

# STEVEN C. MUNGER, Ph.D.

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## PROFILE

### *Using Genetic Diversity as a Tool for Biological Discovery*

The Munger Lab combines multi-scale genomics technologies with advanced statistical methods in genetically diverse mice and stem cell models – an integrative approach called “systems genetics” – to decode how population-level genetic differences influence gene regulation, cell differentiation, organ function, and disease. My highly collaborative team of computational and experimental scientists study diverse systems ranging from embryonic stem cells to mouse models of cancer cachexia, with the common thread being our embrace and use of genetic diversity to discover new biology. Projects in my lab take advantage of the Diversity Outbred (DO) heterogeneous stock and Collaborative Cross (CC) recombinant inbred lines, complementary mouse populations that were specifically designed to segregate high gene diversity with a balanced population structure to provide high genetic mapping power and resolution. This abundance of genetic variation has important consequences for studies of gene regulation, as nearly every gene harbors multiple variants that may alter its regulation or function. The effects of these natural gene perturbations can be measured and combined with genetic mapping to identify the variant(s) underlying a phenotype of interest *and* reconstruct the causal chain of molecular and cellular events that link the two. Over the past 8 years, my lab has utilized these powerful mouse resources and systems genetics approaches to define the consequences of genetic variation on post-transcriptional regulation of the adult liver proteome and establishment and maintenance of ground state pluripotency in embryonic stem cells, and we are now applying our genetic understanding of gene regulation to build better cell and animal models of human disease.

## 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**

2022 – Present

The Jackson Laboratory, Bar Harbor, ME

*Associate Professor*

2015 – 2022

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**

2023 Appointed as mammalian field representative to the Allied Program Committee  
*The Allied Genetics Conference 2024, Genetics Society of America*

2022 Appointed to the Nominating Committee, Genetics Society of America

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 the Allied Program Committee  
*The Allied Genetics Conference 2020, Genetics Society of America*

2018 Commencement Speaker, Sumner Memorial High School, Sullivan, Maine

2017 Recipient of the Alford Leaders Award, The Harold Alford Foundation

2016 Reviewer's Choice Abstract Award  
*American Society of Human Genetics Meeting*

2015 – 2017 term Elected to Secretariat of the International Mammalian Genome Society

2013 – 2015 Ruth L. Kirschstein National Research Service Award  
*Individual postdoctoral fellowship*

2011 – 2013 The Jackson Laboratory Fellowship  
*Institution-awarded competitive fellowship*

2013 Chicago Prize for Outstanding Oral Presentation  
*12<sup>th</sup> Annual Meeting of the Complex Trait Community*

2012 Best Oral Presentation by a Post-Doctoral Fellow  
*11<sup>th</sup> Annual Meeting of the Complex Trait Community*

2011 Verne Chapman Memorial Young Scientist Award  
*International Mammalian Genome Society*

2008 Best Oral Presentation by a Graduate Student  
*7<sup>th</sup> Annual Meeting of the Complex Trait Consortium*

2004 – 2006 NIH Predoctoral Training Grant  
*Institution-awarded fellowship*

## **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

26. Zhang T, Keele GR, Gyuricza IG, Vincent M, Brunton C, Bell TA, Hock P, Shaw GD, **Munger SC**, de Villena FPM, Ferris M, Paulo JA, Gygi SP, Churchill GA. Multi-omics analysis identifies drivers of protein phosphorylation. *Genome Biology* 2023 Mar 21; 24(1):52. <https://doi.org/10.1186/s13059-023-02892-2>.
25. Aydin S, Pham DT, Zhang T, Keele G, Skelly DA, Pankratz M, Choi T, Gygi SP, Reinholdt LG<sup>§</sup>, Baker CL<sup>§</sup>, Churchill GA<sup>§</sup>, **Munger SC**<sup>§</sup>. Genetic dissection of the pluripotent proteome through multi-omics data integration. *Cell Genomics* 2023 Mar 23;3(4):100283. <https://doi.org/10.1016/j.xgen.2023.100283>.  
<sup>§</sup>Corresponding authors.
24. 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>.
23. 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>.
22. 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>.
21. 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 reproduce clinical variation and cytokine responses in COVID-19. *bioRxiv* 2023 Apr 21; 2021.09.17.460664. <https://doi.org/10.1101/2021.09.17.460664>. (Article in press at *Nature Communications*)
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, Ndukum 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 Hallgrímsson 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<sup>§</sup>, **Munger SC**<sup>§</sup>, Baker CL<sup>§</sup>, and Reinholdt LA<sup>§</sup>. 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>.  
<sup>§</sup>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<sup>§</sup>, and Gygi SP<sup>§</sup>. Defining the consequences of genetic variation on a proteome-wide scale. *Nature* 2016, 534: 500-505. \*Equal contributors. <sup>§</sup>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 26<sup>th</sup> 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

“The stories that SNPS tell: Genetic diversity as a tool for biological discovery.”

Invited Speaker

Michigan Tech University Biological Sciences Seminar Series

January 2023 [[Link](#)]

Virtual Symposium - “Using New Approach Methodologies to Address Variability and Susceptibility Across Populations”

Invited Panelist

National Institute of Environmental Health Sciences

October 2022

“The stories that SNPS tell: Genetic diversity as a tool for biological discovery.”

Invited Lecturer

Mouse Development, Stem Cells, & Cancer Course

Cold Spring Harbor Laboratory

June 2022

“Using genetic diversity in mice to understand complex biology in humans.”

Invited Speaker

Duke University Program in Genetics and Genomics

April 6, 2021

Invited guest on the Maine Science Podcast

April 1, 2021 [[Link](#)]

"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."  
3<sup>rd</sup> 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."  
43<sup>rd</sup> 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)  
28<sup>th</sup> 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)  
13<sup>th</sup> 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)  
27<sup>th</sup> International Mammalian Genome Conference 2013, Salamanca, Spain

“RNA-seq alignment to individualized genomes.”  
(oral presentation selected from submitted abstract)  
12<sup>th</sup> 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)  
40<sup>th</sup> 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)  
26<sup>th</sup> 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)  
11<sup>th</sup> 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 1<sup>st</sup> 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)

3<sup>rd</sup> 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)

7<sup>th</sup> 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**

Winter 2023	Mentored UMaine rotating graduate student Courtney Willey
Spring/Fall 2017-2023	Primary course instructor for The Genome Access Course (Cold Spring Harbor Laboratory, NY)
Fall 2022	Taught two sessions of the Tufts Mammalian Genetics Course
Summer 2015-2023	Annual McKusick Short Course on Medical and Experimental Mammalian Genetics Taught workshops on RNA-seq statistical experimental design and analysis.
Summer 2022	Mentored JAX Summer Student Program student Bryant Luna Ramos
Spring 2022	Taught two sessions of the Tufts Mammalian Genetics Course
Spring 2022	Lectured on gene expression regulation at the JAX Short Course on the Genetics of Addiction
Winter 2022	Mentored JAX Post-doctoral Fellow Dr. Abdulfatai Tijjani
Fall 2021	Mentored Tufts rotating graduate student Jaycee Choi
Fall 2021	Mentored Post-baccalaureate researcher Samantha Ardery
Summer 2021	Mentored JAX Summer Student Program student Samantha Ardery
Summer 2021-2023	Lectured on “21 <sup>st</sup> Century Mouse Models” at the McKusick Short Course on Medical and Experimental Mammalian Genetics
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 <sup>st</sup> 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
Winter 2018	Mentored JAX Post-doctoral Fellow Dr. Selcan Aydin
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 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*  
*Molecular Biology and Evolution*  
*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, 2023 – 2024 term; Elected to the Board of Directors 2020 – 2022 term; Executive Committee 2021 – 2022, Nominating Committee 2022 – 2024 term)  
International Mammalian Genome Society (2010 – current; Served on the Secretariat 2011 – 2013 [Verne Chapman Award winner 2011], Elected to the Secretariat for 2015 – 2017 term)  
American Society of Human Genetics (2011 – current; ASHG2017 Abstract Reviewer)  
Complex Trait Community (2009 – current)
- Session Chair: The Allied Genetics Meeting 2020, Washington DC (Moved to Virtual Format)  
Mammalian Genetics and Genomics: From Molecular Mechanisms to Translational Applications 2017, EMBL, Heidelberg, Germany  
44<sup>th</sup> Maine Biological Medical Sciences Symposium 2017, Bar Harbor, ME  
The Allied Genetics Meeting 2016, Orlando, FL  
13<sup>th</sup> Annual Meeting of the Complex Trait Community 2014, Berlin, Germany  
27<sup>th</sup> International Mammalian Genome Conference 2013, Salamanca, Spain  
26<sup>th</sup> International Mammalian Genome Conference 2012, St. Pete Beach, FL  
11<sup>th</sup> Annual Meeting of the Complex Trait Community 2012, Paris, France
- Service: Member, Allied Planning Committee 2024, Genetics Society of America  
Member, Board of Directors, Genetics Society of America 2020 – 2022 term  
Member, Executive Committee, Genetic Society of America 2021 – 2022 term  
Chair, Conferences Committee, Genetics Society of America 2021 – current  
Member, Nominating Committee, Genetics Society of America 2022  
Mouse Representative, Allied Planning Committee 2020, Genetics 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