

STEVEN C. MUNGER, Ph.D.

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PROFILE

I combine advanced computational methods with experimental validation techniques in high-resolution genetic mapping populations—an integrative approach called ‘systems genetics’—to elucidate the gene regulatory architecture governing cell fate decisions during early development and tissue homeostasis in adulthood. My research takes advantage of the emerging Diversity Outbred (DO) and Collaborative Cross (CC) mouse populations, complementary reservoirs of natural genetic perturbations that segregate high genetic diversity with a balanced population structure ideal for high-resolution genetic mapping, to characterize the effects of genetic variation on multiple layers of gene regulation and infer predictive network models underlying cell fate decisions. This systems genetic approach has enabled me to (1) define the consequences of genetic variation on transcript and protein abundance in the adult liver, and in so doing discover that pervasive transcriptional variation is largely constrained at the level of protein abundance by the relative stoichiometry of protein binding partners and complex members, and (2) predict and validate genetic variants that influence multiple layers of gene regulation and ultimately underlie ground state pluripotency in mouse embryonic stem cells. Through my training and research over the past fifteen years, I have purposefully acquired expertise in developmental biology, complex trait genetics, genomics and proteomics, statistical inference, and bioinformatics, with the goal of applying this interdisciplinary skillset to dissect and manipulate the gene regulatory networks that drive cell fate processes and influence disease risk.

EDUCATION & TRAINING

2011 – 2015

The Jackson Laboratory, Bar Harbor, ME
Postdoctoral Training
Advisor: Gary Churchill, Ph.D.

Led an interdisciplinary team of post-docs and software engineers to develop advanced analytical methods and computational tools for analyzing genomic data from genetically diverse mice. Developed Seqnare software to impute and construct individualized diploid genome sequences for RNA-seq read alignment. Demonstrated that the individualized alignment strategy increases read mapping accuracy, improves estimates of transcript abundance, yields direct estimates of allele-specific expression, reduces spurious expression quantitative trait locus (eQTL) associations, and unmasks thousands of real eQTL confounded by the common reference alignment strategy. Integrated transcriptomic and proteomic data from DO mice and showed that post-transcriptional mechanisms attenuate much of the local genetic variation impacting transcript abundance and also impose an additional layer of quantitative regulation on protein complex members via stoichiometric buffering.

2010 – 2011

Duke University, Durham, NC
Postdoctoral Training
Advisor: Blanche Capel, Ph.D.

Developed and optimized a gonad primary cell assay and lentiviral-mediated RNAi knockdown method to experimentally validate genetic interactions predicted from the temporal expression and eQTL data.

- 2010 Duke University, Durham, NC
Ph.D. Genetics
Advisor: Blanche Capel, Ph.D.
A systems-level view of mammalian sex determination.
Designed and conducted a systems genetics analysis of the embryonic mouse gonad at the critical time point of sex determination, the first such eQTL study in a developing vertebrate organ. Characterized the fine temporal patterns of gene activation and repression in the critical 24-hour window of sex determination and showed that sensitivity to sex reversal in the C57BL/6J strain background stems from delayed activation of the testis pathway and delayed repression of the ovarian pathway.
- 1999 The University of Michigan, Ann Arbor, MI
B.S. Biology

ADDITIONAL TRAINING

- 2014 The Jackson Laboratory, Bar Harbor, ME
The Whole Scientist Course (one-week course)
- 2012 – 2014 The Jackson Laboratory, Bar Harbor, ME
Short Course on Medical and Experimental Mammalian Genetics (two-week course)
- 2011 – 2013 The Jackson Laboratory, Bar Harbor, ME
Short Course on Systems Genetics (one-week course)
- 2000 – 2003 Dow Chemical Company, Midland, MI
Research & Development Technologist
Advisor: Mark Bernius, Ph.D.
Developed flexible flat panel displays to test new light-emitting polymers.

POSITIONS HELD

- 2015 – Present The Jackson Laboratory, Bar Harbor, ME
Assistant Professor
- 2011 – 2015 The Jackson Laboratory, Bar Harbor, ME
Postdoctoral Research Fellow
- 2010 – 2011 Duke University Medical Center, Durham, NC
Postdoctoral Associate
- 2003 – 2004 Dow Chemical Company, Midland, MI
Quality Control Technologist
- 2000 – 2003 Dow Chemical Company, Midland, MI
Research & Development Technologist
- 1999 – 2000 Waterford Kettering High School, Waterford, MI
Substitute 9 – 12 Grade Science Teacher

HONORS & AWARDS

2021 – 2022	Appointed to Executive Committee, Genetics Society of America
2019 – 2022	Elected to the Board of Directors of the Genetics Society of America
2018	Appointed as mouse field representative to Allied Program Committee <i>The Allied Genome Conference 2020, Genetic Society of America</i>
2018	Commencement Speaker, Sumner Memorial High School, Sullivan, Maine
2017	Alfond Leaders Award, The Harold Alfond Foundation
2016	Reviewer's Choice Abstract Award <i>American Society of Human Genetics Meeting</i>
2015 – 2017 term	Elected to Secretariat of the International Mammalian Genome Society
2013 – 2015	Ruth L. Kirschstein National Research Service Award <i>Individual postdoctoral fellowship</i>
2011 – 2013	The Jackson Laboratory Fellowship <i>Institution-awarded fellowship</i>
2013	Chicago Prize for Outstanding Oral Presentation <i>12th Annual Meeting of the Complex Trait Community</i>
2012	Best Oral Presentation by a Post-Doctoral Fellow <i>11th Annual Meeting of the Complex Trait Community</i>
2011	Verne Chapman Memorial Young Scientist Award <i>International Mammalian Genome Society</i>
2008	Best Oral Presentation by a Graduate Student <i>7th Annual Meeting of the Complex Trait Consortium</i>
2004 – 2006	NIH Predoctoral Training Grant <i>Institution-awarded fellowship</i>

PUBLICATIONS

Google Scholar page: <http://scholar.google.com/citations?user=j6C32yAAAAAJ&hl=en>

Complete List of Published Work in My Bibliography:

<https://www.ncbi.nlm.nih.gov/sites/myncbi/steven.munger.1/bibliography/44191189/public/?sort=date&direction=descending>

Primary Research Articles

24. Robertson SJ, Bedard O, McNally KL, Lewis M, Clancy C, Shaia C, Broeckel RM, Chiramel AI, Sturdevant GL, Forte E, Preuss C, Baker CN, Brunton C, **Munger SC**, Martens C, Holland SM, Rosenthal NA, Best SM. Genetically diverse mouse models of SARS-CoV-2 infection model clinical variation and cytokine responses in COVID-19. *BioRxiv* 2021. <https://doi.org/10.1101/2021.09.17.460664>.

23. Gyuricza IG, Chick JM, Keele GR, Deighan AG, **Munger SC**, Korstanje R, Gygi SP, Churchill GA. Genome-wide transcript and protein analysis reveals distinct features of aging in the mouse heart. *Genome Research* 2022 fr.275672.121. <https://doi.org/10.1101/gr.275672.121>.
22. Kuffler L, Skelly DA, Czechanski A, **Munger SC**, Baker CL, Reinholdt LG, Carter GW. Imputation of 3D genome structure by genetic-epigenetic interaction modeling in mice. *BioRxiv* 2022. <https://doi.org/10.1101/2022.02.07.479436>.
21. Byers C, Spruce C, Fortin HJ, Hartig EI, Czechanski A, **Munger SC**, Reinholdt LG, Skelly DA, Baker CL. Genetic control of pluripotency epigenome determines differentiation bias in mouse embryonic stem cells. *The EMBO Journal* 2022 41:e109445. <https://doi.org/10.15252/embj.2021109445>.
20. Keele GR, Zhang T, Pham DT, Vincent M, Bell TA, Hock P, Shaw GD, Paulo JA, **Munger SC**, de Villena FPM, Ferris MT, Gygi SP, Churchill GA. Regulation of protein abundance in genetically diverse mouse populations. *Cell Genomics* 2021 1(1) 100003. <https://doi.org/10.1016/j.xgen.2021.100003>
19. Wells AE, Raghupathy N, Robledo RF, Gatti DM, **Munger SC**, Phillips C, Ndikum J, Wilcox J, Graber JH, Hibbs M, Langston MA, Churchill GA, Carter GW, Chesler EJ. Natural genetic variation alters Alzheimer's-related gene expression modules in mice: Development of new models and analysis methods/novel assays and technologies. *Alzheimer's & Dementia* 2020 Dec: e042019. <https://doi.org/10.1002/alz.042019>.
18. Choi KB, He H, Gatti DM, Philip VM, Raghupathy N, Gyuricza IG, **Munger SC**, Chesler EJ, Churchill GA. Genotype-free individual genome reconstruction of Multiparental Population Models by RNA sequencing data. *BioRxiv* 2020. <https://doi.org/10.1101/2020.10.11.335323>.
17. Liang ZS, Cimino I, Yalcin B, Raghupathy N, Vancollie VE, Ibarra-Soria X, Firth HV, Rimmington D, Farooqi S, Lelliott CJ, **Munger SC**, O'Rahilly S, Ferguson-Smith AC, Coll AP, and Logan DW. Trappc9 deficiency causes parent-of-origin dependent microcephaly and obesity. *PLoS Genetics* 2020 Sep 2;16(9)e1008916 <https://doi.org/10.1371/journal.pgen.1008916>.
16. Katz DC, Aponte D, Liu W, Green RM, Mayeux JM, Pollard KM, Pomp D, **Munger SC**, Murray SA, Roseman CC, Percival CJ, Cheverud J, Marcucio RS, and Hallgrimsson B. Facial shape and allometry quantitative trait locus intervals in the Diversity Outbred mouse are enriched for known skeletal and facial development genes. *PLoS One* 2020 Jun 5;15(6):e0233377. <https://doi.org/10.1371/journal.pone.0233377>.
15. Skelly DA, Czechanski A, Byers C, Aydin S, Spruce C, Olivier C, Choi KB, Gatti DM, Raghupathy N, Stanton A, Vincent M, Dion S, Greenstein I, Pankratz M, Porter DK, Martin W, Qi W, Harrill AH, Choi T, Churchill GA[§], **Munger SC**[§], Baker CL[§], and Reinholdt LA[§]. Genetic variation influences pluripotent ground state stability in mouse embryonic stem cells through a hierarchy of molecular phenotypes. *Cell Stem Cell* 2020 Sep 3;27(3):459-469.e8. <https://doi.org/10.1016/j.stem.2020.07.005>.
[§]Corresponding authors.
 - Research Preview in Cell Stem Cell: <https://doi.org/10.1016/j.stem.2020.08.012>
 - JAX Research Highlight: <https://www.jax.org/news-and-insights/2020/october/exploring-early-development>
14. Ortmann D, Brown S, Czechanski A, Aydin S, Tomaz RA, Osnato A, Skelly DA, Choi T, Churchill GA, Baker CL, **Munger SC**, Reinholdt LG, and Vallier L. Genetic background impacts on variability of ground state pluripotent stem cell lines. *Cell Stem Cell* 2020 Sep 3;27(3):470-481.e6. <https://doi.org/10.1016/j.stem.2020.07.019>.

13. Ruthig VA, Friedersdorf MB, Garness JA, **Munger SC**, Bunce C, Keene JD, and Capel B. The RNA-binding protein DND1 acts sequentially as a negative regulator of pluripotency and a positive regulator of epigenetic modifiers required for germ cell reprogramming. *Development* 2019 Jul 25; 146(19).
12. Raghupathy N, Choi K, Vincent MJ, Beane GL, Sheppard KS, **Munger SC**, Korstanje R, Pardo-Manual de Villena F, and Churchill GA. Hierarchical analysis of RNA-seq reads improves the accuracy of allele-specific expression. *Bioinformatics* 2018, 34(13):2177-2184.
11. Tyler AL, Ji B, **Munger SC**, Churchill GA, Svenson KL, and Carter GW. Epistatic networks jointly influence phenotypes related to Metabolic Disease and gene expression in Diversity Outbred mice. *GENETICS* 2017, 206(2): 621-639.
10. Chick JM*, **Munger SC***, Simecek P, Huttlin EL, Choi KB, Gatti DM, Raghupathy N, Svenson KL, Churchill GA§, and Gygi SP§. Defining the consequences of genetic variation on a proteome-wide scale. *Nature* 2016, 534: 500-505. *Equal contributors. §Corresponding authors.
9. Morton NM, Beltram J, Carter RE, Michailidou Z, Gorjanc G, McFadden C, Barrios-Llerena M, Rodriguez-Cuenca S, Gibbins M, Aird R, Moreno-Navarrete JM, **Munger SC**, Svenson KL, Gastaldello A, Ramage L, Naredo, G, Zeyda M, Wang ZV, Howie AF, Saari A, Sipila P, Stulnig TM, Gudnasson V, Kenyon CJ, Seckl JR, Walker BR, Webster SP, Dunbar DR, Churchill GA, Vidal-Puig A, Fernandez-Real JM, Emilsson V, and Horvat S. Genetic identification of an adipocyte expressed anti-diabetic target in mice selected for resistance to diet-induced obesity. *Nature Medicine* 2016, 22: 771-779.
8. French JE, Gatti DM, Morgan DL, Kissling GE, Shockley KR, Knudsen GA, Shepard KG, Price HC, King D, Witt KL, Pedersen LC, **Munger SC**, Svenson KL, and Churchill GA. Diversity Outbred mice identify population-based exposure thresholds and genetic factors that influence benzene-induced genotoxicity. *Environmental Health Perspectives* 2014, DOI:10.1289/ehp.1408202.
7. **Munger SC**, Raghupathy N, Choi K, Simons AK, Gatti DM, Hinerfeld DA, Svenson KL, Keller MP, Attie AD, Hibbs MA, Graber JH, Chesler EJ, and Churchill GA. RNA-seq alignment to individualized genomes improves transcript abundance estimates in multiparent populations. *Genetics* 2014, 198(1): 59-73.
6. **Munger SC***, Natarajan A*, Looger LL, Ohler U, and Capel B. Fine timecourse expression analysis reveals cascades of activation and repression and maps a regulator of mammalian sex determination. *PLoS Genetics* 2013, 9(7): e1003630. * Equal contributors.
5. Churchill GA, Gatti DM, **Munger SC**, and Svenson KL. The diversity outbred mouse population. *Mammalian Genome* 2012, 23(9-10): 713-718.
4. Jameson SA, Natarajan A, Maatouk DM, DeFalco T, Cool J, Mork L, **Munger SC**, and Capel B. Temporal transcriptional profiling of somatic and germ cells reveals lineage priming of sexual fate in the fetal mouse gonad. *PLoS Genetics* 2012, 8 (3): e1002575.
3. Cook MS, **Munger SC**, Nadeau JH, and Capel B. (2011) Regulation of male germ cell cycle arrest and differentiation by DND1 is modulated by genetic background. *Development* 2011, 138 (1): 23-32.
2. **Munger SC**, Aylor DL, Syed HA, Magwene PM, Threadgill DW, and Capel B. Elucidation of the transcription network governing mammalian sex determination by exploiting strain-specific susceptibility to sex reversal. *Genes & Development* 2009, 23: 2521-2536.
1. Ross A, **Munger SC**, and Capel B. Bmp7 regulates germ cell proliferation in mouse fetal gonads. *Sexual Development* 2007, 1 (2): 127-137.

Review Articles/ Meeting Reports

2. Musser MA*, **Munger SC***, and Gunn TM. Meeting report of the 26th International Mammalian Genome Conference. *Mammalian Genome* 2013, 24(5-6): 179-89. Meeting Report.
* Equal contributors.
1. **Munger SC** and Capel B. Sex and the circuitry: Progress toward a systems-level understanding of vertebrate sex determination. *Wiley Interdisciplinary Reviews – Systems Biology and Medicine* 2012, doi: 10.1002/wsbm. 1172. Review article.

INVITED PRESENTATIONS

"Using genetic diversity in mice to understand complex biology in humans."

Invited Speaker

Duke University Program in Genetics and Genomics

April 6, 2021

"Using genetic diversity in mice to understand complex biology in humans."

Invited Speaker

Pasteur Institute, Paris, France

September 30, 2019

"Genetic control of pluripotency in embryonic stem cells."

Invited Speaker, Bates Seminar Series

Bates College, Lewiston, ME

February 4, 2019

"Harnessing genetic diversity to discover protein regulatory networks."

Invited Speaker, Genetics & Molecular Biology Seminar Series

University of North Carolina, Chapel Hill, NC

April 6, 2018

"Harnessing genetic diversity to discover protein regulatory networks."

Invited Guest Lecture, Next Generation Sequencing Analysis Course

Wellcome Trust Sanger Institute, Genome Campus, Hinxton, UK

October 5, 2017

"Harnessing genetic diversity to discover protein regulatory networks."

3rd Annual JAX-EWHA Scientific Symposium

EWHA Women's University, Seoul, South Korea

August 30, 2017

"Harnessing genetic diversity to discover protein regulatory networks."

Applied Bioinformatics Course

Mount Desert Biological Laboratory, Salisbury Cove, ME

July 13, 2017

"Harnessing genetic diversity to discover protein regulatory networks."

Vanderbilt Genetics Institute

Vanderbilt University, Nashville, TN

May 21, 2017

"Death by a thousand (genetic) cuts."

Maine Science Festival, Invited "5-Minute Genius" Talk
Link: <https://www.youtube.com/watch?v=GRbWtyJ2n9I>
March 19, 2017

"Harnessing genetic diversity to discover protein regulatory networks."
School of Biology and Ecology Seminar
University of Maine, Orono, ME
March 3, 2017

"Harnessing genetic diversity to discover protein regulatory networks."
Department of Genetics Invited Seminar
Tufts University Sackler Medical School, Boston, MA
September 14, 2016

"Defining the consequences of genetic variation on a proteome-wide scale."
43rd Maine Biological and Medical Sciences Symposium
Mount Desert Biological Laboratory, Hulls Cove, ME
April 29, 2016

"Systems genetic approaches to understanding normal development, disorder, and disease."
Genome Science Seminar Series, Host: Charles Farber
University of Virginia, Charlottesville, VA
November 19, 2014

"Exploring the genetics of transcript and protein abundance in the murine liver."
Invited Seminar, Host: Steven Gygi, Harvard Medical School, Boston, MA
October 10, 2014

"RNA-seq alignment to individualized genomes."
Environmental Genomics Short Course, Mount Desert Island Biological Laboratory, Salisbury Cove, ME
August 6, 2014

"RNA-seq alignment to individualized genomes."
Invited Seminar, Host: Darren Logan, Wellcome Trust Sanger Institute, Hinxton, UK
May 23, 2014

"Finding sex in the circuitry: Toward a predictive network model of mammalian sex determination."
Behavior, Ecology, Evolution, and Systematics Invited Seminar, Host: Thomas Kocher
University of Maryland, College Park, MD
March 24, 2014

"A systems genetic analysis of the dynamic transcription network governing primary sex determination."
Invited Seminar, Host: April Binder, National Institute of Environmental Health Sciences, Triangle Park, NC
August 22, 2011

PRESENTATIONS & POSTERS

"Genetic dissection of chromatin accessibility and transcript abundance underlying ground state pluripotency in mouse embryonic stem cells."
(oral platform presentation selected from submitted abstract)
Population, Evolutionary, and Quantitative Genetics (PEQG-GSA) 2018 Meeting, Madison, WI

“Lessons from combined transcriptomic and proteomic studies in genetically diverse mice.”
(oral platform presentation selected from submitted abstract)
Mammalian Genetics and Genomics: From Molecular Mechanisms to Translational Applications
EMBL-Heidelberg, Germany 2017

“Conserved and tissue-specific effects of natural genetic variation on transcript and protein abundance.”
(poster talk and Reviewer’s Choice Abstract Award)
American Society of Human Genetics 2016, Vancouver, BC

“Conserved and tissue-specific effects of natural genetic variation on transcript and protein abundance.”
(oral platform presentation selected from submitted abstract)
The Allied Genetics Conference 2016, Orlando, FL

“Post-translational mechanisms buffer protein abundance against transcriptional variation.”
(oral platform presentation selected from submitted abstract)
International Mammalian Genome Conference 2015, Yokohama, Japan

“Post-translational mechanisms buffer protein abundance against transcriptional variation.”
(oral platform presentation selected from submitted abstract)
American Society of Human Genetics Meeting 2015, Baltimore, MD

“Genetic control of transcript and protein abundance in the liver.” (oral presentation)
Meeting of the National Centers for Systems Biology 2015, Albuquerque, NM

“Genetic control of transcript and protein abundance in the liver.”
(oral presentation selected from submitted abstract)
28th International Mammalian Genome Conference 2014, Bar Harbor, Maine

“Allele specific expression and eQTL in diploid genomes.” (poster)
American Society of Human Genetics Meeting 2014, San Diego, CA

“Reconsidering the laboratory mouse.” (oral presentation)
Genomics of Common Diseases 2014 Meeting, Potomac, MD

“Dissection of expression quantitative trait loci in the Diversity Outbred mouse population.”
(oral presentation selected from submitted abstract)
13th Annual Meeting of the Complex Trait Community 2014, Berlin, Germany

“RNA-seq alignment to individualized transcriptomes.” (poster)
American Society of Human Genetics Meeting 2013, Boston, MA

“RNA-seq alignment to individualized diploid transcriptomes reveals extensive local genetic regulation and differential allelic expression in outbred DO mice.” (oral presentation selected from submitted abstract)
27th International Mammalian Genome Conference 2013, Salamanca, Spain

“RNA-seq alignment to individualized genomes.”
(oral presentation selected from submitted abstract)
12th Annual Meeting of the Complex Trait Community 2013, Madison, WI
Chicago Prize for Outstanding Oral Presentation

“RNA-seq alignment to individualized genomes.”
(oral presentation selected from submitted abstract)
40th Maine Biological and Medical Sciences Symposium 2013, Salisbury Cove, ME

“Expression QTL mapping in the Diversity Outbred mouse population.”
(oral presentation selected from submitted abstract)
26th International Mammalian Genome Conference 2012, St. Pete Beach, FL

“Expression QTL mapping in the Diversity Outbred mouse population.” (poster)
Annual Meeting of the National Centers for Systems Biology 2012, Chicago, IL

“Expression QTL mapping in the Diversity Outbred mouse population.”
(oral presentation selected from submitted abstract)
11th Annual Meeting of the Complex Trait Community 2012, Paris, France
Best Oral Presentation by a Post-Doctoral Fellow

“Systems genetic analysis reveals a complex and highly dynamic transcription network governing sex determination.” (oral presentation selected from submitted abstract)
Mouse Genetics 2011, Washington, DC
Awarded the Verne Chapman Memorial Young Scientist Prize

“Systems genetic analysis of gonadogenesis in mice reveals a dynamic transcription network governing sex determination and testis organogenesis.” (poster)
Duke School of Medicine 1st Annual Basic Science Day 2010, Durham, NC

“Systems genetic analysis of gonadogenesis in mice reveals a dynamic transcription network governing sex determination and testis organogenesis.” (poster)
Annual Meeting of the National Centers for Systems Biology 2009, Bethesda, MD

“Integrating genetics and genomics to elucidate the transcription networks governing sex determination and testis organogenesis in mice.”
(oral presentation selected from submitted abstract)
Symposium on the Biology of Vertebrate Sex Determination 2009, Kona, HI

“Integrating genetics and genomics to elucidate the transcription networks governing sex determination and testis organogenesis in mice.” (oral presentation)
3rd Annual Duke Center for Systems Biology Symposium 2008, Durham, NC

“Integrating genetics and genomics to elucidate the transcription networks governing organogenesis.”
(oral presentation selected from submitted abstract)
7th Annual Meeting of the Complex Trait Consortium 2008, Montreal, Quebec
Best Oral Presentation by a Graduate Student

“Whole-genome expression profiling of embryonic male gonads at the time of sex determination reveals significant differences between the C57BL/6J and 129S1/ImJ inbred mouse strains.” (poster)
Society for Developmental Biology Southeast Regional Conference 2007, Chapel Hill, NC

TEACHING EXPERIENCE & MENTORING

Spring 2022	Taught two sessions of the Tufts Mammalian Genetics Course
Fall 2021	Mentored Tufts rotating graduate student Jaycee Choi
Summer 2021	Mentored JAX Summer Student Program student Samantha Ardery
Spring 2021	Taught two sessions of the Tufts Genetics Course
Winter 2021	Mentored Tufts rotating graduate student Sherrea Brown
Fall 2020	Gave the opening lecture on complex traits for the JAX Cube Educational Series
Summer 2020	Lectured on “21 st Century Mouse Models” at the McKusick Short Course on Medical and Experimental Mammalian Genetics
Spring 2020	Mentored Tufts rotating graduate student Luke Parsley

Summer 2019	Mentored JAX Summer Student Program student Stephanie Hoyt
Summer 2018	Mentored JAX Summer Student Program student Benjamin Allen-Rahill
Spring/Fall 2017-2021	Primary course instructor for The Genome Access Course (Cold Spring Harbor Laboratory, NY)
Summer 2017-2018	Mentored JAX Summer Student Program student Douglas Perkins
Fall 2016-Current	Served on eight graduate student thesis committees
Fall 2016	Taught 1-hour systems genetics lecture at The Genome Access Course (Cold Spring Harbor Laboratory, NY)
Fall 2016-Spring 2017	Mentored two MDI high school students on independent research projects
Summer 2015-2020	Annual McKusick Short Course on Medical and Experimental Mammalian Genetics Taught two 1-hour workshops on RNA-seq statistical experimental design and analysis.
Summer 2016	Mentored Tufts rotating graduate student Candice Byers
Spring 2016	Mentored Tufts rotating graduate student Alex Stanton (joined lab Summer 2016).
Fall 2014	Mentored local high school student on senior independent research project.
Summer 2014 & Summer 2015	Annual JAX Short Course on Experimental Models of Human Cancer Developed and led a 2-hour problem-driven training session that explored the power of common genome browsers for guiding gene discovery in cancer biology.
Summer 2014 & Summer 2013	Journal Club – The Jackson Laboratory Summer Student Program Mentored two groups of talented high school and college students to present and critique recent high-profile genome-wide association and next generation sequencing studies.
Spring 2014 - Spring 2019	Mammalian Genetics Course - Tufts University/University of Maine Taught two 2-hour classes on genetic mapping and RNA-seq analysis. Designed data-driven exam questions to test students' comprehension of concepts and applications.
October 2012-2014 Summer 2013-2014 2016-2019	Developed and led a 3-hour training session on all aspects of RNA-seq analysis. Applied Bioinformatics Course – Mount Desert Island Biological Laboratory Presented a lecture on methods for RNA-seq analysis in diverse populations.
Fall 2013 & 2014	Computational Methods in Biology/Genomics – University of Maine Presented a one-hour lecture on methods for RNA-seq alignment and quantitation.
May 2013	Workshop on Modern Approaches to High Throughput Sequencing Presented a one-hour lecture on methods for RNA-seq alignment and quantitation.
Spring 2016-2019	Genetics Journal Club – Tufts University Facilitated three journal club sessions focused on genome-wide association studies. Mentored student presenters on experimental design and results.
Spring 2012	RNA-seq Interest Group – The Jackson Laboratory Initiated a new interest group at the laboratory centered on RNA-seq, and led seven monthly 1-hour sessions covering all aspects of RNA-seq analysis from RNA extraction to expression quantitation and differential expression analysis.
Summer 2011	Summer Fellows Program – Duke IGSP Center for Systems Biology Mentored a talented undergraduate student from North Carolina State University on an independent systems biology research project.
Spring 2010 & Spring 2009	Undergraduate Independent Study Program – Duke University Mentored two Duke undergraduate students on independent research projects.
Spring 2007	Genetics and Molecular Biology – Biology 118, Duke University Served as a graduate teaching assistant in a large undergraduate genetics course. Led weekly study sections, held office hours, and graded midterm and final exams.

PROFESSIONAL MEMBERSHIPS & SERVICE

Ad hoc reviewer for: *Nature*
Nature Genetics
Genome Research
GENETICS
G3: Genes | Genomes | Genetics
Bioinformatics
Circulation: Cardiovascular Genetics
ELife
Experimental Cell Research
Frontiers Neuroscience
Nucleic Acids Research
NPG Systems Biology and Applications
mBio
PLoS Genetics
PLoS Computational Biology
BMC Developmental Biology
NIEHS Environmental Health Perspectives

Guest associate editor: *PLoS Genetics*

Member of: Genetics Society of America (2011 - current; APC member 2018 – 2020 term; Elected to the Board of Directors 2020 – 2022 term; Executive Committee 2021 – 2022)
International Mammalian Genome Society (2010 – current; Served on the Secretariat 2011 – 2013, Elected to the Secretariat for 2015 – 2017 term)
American Society of Human Genetics (2011 - current)
Genetics Society of America (2011 - current; APC member 2018 – 2020 term; Board of Complex Trait Community (2009 – current)

Session Chair: Mammalian Genetics and Genomics: From Molecular Mechanisms to Translational Applications 2017, EMBL, Heidelberg, Germany
44th Maine Biological Medical Sciences Symposium 2017, Bar Harbor, ME
The Allied Genetics Meeting 2016, Orlando, FL
13th Annual Meeting of the Complex Trait Community 2014, Berlin, Germany
27th International Mammalian Genome Conference 2013, Salamanca, Spain
26th International Mammalian Genome Conference 2012, St. Pete Beach, FL
11th Annual Meeting of the Complex Trait Community 2012, Paris, France

External Service: Chair, Conferences Committee, Genetics Society of America 2021 – 2023 term
Board of Directors, Genetics Society of America 2020 – 2022 term
Mouse Representative, Allied Planning Committee 2020, Genetic Society of America
Secretariat of International Mammalian Genome Society 2011 – 2013, 2015 – 2017
Organizing committee for Maine Biological Medical Sciences Symposium 2016 – 2018
Abstract Review Committee, American Society of Human Genetics 2018 Meeting