

# Graham P. McVicker

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## Education

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

## Professional Experience

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

## Peer-Reviewed Publications (\* equal contribution)

1. 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.  
<http://www.nature.com/nmeth/journal/v12/n11/abs/nmeth.3582.html>
2. 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.  
<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC4169251/>
3. 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.  
<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3928079/>

4. **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.  
<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3947669/>
5. 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.  
<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3499251/>
6. 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.  
<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3037005/>
7. 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.  
<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3202285/>
8. **McVicker G**, Green P (2010). Genomic signatures of germline gene expression. *Genome Research*, 20(11):1503-11.  
<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2963814/>
9. **McVicker G**, Gordon D, Davis C, Green P (2009). Widespread genomic signatures of natural selection in hominid evolution. *PLOS Genetics*, 5(5):e1000471.  
<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2669884/>
10. Birney E *et al.* [one of 55 authors] (2005). Ensembl 2005. *Nucleic Acids Research*, 33:D447-53.  
<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC540092/>
11. Stabenau A, **McVicker G**, Melsopp C, Proctor G, Clamp M, Birney E (2004). The Ensembl Core Software Libraries. *Genome Research*, 14(5):929-33.  
<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC479122/>
12. Birney E *et al.* [one of 48 authors] (2004). An overview of Ensembl. *Genome Research*, 14(5):925-8.  
<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC479121/>
13. Birney E *et al.* [one of 48 authors] (2004). Ensembl 2004. *Nucleic Acids Research*, 32:D468-70.  
<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC308772/>
14. 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  
<http://bioinformatics.oxfordjournals.org/content/19/10/1296.long>

## Other Publications

15. Raj A, **McVicker G** (2014) The genome shows its sensitive side. *Nature Methods (News & Views)*, 11(1):39-40  
<http://www.nature.com/nmeth/journal/v11/n1/full/nmeth.2770.html>

16. Elyashiv E, Sattah S, Hu TT, Strustovsky A, **McVicker G**, Andolfatto P, Coop G, Sella G. (2014) A genomic map of linked selection in *Drosophila*. arXiv preprint. <http://arxiv.org/abs/1408.5461>

### Awards

- 2009 Society for Molecular Biology and Evolution Graduate Student Travel Award (\$1,000)
- 2007-2009 Natural Science and Engineering Research Council (NSERC) Post Graduate Scholarship, PGS-D2 (\$42,000)
- 2005-2007 Natural Science and Engineering Research Council (NSERC) Post Graduate Scholarship, PGS-M (\$38,500)
- 1997 University of British Columbia Outstanding Student Initiative Scholarship (\$5,000)

### 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

- 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

### Poster Presentations

- 2014 “Accurate inference of causal variants in autoimmune diseases using cell-type specific functional genomic data” Gordon Research Conference on Single Nucleotide Polymorphisms and Human Disease, Stonehill College, Easton, MA
- 2013 “Identification of Genetic Variants that affect Histone Modifications in Human Cells” American Society for Human Genetics, Boston
- 2013 “Identification of Genetic Variants that affect Histone Modifications in Human Cells” The Biology of Genomes, Cold Spring Harbor
- 2012 “A Large Fraction of Nucleosomes in the Human Genome are Consistently Positioned” Systems Biology: Global Regulation of Gene Expression, Cold Spring Harbor
- 2009 “Genomic Signatures of Germline Gene Expression” HHMI Scientific Meeting, Janelia Farm Research Campus
- 2008 “Background Selection in Hominid Evolution” International Conference on Primate Genomics, Seattle

### Teaching Experience

- 2011 Tutor, *Okinawa Institute of Science and Technology*  
Quantitative Evolutionary and Comparative Genomics Summer School

Invited presenter at 3 week intensive workshop. Taught 6 hour course on natural selection. Voted best teacher.

- 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  
Taught workshop on using the Ensembl API and database.

### **Peer Review**

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