

# Graham P. McVicker

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## Education

- 2005-2010 **Ph.D. Genome Sciences**, University of Washington  
Mentor: Phil Green  
Thesis: The Roles of Natural Selection and Germline Gene Expression in Primate Genome Evolution
- 1997-2002 **B.Sc. Computer Science**, University of British Columbia  
Co-op program with 20 months of industry work experience

## Professional Experience

- 2016-Present **Assistant Professor**  
*Salk Institute for Biological Studies, La Jolla, CA*
- 2010-2015 **Postdoctoral Scholar**, Stanford University  
Mentor: Jonathan Pritchard  
Note: Moved from University of Chicago to Stanford in 2013
- 2013-2015 **Visiting Scholar**, Dana-Farber Cancer Institute,  
Harvard T.H. Chan School of Public Health  
Mentor: X. Shirley Liu
- 2004-2005 **Team Leader**  
*UBC Bioinformatics Centre, Vancouver, Canada*
- 2002-2004 **Scientific Software Developer**  
*European Bioinformatics Institute, Hinxton, UK*
- 2001 **Software Developer** (4-month paid internship)  
*Department of National Defense, Ottawa, Canada*
- 1999-2000 **Software Developer** (two 8-month paid internships)  
*MDSI Mobile Data Solutions, Richmond, Canada*

## Preprints

1. Fiaux P, Chen H, **McVicker G** (2019). Discovering functional sequences with RELICS, an analysis method for CRISPR regulatory screens. BioRxiv 687293v1 [**Preprint**] June 30, 2019. Available from: <https://doi.org/10.1101/687293>
2. Sen A, Tyndale ST, Fu R, Erikson G, **McVicker G** (2019). BreakCA, a method to discover indels using ChIP-seq and ATAC-seq reads, finds recurrent indels in regulatory regions of neuroblastoma genomes. BioRxiv 605642v1 [**Preprint**] April 11, 2019. Available from: <https://doi.org/10.1101/605642>

## Peer-Reviewed Publications

1. Nott A\*, Holtman IR\*, Coufal NG\*, Schlachetzki JCM, Yu M, Hu R, Han CZ, Pena M, Xiao J, Wu Y, Keulen Z, Pasillas MP, O'Connor C, Nickl CK, Schafer ST, Shen Z, Rissman RA, Brewer JB, Gosselin D, Gonda DD, Levy ML, Rosenfeld MG, **McVicker G**, Gage FH, Ren B, Glass CK. (2019) Brain cell type-specific enhancer-promoter interactome maps and disease risk association. *Science*, 366(6469):1134-1139 (\*=equal contribution)

2. Ha B, Greenbaum JA, Shmiedel BJ, Singh D, Madrigal A, Valdovino-Gonzalez AG, White BM, Zapardiel-Gonzalo J, Altay G, **McVicker G**, Seumois G, Rao A, Kronenberg M, Vijayanand P, Peters B. (2019) Database of Immune Cell EQTLs, Expression, Epigenomics. *J. Immunology*, 202(1):131.18-131.18
3. Schmiedel BJ, Singh D, Madrigal A, Valdovino-Gonzalez AG, White BM, Zapardiel-Gonzalo J, Ha B, Altay G, Greenbaum JA, **McVicker G**, Seumois G, Rao A, Kronenberg M, Peters B, Vijayanand P. (2018) Impact of Genetic Polymorphisms on Human Immune Cell Gene Expression. *Cell*, 175(6):1701-1715
4. Martin RL, Maiorano J, Beitel GJ, Marko JF, **McVicker G**, Fondufe-Mittendorf YN. (2017) A Comparison of nucleosome organization in Drosophila cell lines. *PLOS One*, 12(6):e0178590
5. Elyashiv E, Sattah S, Hu TT, Strustovsky A, **McVicker G**, Andolfatto P, Coop G, Sella G. (2016) A genomic map of linked selection in Drosophila. *PLOS Genetics*, 12(8):e1006130
6. van de Geijn B\*, **McVicker G**\*, Gilad Y, Pritchard JK (2015) WASP: allele-specific software for robust discovery of molecular quantitative trait loci. *Nature Methods*, 12(11):1061-3. (\*=equal contribution)
7. Banovich NE\*, Lan X\*, **McVicker G**, van de Geijn B, Degner JF, Blischak JD, Roux J, Pritchard JK, Gilad Y. (2014). Methylation QTLs are associated with coordinated changes in transcription factor binding, histone modifications, and gene expression levels. *PLOS Genetics*, 10(9):e1004663. (\*=equal contribution)
8. Nalabothula N\*, **McVicker G**\*, Maiorano J, Martin R, Pritchard JK, Fondufe-Mittendorf YN (2014) The chromatin architectural proteins HMGD1 and H1 bind reciprocally and have opposite effects on chromatin structure and gene regulation. *BMC Genomics*, 15:92. (\*=equal contribution)
9. **McVicker G**\*, van de Geijn B\*, Degner JF, Cain CE, Banovich NE, Lewellen N, Myrthil M, Gilad Y, Pritchard JK (2013). Identification of genetic variants that affect histone modification in human cells. *Science*, 342(6159):747-9. (\*=equal contribution)
10. Gaffney DJ\*, **McVicker G**\*, Pai AA, Fondufe-Mittendorf YN, Lewellen N, Michelini K, Widom J, Gilad Y, Pritchard JK (2012). Controls of nucleosome positioning in the human genome. *PLOS Genetics*, 8(11):e1003036. (\*=equal contribution)
11. D'Souza CA *et al.* [one of 41 authors] (2011) Genome variation in *Cryptococcus gattii*, an emerging pathogen of immunocompetent hosts. *MBio*, 2(1):e00342-10.
12. George RD, **McVicker G**, Diederich R, Ng SB, MacKenzie AP, Swanson WJ, Shendure J, Thomas JH (2011). *Trans* genomic capture and sequencing of primate exomes reveals new targets of positive selection. *Genome Research*, 14(5):929-33.
13. **McVicker G**, Green P (2010). Genomic signatures of germline gene expression. *Genome Research*, 20(11):1503-11.
14. **McVicker G**, Gordon D, Davis C, Green P (2009). Widespread genomic signatures of natural selection in hominid evolution. *PLOS Genetics*, 5(5):e1000471.
15. Birney E *et al.* [one of 55 authors] (2005). Ensembl 2005. *Nucleic Acids Research*, 33:D447-53.
16. Stabenau A, **McVicker G**, Melsopp C, Proctor G, Clamp M, Birney E (2004). The Ensembl Core Software Libraries. *Genome Research*, 14(5):929-33.
17. Birney E *et al.* [one of 48 authors] (2004). An overview of Ensembl. *Genome Research*, 14(5):925-8.
18. Birney E *et al.* [one of 48 authors] (2004). Ensembl 2004. *Nucleic Acids Research*, 32:D468-70.
19. Shah S, **McVicker G**, Mackworth A, Rogic S, Ouellette BFF (2003) GeneComber: Combining outputs of gene prediction programs for improved results. *Bioinformatics*, 19(10): 1296-7

## Other Publications

20. Raj A, **McVicker G** (2014) The genome shows its sensitive side. *Nature Methods (News & Views)*, 11(1):39-40

## Research Support

- 2019-2024 P30 CA014195-46 (Shaw, PI) NIH/NCI: "Cancer Center Support Grant" Role: Co-Investigator
- 2019-2022 R01 AI107027-06 (Zheng, PI) NIH/NIAID: "Treg development and function controlled by cis-regulatory circuits" Role: Co-Investigator
- 2019-2023 R01 DK122607-01 (Gaulton/Sander PIs) NIH/NIDDK: "Genetic mechanisms of type 1 diabetes risk in stress-induced pancreatic islets" Role: Co-Investigator
- 2019-2020 Padres Pedal the Cause Rady Children's Hospital Translational Pediatric Cancer Research Award (McVicker/Elster PIs) "Detecting dysregulated genes in neuroblastoma using allele-specific expression"

## Completed Research Support

- 2018-2019 Padres Pedal the Cause Collaborative Translational Pilot Grant (McVicker/Carter PIs) "Enhanced Breast Cancer Risk Prediction from Imputed Gene Expression"
- 2018-2019 Salk Cancer Center Pilot Grant (Dixon/McVicker PIs) "The effects of DNA hypomethylating agents on genome-wide enhancer-promoter landscapes"
- 2017-2018 Padres Pedal the Cause Rady Children's Hospital Translational Pediatric Cancer Research Award (McVicker/Dixon/Kuo PIs) "Discovery of non-coding oncogenic mutations in pediatric acute lymphoblastic leukemia using ATAC-seq and Hi-C"
- 2016-2017 Salk Institute Innovation Grant (McVicker/Manor/Hsu PIs): "Imaging the spatiotemporal dynamics of arbitrary genomic loci in living cells"
- 2007-2009 Natural Science and Engineering Research Council (NSERC) Post Graduate Scholarship, PGS-D2
- 2005-2007 Natural Science and Engineering Research Council (NSERC) Post Graduate Scholarship, PGS-M

## Conference Talks

- 2014 "Genetic Control of Chromatin State" American Society for Human Genetics, San Diego, CA
- 2014 "Accurate inference of causal variants in autoimmune diseases using cell-type specific functional genomic data" ENCODE Consortium Meeting, Stanford, CA
- 2009 "Genomic Signatures of Germline Transcription" Society for Molecular Biology and Evolution, Iowa City, IA
- 2008 "Background Selection Explains Patterns of Primate Diversity" The Biology of Genomes, Cold Spring Harbor, NY
- 2005 "Pegasys: A Parallel Genome Annotation System" BCNet Advanced Network Conference, Vancouver, BC

**Seminars and Invited Talks**

- 2017 "New approaches for identifying regulatory variants in the human genome" Genetics, Bioinformatics & Systems Biology Colloquium, UCSD, San Diego, CA
- 2017 "Identifying regulatory variants in the human genome" San Diego Chromatin Club, San Diego, CA
- 2017 Panel Discussion: "Personalized medicine... curb your enthusiasm?" Festival of Genomics, San Diego, CA
- 2017 "Interpreting human genetic variation by molecular trait mapping" Department of Biology, San Francisco State University, San Francisco, CA
- 2016 "Interpreting human genetic variation by molecular trait mapping" UCLA Bioinformatics Seminar, Los Angeles, CA
- 2016 "Allele-specific methods for discovery of molecular quantitative trait loci" Genetics, Bioinformatics and Systems Biology Colloquium, UCSD, San Diego, CA
- 2015 "Interpreting human genetic variation by molecular trait mapping" Department of Genetics, Yale University, New Haven CT
- 2015 "Interpreting human genetic variation by molecular trait mapping" Simons Center for Quantitative Biology, Cold Spring Harbor Laboratory, NY
- 2015 "Interpreting human genetic variation by molecular trait mapping" Department of Cellular and Molecular Medicine, University of California San Diego
- 2015 "Interpreting human genetic variation by molecular trait mapping" The Salk Institute, San Diego, CA
- 2015 "Interpreting human genetic variation by molecular trait mapping" Department of Molecular Biosciences, University of Texas at Austin
- 2015 "New methods for robust discovery of molecular quantitative trait loci" Department of Computer Science, University of Texas at Austin
- 2015 "Interpreting human genetic variation by molecular trait mapping" La Jolla Institute for Allergy and Immunology, San Diego, CA
- 2015 "Interpreting human genetic variation by molecular trait mapping" Department of Human Genetics, University of Utah
- 2015 "Interpreting human genetic variation by molecular trait mapping" Department of Molecular Biology and Genetics, Cornell University
- 2015 "Interpreting human genetic variation by molecular trait mapping" The Jackson Laboratory for Genomic Medicine, Farmington, CT
- 2014 "Interpreting human genetic variation by molecular trait mapping" Department of Genetics, University of Pennsylvania
- 2014 "Interpreting human genetic variation by molecular trait mapping" Genome Institute of Singapore
- 2013 "Identification of genetic variants that affect histone modifications in human cells" CSAIL Stata Center Seminar, MIT
- 2013 "How Does Natural Selection Affect Linked Neutral Diversity in Primate Evolution" Boston Evolutionary Genomics Retreat, Broad Institute
- 2013 "Mapping of Histone Modification and DNA Methylation QTLs" ENCODE GWAS Working Group Conference Call

- 2005 "Pegasys: Workflow Management Software for Bioinformatics" BC Genome Sciences Centre, Vancouver, Canada
- 2004 "The Ensembl Core API & Database Schema" Swiss Institute of Bioinformatics, Geneva, Switzerland
- 2003 "The Ensembl Databases and API" Serono/Merck, Paris, France

### Current Students and Postdocs

- 2016-Present Patrick Fiaux (Ph.D. student, UCSD Bioinformatics and Systems Biology)
- 2018-Present Jessica Zhou (Ph.D. student, UCSD Bioinformatics and Systems Biology; Joint with Hannah Carter)
- 2016-Present Arko Sen (Postdoc)
- 2016-Present Hsiuyi Chen (Postdoc)
- 2018-Present Aaron Chen (B.Sc. student, UCSD Biochemistry and Cell Biology)

### Previous Students and Postdocs

- 2018-2019 Arya Massarat (B.Sc. student, Harvey Mudd College)  
Current Position: B.Sc. student, Harvey Mudd College
- 2019 Lillian Petersen (High school summer student)  
Current Position: High school student, Los Alamos High School
- 2016-2017 Jing Gu (M.Sc. Student, UCSD Chemistry and Biochemistry)  
Current Position: Ph.D. student, University of Chicago
- 2016-2017 Kayla Chase (Postdoc, Joint with Abe Palmer).  
Current Position: Medical Science Liaison, Collegium Pharmaceutical, Inc.
- 2016-2017 Ishika Luthra (Undergraduate Co-op student, Simon Fraser University)  
Current Position: M.Sc. student, Mostafavi Lab, University of British Columbia

### Rotation Students

- 2019 Joe Solvason, UCSD Bioinformatics and Systems Biology (Spring)
- 2018 Jennifer Havens, UCSD Bioinformatics and Systems Biology (Fall)
- 2018 Adam Jussila, UCSD Bioinformatics and Systems Biology (Fall)
- 2017 James Sorrentino, UCSD Bioinformatics and Systems Biology (Fall)
- 2017 Jessica Zhou, UCSD Bioinformatics and Systems Biology (Summer)
- 2016 Patrick Fiaux, UCSD Bioinformatics and Systems Biology (Spring)

### Student Dissertation Committees

- 2019-Present Shubham Saini (Gymrek Lab), UCSD Computer Science and Engineering
- 2016-Present Anthony Aylward (Gaulton Lab), UCSD Bioinformatics and Systems Biology
- 2017-2019 William Greenwald (Fraser Lab), UCSD Bioinformatics and Systems Biology
- 2016-2019 Yunjiang Qiu (Ren Lab), UCSD Bioinformatics and Systems Biology

2016-2019 Dylan Skola (Glass Lab), UCSD Bioinformatics and Systems Biology

### Student Qualifying Exam Committees

2019 Yue Qin (Ideker Lab), UCSD Bioinformatics and Systems Biology  
 2018 Ileana Mitra (Gymrek Lab), UCSD Bioinformatics and Systems Biology  
 2017 William Greenwald (Fraser Lab), UCSD Bioinformatics and Systems Biology  
 2016 Arjun Chandrasekhar (Navlakha Lab), UCSD Bioinformatics and Systems Biology

### Teaching

2017-Present Co-organizer, CSE290: Seminar in Medical and Population Genetics  
 2017-Present Guest lecturer (6 hrs/yr) BIOM262: Quantitative Methods in Genetics and Genomics (Graduate Class)  
 2016-2018 Guest lecturer (1.5 hrs/yr) BGGN220D: Chromatin Structure and Transcriptional Regulation (Graduate Class)  
 2011 Tutor, *Okinawa Institute of Science and Technology*  
 Quantitative Evolutionary and Comparative Genomics Summer School  
 Invited presenter at 3 week intensive workshop. Taught 6hr course on natural selection.  
 2009 Graduate Teaching Assistant, *University of Washington*  
 Genome 540: Computational Molecular Biology (Graduate Class)  
 2008 Graduate Teaching Assistant, *University of Washington*  
 Genome 371: Introduction to Genetics (Undergraduate Class)  
 2004 Presenter, *European Bioinformatics Institute*  
 Industry Programme Workshop, Cambridge, UK

### Peer Review

Reviewer for *eLife*, *Science*, *PNAS*, *Nature Genetics*, *Nature Methods*, *Nature Communications*, *PLOS Biology*, *PLOS Computational Biology*, *PLOS Genetics*, *PLOS ONE*, *Genome Research*, *Genome Biology*, *Molecular Biology and Evolution*, *BMC Genomics*, *Genetics*, *Bioinformatics*, *Scientific Reports*, *Nucleic Acids Research*, among others.

### Other Academic Service

2019-Present Member, Salk Innovation Review Committee  
 2017-Present Member, Admissions Committee for UCSD Bioinformatics and Systems Biology  
 2016-Present Faculty member, UCSD Bioinformatics and Systems Biology  
 2013-Present Member, American Society for Human Genetics  
 2019 Co-organizer, Inaugural Salk Integrative Biology Symposium  
 2018 Ad hoc reviewer, Salk Innovation Grant Proposals  
 2017 Platform session moderator for "Transcriptomic Analysis of Genetic Variation and Disease", American Society of Human Genetics 2017 Meeting.