

Scott Allen Funkhouser

Updated January 2017

Education

- 2013-2019** **PhD, Genetics and Quantitative Biology**; Michigan State University
- 2007-2011** **BSc, Biochemistry**; University of Washington
- 2005-2007** **Valedictorian**; Graham-Kapowsin HS

Research Positions

- 2014 - Present** **Graduate Research Assistant**; Mentor: Catherine Ernst PhD; Michigan State University
Investigating the role of A-to-I RNA editing in mammalian genomes and developing methods for the genomic prediction of complex phenotypes.
- 2012 - 2013** **Research Scientist I**; Mentor: Mary Philip MD PhD; University of Washington
Investigated the role of a heme exporter, FLVCR, in the development of T lymphocytes.
- 2010 - 2011** **Undergraduate Research Assistant**; Mentor: Chris Hague PhD; University of Washington
Studied novel binding partners to pertinent G-Protein coupled receptors.

Awards, Grants, Scholarships

USDA Pre-doctoral Fellowship

2017-2019 • \$95,000

ISAG Travel Award

\$2,000 to attend the 2016 ISAG Conference in Salt Lake City, UT

NSIF Graduate Student Travel Award

\$500 to attend 2016 NSIF meeting in Raleigh, NC

Fred and Lucille Stamper Academic College Scholarship

2007 - 2011 • \$16,256

Memberships

ASAS PhD Student Member

2015 – Present

Genetics Student Organization Officer

- 2016-Present: *President*
- 2014-2015: *Second-year Representative*
- 2015-2016: *Third-year Representative and Social Chair*

Selected Graduate Coursework

- Molecular Biology (BMB 801)
- Eukaryotic Molecular Genetics (MMG 835)
- R Programming for Quantitative Genetics (ANS 824)
- Advanced Statistics for Biologists (STT 814)
- Intro to Statistical Genetics (STT 855)
- Bayesian Inference using MCMC (FW 849)

Skills

Programming Listed in order from most skilled to least skilled

- The R language
- C++
- Bash
- Fortran
- Python
- Java

Familiar with others for web development including:

- Markdown
- HTML
- CSS
- Javascript

Bioinformatics Experience using various tools, including:

- Bowtie
- Tophat
- Picard
- SAMTools
- bcftools
- Variant Effect Predictor
- UCSC Genome Browser

Software development

- Git
- Github
- R Studio
- GNU Make

R development packages:

- devtools
- roxygen
- testthat

Literate programming

- knitr
- Rmarkdown
- Shiny

Molecular Biology

- Flow cytometry
- immunostaining
- qPCR
- PCR
- molecular cloning and techniques therein
- cell culture

Publications

1. **Funkhouser SA**, Bates RO, Ernst CW, Newcom D, Steibel JP. Estimation of genome-wide and locus-specific breed composition in pigs. *TAS*. 2017; doi: 10.2527/tas2016.0003
2. Zhao D, Hamilton JP, Hardigan M, Yin D, He T, Vaillancourt B, Reynoso M, **Funkhouser SA** et al. Analysis of ribosome-associated mRNAs in rice reveals the importance of transcript size and GC content in translation. *G3 (Bethesda)*. 2016;7: 203–219. doi:10.1534/g3.116.036020
3. Philip M, **Funkhouser SA**, Chiu EY, Phelps SR, Delrow JJ, Cox J, et al. Heme Exporter FLVCR Is Required for T Cell Development and Peripheral Survival. *J Immunol*. 2015; doi:10.4049/jimmunol.1402172

Pending Publications

1. **Funkhouser SA**, Steibel JP, Bates RO, Raney NE, Schenk D, Ernst CW. Evidence for Transcriptome-wide RNA Editing Among *Sus scrofa* PRE-1 SINE Elements. *bioRxiv*. 2017; Available: [here](#)
2. Reeb PD, **Funkhouser SA**, Ernst CW, Steibel JP. Assessing genotype call accuracy from RNA sequencing data.

Conference Presentations and Posters

- **Funkhouser SA**, Bates RO, CW Ernst, Newcom D, Steibel JP. (2016) Estimation of the composition of four U.S. swine breeds using genomic data. ePoster presented at the 2016 ASDA/AAS Joint Annual Meeting.
- **Funkhouser SA**, Steibel JP, Bates RO, Raney NE, Ernst CW. (2016) RNA editing in swine is associated with PRE-1 retrotransposons. ePoster presented at the 2016 International Society for Animal Genetics Conference.
- **Funkhouser SA**, Steibel JP, Bates RO, Raney NE, Ernst CW. (2015) Evidence of RNA editing in pig *longissimus dorsi* muscle. Oral presentation given at the American Dairy Science / American Society of Animal Science Midwest Conference.

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