature Communications, PLoS Computational Biology, Scientific Reports

2019 (5)

eBioMedicine, European Urology, Genome Biology, Genome Medicine, Journal of Clinical Investigation

2020 (5)

Genome Medicine, Journal of the National Cancer Institute, Nature Methods, Science Advances, Molecular Therapy – Nucleic Acids,

2021 (6)

Genome Biology, Genome Medicine (x2), Genome Research, Nature Communications (x2)

2022 (4)

Cell Genomics, Genome Medicine, Nature Communications (x2), Nucleic Acids Research Cancer

2023 (4)

Nature Medicine, Nature Methods, Cancer Discovery, Cell Reports Medicine

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Nature Genetics

## PUBLICATIONS

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

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### PRE-PRINT SERVER ARTICLES

1. Moorthi S, Paguirigan A, Ko M, Pettinger M, Hoge ACH, Nag A, Patel NA, Wu F, Sather C, Fitzgibbon MP, Thorne AR, Anderson GL, **Ha G**<sup>‡</sup>, Berger AH<sup>‡</sup>. Somatic mutation but not aneuploidy differentiates lung cancer in never-smokers and smokers. *bioRxiv*. Published online January 6, 2023:2023.01.05.522947. doi:[10.1101/2023.01.05.522947](https://doi.org/10.1101/2023.01.05.522947)

### PEER-REVIEWED ARTICLES

*Independent Lab (20 total, 6 corresponding author, 1 first author)*

1. Ajkunic A, Sayar E, Roudier MP, Patel RA, Coleman IM, De Sarkar N, Hanratty B, Adil M, Zhao J, Zaidi S, True LD, Sperger JM, Cheng HH, Yu EY, Montgomery RB, Hawley JE, **Ha G**, Persse T, Galipeau P, Lee JK, Harmon SA, Corey E, Lang JM, Sawyers CL, Morrissey C, Schweizer MT, Gulati R, Nelson PS, Haffner MC. [Assessment of TROP2, CEACAM5 and DLL3 in metastatic prostate cancer: Expression landscape and molecular correlates](#). *NPJ Precis Oncol*. 2024 May 17;8(1):104. [PMCID: PMC11101486].
2. Hiatt JB, Doebley AL, Arnold HU, Adil M, Sandborg H, Persse TW, Ko M, Wu F, Quintanal Villalonga A, Santana-Davila R, Eaton K, Dive C, Rudin CM, Thomas A, Houghton AM, **Ha G**<sup>‡</sup>, MacPherson D<sup>‡</sup>. [Molecular phenotyping of small cell lung cancer using targeted cfDNA profiling of transcriptional regulatory regions](#). *Science Advances*. 2024 Apr 12;10(15):eadk2082. doi: 10.1126/sciadv.adk2082. [PMCID: PMC11006233].
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4. Schuster SL, Arora S, Wladyka CL, Itagi P, Corey L, Young D, Stackhouse BL, Kollath L, Wu QV, Corey E, True LD, **Ha G**, Paddison PJ, Hsieh AC. [Multi-level functional genomics reveals molecular and cellular](#)



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5. De Sarkar N<sup>^</sup>, Patton RD<sup>^</sup>, Doebley AL, Hanratty B, Adil M, Kreitzman AJ, Sarthy JF, Ko M, Brahma S, Meers MP, Janssens DH, Ang LS, Coleman IM, 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 RB, Corey E, Henikoff S, Nelson PS<sup>‡</sup>, Ha G<sup>‡</sup>. [Nucleosome Patterns in Circulating Tumor DNA Reveal Transcriptional Regulation of Advanced Prostate Cancer Phenotypes](#). *Cancer Discovery*. 2023;13(3):632-653. doi:10.1158/2159-8290.CD-22-0692 [PMCID: PMC9976992]
  6. Doebley AL, Ko M, Liao H, Cruikshank AE, Santos K, Kikawa C, Hiatt JB, Patton RD, De Sarkar N, Collier KA, Hoge ACH, Chen K, Zimmer A, Weber ZT, Adil M, Reichel JB, Polak P, Adalsteinsson VA, Nelson PS, MacPherson D, Parsons HA, Stover DG, Ha G<sup>‡</sup>. [A framework for clinical cancer subtyping from nucleosome profiling of cell-free DNA](#). *Nature Communications*. 2022 Dec 3;13(1):7475. doi: 10.1038/s41467-022-35076-w. [PMCID: PMC9719521].
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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. [PMCID: PMC5673918]
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. [PMCID: PMC5815405]
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

### 2024

1. **Coffey-Holden Prostate Cancer Academy Meeting**, UCLA, Los Angeles, CA  
Date: June 20-23, 2024  
Invited speaker
2. **UTSW Pathology Seminar Series**, UT Southwestern Dept. of Pathology, Dallas, TX  
Date: April 23, 2024  
Title: Methods for Tumor Phenotype Classification from Circulating Tumor DNA
3. **COMBI Seminar Series**, Department of Genome Sciences, University of Washington, Seattle, WA  
Date: January 31, 2024  
Title: "Characterizing tumor heterogeneity and evolution in bladder cancer rapid autopsies"

2023

4. **Liquid Biopsy in GI Oncology Mini-symposium**, Fred Hutch, Seattle, WA  
Date: September 11, 2023  
Title: "Methods for tumor phenotype classification from circulating tumor DNA"
5. **PNW Prostate Cancer SPORE Research Symposium**, Vancouver, BC, Canada  
Date: July 23, 2023  
Title: "Classifying prostate cancer phenotypes using circulating tumor DNA"
6. **Cancer Early Detection Advanced Research (CEDAR) Seminar Series**, OHSU, Portland, OR  
Date: July 18, 2023  
Title: "Methods for tumor phenotype classification from circulating tumor DNA"
7. **GU Oncology Faculty Retreat**, Seattle WA  
Date: June 15, 2023  
Title: "Characterizing tumor heterogeneity and evolution in bladder cancer rapid autopsies"
8. **Seattle Translational Tumor Research (STTR) 10-Year Retreat**, Seattle WA  
Date: June 8, 2023  
Title: "Classifying Tumor Phenotypes from Cell-free DNA for Precision Oncology"
9. **UW Public Health Genetics Student Seminar Series**, Seattle WA  
Date: March 29, 2023 (Virtual Seminar)  
Title: "Innovations in Liquid Biopsies: Enabling Precision Oncology"
10. **Memorial Sloan Kettering Computational Oncology Seminar Series**, New York, NY  
Date: March 21, 2023  
Title: "Methods for tumor phenotype classification from circulating tumor DNA"
11. **Dana-Farber Cancer Institute Center for Functional Cancer Epigenetics Seminar Series**  
Date: March 10, 2023 (Virtual Seminar)  
Title: "Transcriptional regulation of cancer phenotypes revealed by circulating tumor DNA"

2022

12. **Prostate Cancer Foundation 29th Annual Scientific Retreat**, Carlsbad, CA  
Date: October 27-29, 2022  
Poster title: "Predicting transcriptional regulation of prostate cancer phenotypes from circulating tumor DNA"
13. **NIH/NCI Informatics Technology for Cancer Research (ITCR) 2022 Annual Meeting**, St. Louis, MI  
Date: September 12-15, 2022  
Title: "Predicting transcriptional signatures and tumor subtypes from circulating tumor DNA"
14. **Prostate Cancer Foundation Working Group Seminar (Genomes/Genetics/Epigenetics)**  
Date: August 10, 2022 (Virtual Seminar)  
Title: "Transcriptional regulation in CRPC tumor phenotypes revealed by circulating tumor DNA"
15. **Fred Hutch Early Detection Research Network Methods Group Meeting**  
Date: August 4, 2022 (Virtual Seminar)  
Title: "Methods for cancer detection using circulating tumor DNA"
16. **Dana-Farber Cancer Institute Triple Negative Breast Cancer Working Group Monthly Meeting**  
Date: August 3, 2022 (Virtual Seminar)  
Title: "Classifying ER status in metastatic breast cancer from circulating tumor DNA"
17. **GU Oncology Seminar Series**, Fred Hutch, Seattle WA  
Date: February 24, 2022  
Title: "Transcriptional regulation in CRPC tumor phenotypes revealed by circulating tumor DNA"
18. **Broad Institute Blood Biopsy Monthly Meeting**  
Date: February 1, 2022 (Virtual Seminar)  
Title: "Tumor subtype and phenotype prediction from cell-free DNA"



## 2021

19. **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"
20. **UCSF Computational Cancer Community Seminar**, San Francisco, CA  
Date: December 3, 2021 (Virtual Seminar)  
Title: "Tumor subtype and phenotype prediction from cell-free DNA"
21. **Prostate Cancer Foundation 28th Annual Scientific Retreat** (Virtual Conference)  
Date: October 28-30, 2021  
Poster Title: "Tumor subtyping in prostate and breast cancers using circulating tumor DNA"
22. **V Foundation Scholar Summit** (Virtual Conference)  
Date: April 27-28, 2021  
Poster Title: "Characterizing molecular signatures in advanced prostate cancer using circulating tumor DNA"
23. **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

24. **Prostate Cancer Foundation 27th Annual Scientific Retreat** (Virtual Conference)  
Date: October 20-23, 2020  
Poster Title: "Multi-omic Profiling of Circulating Tumor DNA in Castration-Resistant Prostate Cancer"
25. **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"
26. **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"
27. **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

28. **Cancer Consortium – Cancer Basic Biology Retreat**, Seattle, WA  
Date: December 2, 2019  
Title: Analysis of cell-free DNA in patients with advanced cancer
29. **Prostate Cancer Foundation 26th Annual Scientific Retreat**, Carlsbad, CA  
Date: October 24-26, 2019  
Poster Title: "Multi-omic profiling of circulating tumor DNA in patients with CRPC"
30. **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
31. **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"
32. **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."

33. **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."
34. **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

35. **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."
36. **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

37. **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"
38. **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)
39. **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"
40. **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"
41. **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"
42. **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

Keraon      Homepage: <https://github.com/GavinHaLab/CRPCSubtypingPaper/tree/main/ctdPheno>  
Description: Probabilistic method to estimate cancer phenotype mixtures from circulation tumor DNA  
Author: Robert Patton, PhD (Postdoc, Ha Lab)  
Publication: [De Sarkar et al. Cancer Discov. 2022](#)

ctdPheno

Homepage: <https://github.com/GavinHaLab/CRPCSubtypingPaper/tree/main/ctdPheno>

Description: Probabilistic method to classify tumor phenotypes from circulation tumor DNA

Author: Robert Patton, PhD (Postdoc, Ha Lab)

Publication: [De Sarkar et al. Cancer Discov. 2023](#)

Griffin

Homepage: <https://github.com/GavinHaLab/Griffin>

Description: A flexible framework for nucleosome profiling of cell-free DNA

Author: Anna-Lisa Doebley, PhD (Graduate student, Ha Lab)

Publication: [Doebley et al. Nat Commun. 2022](#)

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

Author: Gavin Ha

Publication: [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

Author: Gavin Ha

Publication: [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

Authors: Daniel Lai, Gavin Ha, Sohrab Shah

Publication: [Ha et al. Genome Res. 2012](#)

APOLLOH

Homepage: <https://github.com/shahcompbio/apolloh>

Description: Cancer genomics software for detecting loss of heterozygosity from whole genome sequencing data of tumors

Author: Gavin Ha

Publication: [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

Author: Gavin Ha

Publication: [Ha et al. Methods Mol Biol. 2013](#)

## INTELLECTUAL PROPERTY

Priority 2022-08-30

Converted 2023-08-25

CELL-FREE DNA SEQUENCE DATA ANALYSIS TECHNIQUES FOR ESTIMATING FETAL FRACTION AND TO PREDICT PRE-ECLAMPSIA

[PCT/US2023/072909](#)

Inventors: Gavin Ha, Mohamed Adil, Jonathan Reichel, Christina Lockwood, Raj Shree

Assignee: Fred Hutchinson Cancer Center and University of Washington

Description: Method of enhancing cell-free DNA sequence data to estimate the fetal DNA contribution and to predict the risk of pre-eclampsia from fluids of pregnant women.

Gavin Ha, PhD

*Curriculum Vitae*

Priority 2021-04-08 CELL-FREE DNA SEQUENCE DATA ANALYSIS METHOD TO EXAMINE NUCLEOSOME  
Converted 2022-04-08 PROTECTION AND CHROMATIN ACCESSIBILITY

[PCT/US2022/024082](#)

Inventors: Gavin Ha, Anna-Lisa Doebley, Robert Patton, Navonil De Sarkar, Joseph Hiatt,  
David MacPherson, Peter Nelson

Assignee: Fred Hutchinson Cancer Center

Description: Method of enhancing sequence read data from cell-free DNA samples for cell  
type, phenotype, subtype, prediction.

Priority 2016-03-16 METHODS FOR GENOME CHARACTERIZATION

Converted 2017-03-16 WO EP US [US11479878B2](#)

Published 2019-03-14 Status: Active

Granted 2022-10-25 Inventors: Gavin Ha, Viktor Adalsteinsson, Samuel Freeman

Assignee: Dana-Farber Cancer Institute, Inc., Broad Institute, Inc., Harvard College

Description: 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