Amelia Weber Hall, PhD

ahall@broadinstitute.org • Broad Institute of MIT and Harvard • (774) 270-0589

Education

Ph.D. **Microbiology** (2017),
University of Texas at Austin, Austin, TX

B.S. **Molecular Genetics** (2007),
University of Rochester, Rochester, NY

Honors and Awards

Broad Institute Staff Scientists Distinction Award in Management and Mentorship, 2022
AHA GPM Young Investigator Award, 2019
AHA Atrial Fibrillation SFRN Fellowship, 2018, 2019
Outstanding Teaching Assistant Award, 2017
Graduate School Summer Fellowship, 2015, 2016
Ethel and Robert L. Terry Memorial Scholarship, 2012, 2015

Experience

Research Scientist I, Advised by Dr. Charles Epstein, Epigenomic Platform and Gene Regulation Observatory, the Broad Institute of MIT and Harvard, Cambridge, MA. 07/2021 – present

- Standardized a protocol for performing SHARE-seq (a single cell multiomic protocol that profiles ATAC and RNA sequencing data at the same time) with members of the Buenrostro laboratory
- Developed and refined a protocol for isolating intact nuclei from frozen cadaveric human tissue
- Trained three research assistants in the above protocol as well as basic molecular biology and epigenetic techniques (such as qPCR usage, basics of data analysis for ChIP).
- Lead an informal computational biology bootcamp/journal club on the analysis of NGS data using the Google cloud platform Terra, focus was wetbench scientists with minimal computational biology knowledge. Topics covered: R: ggplot2, ArchR, DEseq2, Seurat. Python: scanpy.

Research Fellow, Advised by Dr. Patrick Ellinor, Cardiovascular Research Center, Massachusetts General Hospital, Boston, MA and the Broad Institute of MIT and Harvard, Cambridge, MA. 11/2017 – 07/2021

- Conducted bench and computational research on the genetics of cardiovascular disease, with particular attention to atrial arrhythmias
- Standardized a protocol for performing ChIP-seq in a bank of frozen human left atrial tissue samples
- Developed a computational pipeline for processing ChIP-seq data using Unix, bash scripting, Python, R
- Developed a pipeline for processing RNA-seq data using Kallisto, DEseq2, tximport and R Bioconductor
- Annotated SNP data using external databases to provide genomic context for disease associated SNPs identified in genome wide association studies
- Implemented initial computational processing pipeline for single cell RNA-seq data (10X Genomics), developed transcriptome gtfs for non-model organisms such as rat and pig

Graduate Research Assistant, Advised by Dr. Vishwanath Iyer, Department of Molecular Biosciences, The University of Texas at Austin, Austin, TX 5/2011 – 7/2017

- Directed research on profiling the epigenome and transcriptome of primary human glioblastoma samples
- Established and optimized protocol for performing ChIP in primary brain tumors
- Developed a pipeline for primary analysis of ChIP sequence data (alignment, peak calling, quality control metrics), and visualization of ChIP data using R and Python
- Collaborated on computational modelling of amino acid conservation in calmodulin across a large set of phyla with the Aldrich laboratory

Laboratory Technician, Advised by Dr. Richard Aldrich, Section of Neurobiology, The University of Texas at Austin, Austin, TX 2007 – 2010

- Developed protein mutagenesis protocol to selectively add non-natural amino acids to calcium binding sites for optical measurement of calcium binding strength

Undergraduate Research Assistant, Advised by Dr. Vera Gorbunova, University of Rochester, Rochester, NY 2006 – 2007

- Defended undergraduate thesis: The Effects of Irradiation, Oxidative Damage and Oncogenic Senescence on DNA Repair Efficiency in Human Dermal Fibroblasts, Spring 2007

Student Technician, Educational Technology Center, University of Rochester, Rochester, NY 2003 – 2007

Summer Programming Intern, IntrinsiQ Research, Inc., Waltham, MA 2004 – 2006

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Publications

Nauffal V, Morrill VN, Jurgens SJ, Choi SC, **Hall AW**, et al. Monogenic and Polygenic Contributions to QTc Prolongation in the Population. *Circulation,* 2022. PMID: 35389749; PMCID: PMC9117504.

O'Brien S, Holmes AP, Johnson D, Kabir SN, O'Shea C, O'Rielly M, Avezzu A, Reyat JS, **Hall AW**, et al. Increased atrial effectiveness of flecainide conferred by altered biophysical properties of sodium channels. *J Mol Cell Cardiol.,* 2022. PMID: 35114252.

Jurgens SJ, Choi SC, Morrill VN, Chaffin MD, Pirrucello JP, Halford JL, Weng LC, Nauffal V, Roselli CR, **Hall AW**, et al. Analysis of rare genetic variation underlying cardiometabolic diseases and traits among 200,000 individuals in the UK Biobank. *Nature Genetics,* 2022. PMID: 35177841; PMCID: PMC8930703.

Pirrucello JP, Chaffin MD, Chou EL, Fleming SJ, Lin H, Nekoui M, Khurshid S, Friedman S, Bick AG, Arduini, A, Weng LC, Choi SC, Akkad A-D, Batra P, Tucker NR, **Hall AW**, et al. Deep learning enables genetic analysis of the human thoracic aorta. *Nature Genetics,* 2022. PMID: 34837083 PMCID: PMC8758523.

Choi SC, Jurgens SJ, Haggerty CM, **Hall AW**, et al. Rare Coding Variants Associated With Electrocardiographic Intervals Identify Monogenic Arrhythmia Susceptibility Genes: A Multi-Ancestry Analysis. *Circulation: Precision and Genomic Medicine,* 2021. PMID: 34319147; PMCID: PMC8373440

Hall AW, Chaffin M, Roselli C, et al. Epigenetic Analyses of Human Left Atrial Tissue Identifies Gene Networks Underlying Atrial Fibrillation. *Circulation: Precision and Genomic Medicine,* 2020. PMID: 33155827.

Weng L-C*, **Hall AW***, Choi SC, Jurgens SJ, et al. Genetic Determinants of Electrocardiographic P-wave Duration and Relation to Atrial Fibrillation. *Circulation: Precision and Genomic Medicine,* 2020. PMID: 32822252.

Tucker NR, Chaffin M, Fleming SJ, **Hall AW**, et al. Transcriptional and Cellular Diversity of the Human Heart. *Circulation,* 2020. PMID: 32403949.

van Ouwerkerk AF, **Hall AW**, Kadow ZA, Lazarevic S, et al. Epigenetic and Transcriptional Networks Underlying Atrial Fibrillation. *Circulation Research, 2020*. PMID: 32717170.

Ntalla I, Weng L-C, Cartwright JH, **Hall AW**, et al. Multi-ancestry GWAS of the electrocardiographic PR interval identifies 210 loci underlying cardiac conduction. *Nature Communications, 2020*. PMID: 32439900.

Choi SC, Jurgens SJ, Weng L-C, Pirruccello JP, Roselli C, Chaffin M, Lee C, **Hall AW**, Khera AV, Lunetta K, Lubitz SA, Ellinor PT. Monogenic and Polygenic Contributions to Atrial Fibrillation Risk: Results from a National Biobank. *Circulation Research*, 2019. PMID: 31691645.

Zhang M, Hill MC, Kadow ZA, Suh JH, Tucker NR, **Hall AW**, et al. Long-range *Pitx2c* enhancer–promoter interactions prevent predisposition to atrial fibrillation. *Proc Natl Acad Sci USA*. 2019. PMID: 31636200.

Hall AW, Battenhouse AM, Shivram H, Morris AR, Cowperthwaite MC, Shpak M, Iyer VR. Bivalent Chromatin Domains in Glioblastoma Reveal a Subtype-Specific Signature of Glioma Stem Cells. *Cancer Res*. 2018. PMID: 29549165; PMCID: PMC5955797.

Halling DB, Liebeskind BJ, **Hall AW**, Aldrich RW. Conserved properties of individual Ca2+-binding sites in calmodulin. *Proc Natl Acad Sci USA*. 2016. PMID: 26884197; PMCID: PMC4780646.

Mohanty S*, **Hall AW***, Mohanty P, Prakash S, Trivedi C, et al. Novel association of polymorphic genetic variants with predictors of outcome of catheter ablation in atrial fibrillation: new directions from a prospective study (DECAF). *J Interv Card Electrophysiol.* 2016. PMID: 26497660.

Shpak M, **Hall AW**, Goldberg MM, Derryberry DZ, Ni Y, Iyer VR, Cowperthwaite MC. An eQTL analysis of the human glioblastoma multiforme genome. *Genomics*. 2014. PMID: 24607568.

Ni Y, **Hall AW**, Battenhouse A, Iyer VR. Simultaneous SNP identification and assessment of allele-specific bias from ChIP-seq data. *BMC Genet.* 2012. PMID: 22950704; PMCID: PMC3434080.

Li W, Halling DB, **Hall AW**, Aldrich RW. EF hands at the N-lobe of calmodulin are required for both SK channel gating and stable SK-calmodulin interaction. *J Gen Physiol.* 2009. PMID: 19752189; PMCID: PMC2757765.

Seluanov A, Hine C, Bozzella M, **Hall A**, Sasahara TH, Ribeiro AA, Catania KC, Presgraves DC, Gorbunova V. Distinct tumor suppressor mechanisms evolve in rodent species that differ in size and lifespan. *Aging Cell.* 2008. PMID: 18778411; PMCID: PMC2637185.

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Invited Talks and Posters

Epigenetic Analyses Of Human Left Atrial Tissue Identifies Gene Networks Underlying Atrial Fibrillation, Presented webinar for Diagenode. January 2021

Epigenetic Analyses Of Human Left Atrial Tissue Identifies Gene Networks Underlying Atrial Fibrillation AHA Scientific Sessions Genomic and Precision Medicine Young Investigator Award Finalist presentation, Philadelphia, PA. November 2019

Glioblastoma enhancers and bivalent chromatin domains are subtype specific, Department of Molecular Biosciences Retreat, March 2017. **Awarded "Best Poster."**

Modeling Chromatin States to Elucidate Transcriptional Regulation in Glioblastoma, Chromatin, Non-coding RNAs and RNAP II Regulation in Development and Disease, Austin, TX. March 2016 *

Histone Modification Profiling in Glioblastoma Tumors Identifies Enhancer Variability, Big Data in Biology Symposium 2015, Austin, TX. May 2015 *

Histone Modification Profiling in Glioblastoma Tumors Identifies Enhancer Variability, Lost Pines Conference 2014, Smithville, TX. November 2014 *

Epigenetic Profiling and Clustering of Glioblastoma Multiforme, Big Data in Biology Symposium 2014, Austin, TX, May 2014. **Won "Best Graduate Student Poster," award.**

Optimizing ChIP in Cell Lines and Solid Tumors, M.D. Anderson Science Park, Smithville, TX. Nov. 2013

* indicates a poster and talk were presented together. *Titles in italics* indicate only a poster was presented.

Teaching Experience

Single cell and single nucleus RNA sequencing experiments: a practical guide to design and analysis. American Heart Association: Conference on Vascular Discovery, September 21, 2021.

RNA-seq: A practical guide to differential gene expression and pathway analysis. Medical and Population Genetics Primer Series at the Broad Institute. Lecture given on October 1st, 2020.

Using tximport and DEseq2 to identify differentially expressed genes: an interactive Terra tutorial. Medical and Population Genetics Primer Series at the Broad Institute. Lecture given on October 8th, 2020.

Core Next Generation Sequencing Tools on Stampede. Big Data Summer School at UT Austin, Co-instructor May 2017, May 2016, May 2015. Teaching assistant May 2014.

Public Health Bacteriology Laboratory. Teaching assistant under Dr. Suzanne Barth, (BIO361L, Spring, Fall 2016). **Awarded Outstanding Teaching Assistant Award, April 2017**

Working with MySQL Databases. Short Course for Center for Computational Biology and Bioinformatics. Teaching assistant: December 2015, October 2014.

Introduction to ChIP-seq. Short course for Center for Computational Biology and Bioinformatics. Co-instructor November 2015, December 2014.

Skills

Molecular biology:

- Protocol development/experimental design
- Single cell methods, ATAC, RNA
- Epigenetics protocols/Chromatin IP
- RNA-seq, EM-seq

Bioinformatics:

- Single cell multi-omics (RNA and ATAC)
- Single cell RNA-seq
- ChIP-seq, RNA-seq, WGS
- Unix, R, HPC (SGE/SLURM), Python
- Cloud computing (Terra, GCP, Jupyter)
- Data analysis and visualization (ggplot, dplyr, tidyr, tidyverse)