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| NAME  Robert James Schaefer, PhD | | POSITION TITLE  Postdoctoral Associate  College of Veterinary Medicine  University of Minnesota | | |
| EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education and include postdoctoral training.)* | | | | |
| INSTITUTION AND LOCATION | DEGREE  *(if applicable)* | | YEAR(s) | FIELD OF STUDY |
| University of Minnesota, Minneapolis, MN | BS | | 2006-10 | Computer Science |
| University of Minnesota, Minneapolis, MN | PhD | | 2010-15 | Biomed. Informatics and Comp. Biology |
| University of Minnesota, St Paul, MN | Fellow | | 2016-18 | NIFA-AFRI Postdoctoral Fellowship |

1. **Positions and Honors**

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| May 2018  April 2018 | Guest Associate Editor Frontiers in Genetics Livestock Genomics  Nominated Figshare Ambassador |
| March 2018 – Present | Mozilla Open Leaders Mentor |
| July 2017 – Present | Co-chair if FAANG Integrative Genomics and Network Biology Working Group |
| January 2017 | Awarded UMII Updraft to attend CSHL Network Biology Meeting |
| November 2016 | Awarded FAANG Travel Grant |
| June 2016 | Mozilla All Hands Travel Award |
| January 2016 | Awarded NIFA Postdoctoral Fellowship |
| December 2015 | Functional Analysis of the Animal Genome (FAANG) Travel Grant |
| November 2015 | NRSP-8 Animal genome coordinator Travel Grant |
| August 2015 | NIFA AFRI Postdoctoral Fellowship |
| June 2015 | Microbial and Plant Genomics Institute Travel Grant Award |
| May 2015 | COGS Travel Award |
| November 2014 | Neal A. Jorgenson Travel Grant Recipient |
| April 2014 | Doctoral Dissertation Fellowship |
| Sept. 2013 - March 2014 | Teaching Assistant, Dept. of Computer Science, CSCI 3003 |
| December 2013 | Equine Genome Workshop Travel Award |
| April 2013 | iHUB ionomics collaborative Travel Grant Recipient |
| February 2012 | Microbial and Plant Genomics Institute Travel Grant Recipient |
| Sept. 2010-2011 | University of Minnesota Interdisciplinary Informatics Initiative Fellowship |
| 2008 - 2010 | Research Assist., Dept. of Veterinary Population Medicine, U. of Minnesota |

1. **Selected Peer-Reviewed Papers**
2. Sabine Felkel, Claus Vogl, Doris Rigler, Viktoria Dobretsberger, Bhanu P Chowdhary, Ottmar Distl, Ruedi Fries, Vidhya Jagannathan, Jan E Janečka, Tosso Leeb, Gabriella Lindgren, Molly McCue, Julia Metzger, Markus Neuditschko, Thomas Rattei, Terje Raudsepp, Stefan Rieder, Carl-Johan Rubin, Robert Schaefer, Christian Schlötterer, Georg Thaller, Jens Tetens, Brandon Velie, Gottfried Brem, and Barbara Wallner. The horse Y chromosome as an informative marker for tracing sire lines. **Nature Scientific Reports** (Accepted). 2019.
3. Felipe Avila, James R. Mickelson, **Robert J. Schaefer**, Molly E. McCue. Genome-wide signatures of selection reveal genes associated with performance in American Quarter Horse subpopulations. **Frontiers in Genetics**. 2018
4. Samantha Beeson, **Robert Schaefer**, Victor Mason, Molly E McCue. Robust remapping of equine SNP array coordinates to EquCab3. **Animal Genetics**. 2018.
5. Victor Mason, **Robert Schaefer**, Molly McCue, Tosso Leeb, Vinzenz Gerber. eQTL Discovery and their Association with Severe Equine Asthma in European Warmblood Horses. **BMC Genomics**. 2018.
6. **Robert J Schaefer**, Jean-Michel Michno, Joseph Jeffers, Owen Hoekenga, Brian Dilkes, Ivan Baxter, Chad Myers. Integrating co-expression networks with GWAS to prioritize causal genes in maize. **The Plant Cell 2018**. DOI: https://doi.org/10.1101/221655
7. S.A. Durward-Akhurst, **R.J. Schaefer**, J.R. Mickelson, M.E. McCue. Understanding genetic variation in the equine population. **Journal of Equine Veterinary Medicine**. DOI: https://doi.org/10.1016/j.jevs.2017.03.088
8. **Robert J Schaefer**, Mikkel Schubert, Ernest Bailey, Danika L. Bannasch, Eric Barrey, Gila Kahila Bar-Gal, Gottfried Brem, Samantha A. Brooks, Ottmar Distl, Ruedi Fries, Carrie J. Finno, Vinzenz Gerber, Bianca Haase, Vidhya Jagannathan, Ted Kalbfleisch, Tosso Leeb, Gabriella Lindgren, Maria Susana Lopes, Nuria Mach, Artur da Câmara Machado, James N. MacLeod, Annette McCoy, Julia Metzger, Cecilia Penedo, Sagi Polani, Stefan Rieder, Imke Tammen, Jens Tetens, Georg Thaller, Andrea Verini-Supplizi, Claire M. Wade, Barbara Wallner, Ludovic Orlando, James R. Mickelson, Molly E. McCue. Development of a high-density, 2M SNP genotyping array and 670k SNP imputation array for the domestic horse. **BMC Genomics**. 2017; DOI: https://doi.org/10.1101/112979.
9. Barbara Wallner, Nicola Palmieri, Claus Vogl, Doris Rigler, Elif Bozlak, Thomas Druml, Vidhya Jagannathan, Tosso Leeb, Ruedi Fries, Jens Tetens, Georg Thaller, Julia Metzger, Ottmar Distl, Gabriella Lindgren, Carl-Johan Rubin, Leif Andersson, **Robert Schaefer**, Molly McCue, Markus Neuditschko, Stefan Rieder, Christian Schlötterer, Gottfried Brem. Y Chromosome Uncovers the Recent Oriental Origin of Modern Stallions. **Current Biology**, 2017; DOI: http://doi.org/10.1016/j.cub.2017.05.086
10. Lin Li, Roman Briskine, **Robert Schaefer**, Patrick S. Schnable, Chad L. Myers, Lex E. Flagel, Nathan M. Springer and Gary J. Muehlbauer. Co-expression network analysis of duplicate genes in maize (Zea mays L.) reveals no subgenome bias. **BMC Genomics**. 4 November 2016. doi: https://doi.org/10.1186/s12864-016-3194-0
11. **Robert J. Schaefer**, Jean-Michel Michno, Chad L. Myers. Unraveling gene function in agricultural species using gene co-expression networks. **Biochimica et Biophysica Acta (BBA) - Gene Regulatory Mechanisms**. 30 July 2016. http://dx.doi.org/10.1016/j.bbagrm.2016.07.016.
12. Mitra AK, Stessman HAF, **Schaefer RJ**, Wang W, Myers CL, Van Ness BG and Beiraghi S (2016) Fine-Mapping of 18q21.1 Locus Identifies Single Nucleotide Polymorphisms Associated with Nonsyndromic Cleft Lip with or without Cleft Palate. **Front. Genet**. 7:88. doi: https://doi.org/10.3389/fgene.2016.00088
13. **Robert J. Schaefer**, Roman Briskine, Nathan M. Springer, Chad L. Myers. Discovering Functional Modules Across Diverse Maize Transcriptional Datasets Using COB, The Co-expression Browser. **PLoS ONE** 12 June 2014 doi: https://doi.org/10.1371/journal.pone.0099193.
14. Mikkel Schubert, Luca Ermini, Clio Der Sarkissian, Hákon Jónsson, Aurélien Ginolhac, **Robert Schaefer**, Michael D. Martin, Ruth Fernández, Martin Kircher, Molly McCue, Eske Willerslev, Ludovic Orlando. Characterization of ancient and modern genomes by SNP detection and phylogenomic and metagenomic analysis using PALEOMIX. **Nature Protocols** 9, 1056-1082 (2014) https://doi.org/10.1038/nprot.2014.063.
15. Annette McCoy, **Robert Schaefer**, Jessica Peterson, Peter Morrell, Megan Slamka, James Mickelson, Stephanie Valberg, Molly McCue. Evidence of Positive Selection for a Glycogen Synthase (GYS1) Mutation in Domestic Horse Populations. **Journal of Heredity**. 2013. doi: https://doi.org/10.1093/jhered/est075