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EDUCATION North Carolina State University, Raleigh, NC USA

Ph.D., Animal Sciences, May 2017.

- Dissertation: Utilizing Genomic Information to Manage the Diversity and Minimize the Unfavorable Effects of Inbreeding in Livestock Populations.
- Advisor: Dr. Christian Maltecca
- Committee: Dr. Melissa Merrill, Dr. Jennie Pryce, Dr. Kent Gray, Dr. Mark Knauer & Dr. Arnab Maity.

North Carolina State University, Raleigh, NC USA

M.S., Statistics, May 2017.

University of Nebraska-Lincoln, Lincoln, NE USA

M.S., Animal Sciences, December 2012.

- Thesis: The Impact of Genetic Background on Body Temperature Regulation in Beef Cattle During Periods of Heat and Cold Stress.
- Advisor: Dr. Matthew Spangler
- Committee: Dr. Merlyn Nielsen, Dr. Daniel Ciobanu, Dr. Steve Kachman & Dr. Larry Kuehn

Iowa State University, Ames, IA USA

B.S., Animal Science major & Genetics minor, December 2010.

WORK

EXPERIENCES

Director of Analytics, Smithfield Foods (December 2021 - Present).

Geneticist, Smithfield Premium Genetics (July 2018 - December 2021).

Post-Doctorate Research Associate, University of Nebraska-Lincoln (June 2017-June-2018).

Graduate Research Assistant, North Carolina State University (Aug 2013-May 2017).

Visiting Scholar at La Trobe University (May 2014-July 2014).

Research Technician, University of Nebraska-Lincoln (Jan 2013-July 2013).

Graduate Research Assistant, University of Nebraska-Lincoln (Jan 2011-Dec 2012).

Progressive Swine Technologies Intern, Columbus, NE (May 2010-Aug 2010).

Research Assistant for the Iowa State University Swine Testing Station (April 2009-Dec 2011).

Iowa Select Farms Intern, Iowa Falls, IA (May 2008-Aug 2008).

TECHNICAL SKILLS

MS Office | SAS | ASreml | UGA suite of programs | R | C++ | linux | LaTeX |
R Shiny | HTML, CSS & Javascript Web Design | SQL | Python.

TEACHING EXPERIENCES

University of Nebraska-Lincoln, Lincoln, NE USA

Teaching Assistant:

- Undergraduate - Beef Industry Scholars Freshman Seminar (2 semesters).
- Undergraduate - Animal Breeding and Genetics Lab Instructor (1 semester).

North Carolina State University, Raleigh, NC USA

Teaching Assistant:

- Undergraduate - Animal Breeding and Genetics (1 semester).
- Undergraduate - Agriculture Genetics (2 semesters).
- Guest Lecture - Quantitative Genetics and Breeding (2 semesters).

SHORT COURSES

University of Sao Paulo / ESALQ, Piracicaba, Sao Paulo, Brazil

- Co-Instructor
- Quantitative Genetics and Genomics Workshop
 - Introduction to single-step methods and evaluations.
 - Genotyping strategies and reducing the complexity of single-step GBLUP.
 - Genomic inbreeding

GRADUATE COMMITTEE

- North Carolina State University, Raleigh, NC
 - Dalton Obermier (Spring 2020; Masters).
 - Zack Peppmeier (Summer 2020; Masters).
- University of Georgia, Athens, GA
 - Mary Kate Hollifield (Spring 2021; Masters).

AWARDS

- Smithfield ROI Innovation grand price winner (Smithfield) 2022.
- Kenneth R. Keller Award for Excellence in Doctoral Dissertation Research (NC State) 2018.
- NC State 2016 Animal Science Graduate Student Award (Research).
- US Graduate Student Travel Bursary Award International Society for Animal Genetics Conference 2016.
- Neal A. Jorgenson Genome Travel Award (Swine) Plant Animal Genome Conference 2016.
- National Swine Improvement Federation, Pork Checkoff Graduate Student Travel Award 2015.
- Targeting Excellence Graduate Student Scholarship Award, Targeting Excellence 2015.
- Department of Animal Science Graduate Student Travel Scholarships, North Carolina State University, 2015.
- Shear-Miles Agricultural Fellowship Award, University of Nebraska-Lincoln, 2012.
- Frank Baker Memorial Scholarship Award, Beef Improvement Federation, 2012.
- David H. & Anne E. Larrick Memorial Travel Fund, University of Nebraska-Lincoln, 2012.

PEER REVIEWED JOURNALS

- 34.) Peppmeier, Z.C., **J. T. Howard**, M.T. Knauer, S.M. Leonard. 2023. Estimating backfat depth, loin depth, and intramuscular fat percentage from ultrasound images in swine. *Animal* **17**:10.
- 33.) Obermier, D.R., **J. T. Howard**, K.A. Gray, M.T. Knauer. 2022. The impact of functional teat number on reproductive throughput in swine. *Translational Animal Science* **7**:1.
- 32.) He, Y., F. Tiezzi, J. Jiang, **J. T. Howard**, Y. Huang, K. Gray, C. Maltecca. Exploring methods to summarize gut microbiota composition for microbiability estimation and phenotypic prediction in swine. *Journal of Animal Science* **100**:9.
- 31.) He, Y., F. Tiezzi, **J. T., Howard**, Y. Huang, K. Gray, C. Maltecca. 2022. Exploring the role of gut microbiota in host feeding behavior among breeds. *BMC Microbiology* **22**:1.
- 30.) He, Y., F. Tiezzi, J. Jiang, **J. T. Howard**, Y. Huang, K. Gray, J.W. Choi, C. Maltecca. 2022. Use of Host Feeding Behavior and Gut Microbiome Data in Estimating Variance Components and Predicting Growth and Body Composition Traits in Swine. *Genes* **13**:5.

- 29.) Chen, S. Y., P. H. F. Freitas, H. R. Oliveira, S. F. Lázaro, Y. Huang, **J. T. Howard**, Y. Gu, A. P. Schinckel, L. F. Brito. 2021. Genotype-by-environment interactions for reproduction, body composition, and growth traits in maternal-line pigs based on single-step genomic reaction norms. *Genetic Selection Evolution* **53**: 1.
- 28.) Hollifield, M. K., D. Lourenco, S. Tsuruta, M. Bermann, **J. T. Howard**, I. Misztal. 2021. Impact of including the cause of missing records on genetic evaluations for growth in commercial pigs. *Journal of Animal Science* **99**:8.
- 27.) He, Y., F. Tiezzi, **J. T. Howard**, C. Maltecca. 2021. Predicting body weight in growing pigs from feeding behavior data using machine learning algorithms. *Computers and Electronics in Agriculture* **184**:106085.
- 26.) Chen, S., P. H. F. Freitas, H. R. Oliveira, S. F. Lázaro, Y. Huang, **J. T. Howard**, Y. Gu, A. P. Schinckel, L. F. Brito. 2021. Genomic analyses of genotype-by-environment interaction for growth, carcass, and reproduction traits in maternal line pigs based on single-step-GBLUP, reaction norm models, and incorporation of X-chromosome markers. *Genetic Selection Evolution* **53**: 51.
- 25.) Hollifield, M. K., D. Lourenco, M. Bermann, **J. T. Howard**, I. Misztal. 2021. Determining stability of accuracy of genomic estimated breeding values in future generations in commercial pig populations. *Journal of Animal Science*, **99**(4): 1-8.
- 24.) He, Y., F. Tiezzi, **J. T. Howard**, C. Maltecca. 2021. Predicting body weight in growing pigs from feeding behavior data using machine and deep learning algorithms. *Computers and Electronics in Agriculture*, **184**, 106085.
- 23.) **Howard, J. T.**, W. Abbas, H. A. Paz, K. E. Hales, J. E. Wells, L. A. Kuehn, M. L. Spangler, G. E. Erickson, S. C. Fernando. 2020. Influence of host genetics in shaping the rumen bacterial community in beef cattle. *Scientific Reports*, **10**, 15101.
- 22.) Bergamaschi, M., F. Tiezzi, **J. T. Howard**, Y. Huang, K. A. Gray, C. Shillebecks, N. P. McNulty, C. Maltecca. 2020. Gut microbiome composition differences among breeds impact feed efficiency in swine. *Microbiome*, **8**, 110.
- 21.) Tiezzi, F., L. Brito, **J. T. Howard**, Y. Huang, K. A. Gray, C. Schwab, J. Fix, C. Maltecca. 2020. Genomics of heat tolerance in maternal-line pigs based on reproductive traits and various environmental covariates. *Frontiers in Genetics*. **11**:629.
- 20.) Supakorn, C., M. I. Christianson, **J. T. Howard**, K. A. Gray & K. J. Stalder. 2019. Heritability estimates for sow prolapse. *Livestock Science*, **227**: 111-113.
- 19.) Sollero, B. P., **J. T. Howard** & M. L. Spangler. 2019. The impact of reducing the frequency of animals genotyped at higher density on imputation and

- prediction accuracies using ssGBLUP. *Journal of Animal Science*, **97(7)**: 2780-2792.
- 18.) Baller, J. L., **J. T. Howard**, S. D. Kachman & M. L. Spangler. 2019. The impact of clustering methods for cross-validation on the accuracy of genomic predictions. *Journal of Animal Science*, **97(4)**: 1534-1549.
 - 17.) Baes, C. F., B. Makanjuola, F. Miglior, G. Marras, **J. T. Howard**, A. Fleming & C. Maltecca. 2018. Symposium review: The genomic architecture of inbreeding: How homozygosity affects health and performance. *Journal of Dairy Science*, **102(3)**: 2807-2817.
 - 16.) **Howard, J. T.**, T. A. Rathje, C. E. Bruns, D. F. Wilson-Wells, S. D. Kachman & M. L. Spangler. 2018. The impact of selective genotyping on the response to selection using single-step genomic best linear unbiased prediction. *Journal of Animal Science*, **96(11)**: 4532-4542.
 - 15.) **Howard, J. T.**, T. A. Rathje, C. E. Bruns, D. F. Wilson-Wells, S. D. Kachman & M. L. Spangler. 2018. The impact of truncating data on predictive ability for single-step genomic best linear unbiased prediction. *Journal of Animal Breeding Genetics* **135(4)**: 251-262.
 - 14.) **Howard, J. T.**, R. E. Baynes, J. D. Brooks, J. L. Yeatts, M. S. Ashwell & C. Maltecca. 2018. Genetic parameter estimates for metabolizing two common pharmaceuticals in swine. *Frontiers in Genetics* **9**:40.
 - 13.) **Howard, J. T.**, F. Tiezzi, Y. Huang, K.A. Gray, C. Maltecca. 2017. A heuristic method to identify runs of homozygosity associated with reduced performance in livestock. *Journal of Animal Science* **95(10)**: 4318-4332.
 - 12.) **Howard, J. T.**, F. Tiezzi, J.E. Pryce, C. Maltecca. 2017. A combined coalescence forward in time simulator software for pedigreed populations undergoing selection for complex traits. *Journal of Animal Breeding Genetics* **134(6)**:553-563.
 - 11.) **Howard, J. T.**, J. E. Pryce, C. Baes, C. Maltecca. 2017. Inbreeding, inbreeding depression, and management of genomic variability in the genomic era. *Journal of Dairy Science* **100(8)**: 6009-6024.
 - 10.) **Howard, J. T.**, R. E. Baynes, J. D. Brooks, J. L. Yeatts, M. S. Ashwell, C. Maltecca. 2017. Gene co-expression network analysis identifies porcine genes associated with variation in metabolizing fenbendazole and flunixin meglumine. *Scientific Reports* **7(1)**: 1357.
 - 9.) **Howard, J. T.**, F. Tiezzi, Y. Huang, K.A. Gray, C. Maltecca. 2016. The use of alternative genomic metrics in nucleus herds to manage the diversity of purebred and crossbred animals. *Genetic Selection Evolution* **48**: 91.

- 8.) **Howard, J. T.**, M. Haile-Mariam, C. Maltecca, J. E. Pryce. 2015. Characterizing Regions Impacting Inbreeding Depression Across United States and Australian Jersey cow populations. *BMC Genomics* **16**: 813.
- 7.) **Howard, J. T.**, A. T. O’Nan, C. Maltecca, R. E. Baynes, M. S. Ashwell. 2015. Differential gene expression across breed and sex in commercial pigs administered fenbendazole and flunixin meglumine. *PLOS One* **10(9)**:e0137830.
- 6.) **Howard, J. T.**, M. Haile-Mariam, C. Maltecca, B. J. Hayes & J. E. Pryce. 2015. Characterizing homozygosity across United States, New Zealand and Australian Jersey cow and bull populations. *BMC Genomics*, **16(1)**: 187.
- 5.) **Howard, J. T.**, S. Jiao, F. Tiezzi, Y. Huang, K. A. Gray, C. and C. Maltecca. 2015. Genome-Wide Association Study on Legendre Random Regression Coefficients for Growth and Feed Intake on Duroc Boars. *BMC Genetics*, **16(1)**: 59.
- 4.) Ahlberg, C. M., L.N. Schiermiester, **J. T. Howard**, C. Calkins & M. L. Spangler. 2014. Genome wide association study of cholesterol and poly- and mono-unsaturated fatty acids, protein, and mineral content of beef from crossbred cattle. *Meat Science*, **98(4)**: 804-814.
- 3.) **Howard, J. T.**, R. E. Baynes, J. D. Brooks, J. L. Yeatts, B. Bellis, M. S. Ashwell, P. Routh, A. T. O’Nan & C. Maltecca. 2014. The effect of breed and sex on Sulfamethazine, Enrofloxacin, Fenbendazole and Flunixin pharmacokinetic parameters in swine. *Journal of Veterinary Pharmacology and Therapeutics*, **37(6)**: 531-541.
- 2.) **Howard, J. T.**, S. D. Kachman, W. M. Snelling, E. J. Pollak, D. C. Ciobanu, L. A. Kuehn & M. L. Spangler. 2014. Beef cattle body temperature during climatic stress: A genome wide association study. *International Journal of Biometeorology*, **58(7)**: 1665-1672.
- 1.) **Howard, J. T.**, S. D. Kachman, M. K. Nielsen, T. L. Mader & M. L. Spangler. 2013. The effect of Myostatin genotype on body temperature during extreme temperature events. *Journal of Animal Science*, **91(7)**: 3051-3058.

REFERRED
ABSTRACTS

- 31.) Graham J. R., J. S. Johnson, A. C. Araujo, H. R. Oliveira, **J. T. Howard**, L. F. Brito. Transgenerational epigenetic variance for production and reproduction traits in maternal-line pigs. ASAS-CSAS-WSASAS Annual Meeting 2021.
- 30.) Speckman, E., **J. T. Howard**, J. G. Wiegert. The relationship between litter size and functional teat number at farrowing on litter size at weaning. Midwest ASAS Meeting. 2021.

- 29.) Tiezzi, F., M. Bergamaschi, **J.T. Howard**, C. Maltecca. Feed efficiency and behavior are associated with gut microbiome in three breeds of pigs. ASAS-CSAS-WSASAS Annual Meeting and Trade Show. Madison WI, 2020.
- 28.) Yuqing H., F. Tiezzi, **J. T. Howard**, C. Maltecca. Predicting body weight in growing pigs at finishing stage using feeding behavior by machine and deep learning algorithms. ASAS-CSAS-WSASAS Annual Meeting and Trade Show. Madison WI, 2020.
- 27.) Spangler, M. L., W. Abbas, **J. T. Howard**, H.Paz, J. Wells, L. Kuehn, K. Hales, S. C. Fernando. Moving beyond rumen microbiota composition to identify interactions between the host genotype and rumen functional phenotype to identifying genetic markers and microbial functions that influence feed efficiency. Plant & Animal Genome XXVII Conference. San Diego, CA. 2019.
- 26.) Christianson, M. I., C. Supakorn, **J. T. Howard**, K. A. Gray, K. J. Stalder. 2019. Heritability estimates for sow prolapse. Midwest ASAS Meeting.
- 25.) Abbas, W., **J. T. Howard**, H. A. Paz, K. E. Hales, J. E. Wells, L. A. Kuehn, M. L. Spangler, G. E. Erickson, S. C. Fernando. 2019. Host genetics help shape the rumen microbiome in beef cattle. Midwest ASAS Meeting.
- 24.) Baller, J. L., **J. T. Howard**, S. D. Kachman, & M.L. Spangler. 2019. A comparison of the estimated accuracy of prediction of molecular breeding values in Red Angus cattle using clustering methods for cross-validation. Midwest ASAS Meeting.
- 23.) Sollero, B., **J. T. Howard**, V. Junqueira, F. Cardoso & M. Spangler. 2019 The Impact of Reducing the Frequency of Animals Genotyped at Higher Density on Imputation and Prediction Accuracies Using ssGBLUP. Plant & Animal Genome XXVII Conference. San Diego, CA. 2019.
- 22.) Maltecca, C., **J.T. Howard**, C.F. Baes, J.E. Pryce. 2018. Beyond predictions: managing variability in the genomic era . ASAS National Meeting 2018.
- 21.) Baes, C.F., F. Miglior, B. Mamanuola, C. Vogelzang, F. Schenkel, **J.T. Howard**, C. Maltecca, G. Marras. 2018. The genomic architecture of inbreeding: How homozygosity affects health and performance in dairy cattle. ADSA National Meeting 2018.
- 20.) Maltecca, C., G. Gebregiwergis, **J.T. Howard**, C.F. Baes, F. Tiezzi. 2018. Managing population diversity through optimal contribution selection with the use of genomic information. ADSA National Meeting 2018.
- 19.) **Howard, J. T.**, T. A. Rathje, C. E. Bruns, D. F Wilson-Wells, S. D. Kachman & M. L. Spangler. 2018. The impact of truncating data on the predictive ability of selection candidate EBV in swine using ssGBLUP. J. Anim. Sci. 96: 18-19.

- 18.) Marras, G., **J. T. Howard**, P. Martin, A. Fleming, K. Alves, F. Schenkel, F. Miglior, C. Maltecca & C.F. Baes. 2018. Identification of unfavourable homozygous haplotypes associated with with milk and fertility traits in Holsteins. In the 11th World Congress on Genetics Applied to Livestock Production. Auckland, New Zealand. 11.767.
- 17.) **Howard, J. T.**, S. D. Kachman, & M. L. Spangler. 2018. The impact of utilizing previous generations of genotyped animals in genomic selection. In the 11th World Congress on Genetics Applied to Livestock Production. Auckland, New Zealand. 11.172.
- 16.) **Howard, J. T.**, F. Tiezzi, C. Maltecca. Computational Aspects of Characterizing Genomic Inbreeding in Livestock. ADSA Annual Meeting, Pittsburgh, Pennsylvania, June 25-28.
- 15.) **Howard, J. T.**, F. Tiezzi, J.E. Pryce & C. Maltecca. A combined coalescence forward in time simulator software for pedigreed populations undergoing selection for complex traits. *J. Anim. Sci.* 94(S5): 143-144.
- 14.) **Howard, J. T.**, F. Tiezzi, Y. Huang, K.A. Gray & C. Maltecca. A method for the identification of unfavorable haplotypes contained within runs of homozygosity that impact fitness traits and its application to different swine nucleus lines. *J. Anim. Sci.* 94(S4): 26-27.
- 13.) **Howard, J. T.**, F. Tiezzi, Y. Huang, K.A. Gray & C. Maltecca. The use of alternative genomic metrics in nucleus herds to manage the diversity of purebred and crossbred animals. *J. Anim. Sci.* 94(S2):13.
- 12.) Maltecca C., **J. T. Howard**, K. A. Gray, F. Tiezzi & Y. Huang. Identification of runs of homozygosity in Large White and Landrace sows associated with decreased number of piglets born. Plant & Animal Genome XXII Conference, San Diego, CA, January 9-13, 2016.
- 11.) **Howard, J. T.**, M. S. Ashwell, R. E. Baynes & C. Maltecca. Whole genome transcriptome co-expression network analysis identifies pharmacogenetic variation in individual, breed and gender drug metabolism. Plant & Animal Genome XXII Conference, San Diego, CA, January 9-13, 2016.
- 10.) **Howard, J. T.**, J. E. Pryce, M. Haile-Mariam & C. Maltecca. 2015. Regions impacting inbreeding depression and their association with additive genetic effects for United States and Australia Jersey Cattle. *Proc. Assoc. Advmt. Breed. Genet* 21, 346-349.
- 9.) Pryce J. E., **J. T. Howard**, M. Haile-Mariam & C. Maltecca. 2015. Characterising inbreeding depression using runs of homozygosity in Jersey cattle populations in Australia and the USA. Queenstown Molecular Biology Meeting. Queenstown New Zealand.

- 8.) **Howard, J. T.**, C. Maltecca, M. Haile-Mariam, B. J. Hayes & J. E. Pryce. 2015. Distribution of runs of homozygosity and its association with inbreeding depression in United States and Australia Jersey cattle. ADSA-ASAS National Meeting. Orlando, FL 2015.
- 7.) **Howard, J. T.**, F. Tiezzi, S. Jiao, K. A. Gray, C. & C. Maltecca. 2014. Genome-Wide Association Study for Growth and Feed Intake in Duroc boars Utilizing Random Regression Models. In the 10th World Congress on Genetics Applied to Livestock Production, page 370. Vancouver, BC, Canada.
- 6.) M. S. Ashwell, **J. T. Howard**, R. E. Baynes, A. T. O'Nan, J. D. Brooks, J. L. Yeatts, P. Routh & C. Maltecca. 2014. Effect of breed and gender on drug depletion and differential gene expression associated with drug metabolism after Flunixin and Fenbendazole administration. Swine in Biomedical Research, Raleigh NC, July 6-8, 2014.
- 5.) Spangler, M. L., **J. T. Howard**, S. D. Kachman, D. C. Ciobanu, L. A. Kuehn, M. K. Nielsen & T. L. Mader. 2014. Exploratory Analysis of Genetic Variants Underlying Body Temperature in Beef Cattle. Plant & Animal Genome XXII Conference, San Diego, CA, January 11-15, 2014.
- 4.) **Howard, J. T.**, M. S. Ashwell, R. E. Baynes, J. D. Brooks, J. L. Yeatts, B. Bellis, P. Routh & C. Maltecca. 2014. The effect of breed and sex on drug depletion and differential gene expression associated with drug metabolism after Fenbendazole and Flunixin administration. Plant & Animal Genome XXII Conference, San Diego, CA, January 11-15, 2014.
- 3.) Ahlberg, C. M., L. N. Schiermiester, **J. T. Howard**, C. Calkins, & M. L. Spangler. 2013. Genome Wide Association Study of protein and mineral content of beef from crossbred cattle. J. Anim. Sci 91: E Suppl 2.
- 2.) Schiermiester, L. N., C. M. Ahlberg, **J. T. Howard**, C. Calkins, & M. L. Spangler. 2013. Genome wide association study of cholesterol and poly- and mono-unsaturated fatty acids of beef from crossbred cattle. J. Anim. Sci. 91: E Suppl 2.
- 1.) **Howard, J. T.**, M.K. Nielsen, T. Mader, & M.L. Spangler. 2012. The effect of myostatin genotype on body temperature during extreme temperature events. J. Anim. Sci. 90: E Suppl 2.

INVITED
PRESENTATIONS

- 8.) The SPG Experience: Working with a Integrated Swine Genetics Company. Iowa State University Animal Breeding and Genetics Seminar. Ames, IA, March 9, 2021.
- 7.) The SPG Experience: Working with a Integrated Swine Genetics Company. North Carolina State University Animal Science Seminar. Raleigh, NC,

November 25, 2019.

- 6.) The use of 'Big Data' in a modern swine breeding program now and in the future. Beef Improvement Federation Annual Meeting. Brookings, SD, June 18-21, 2019.
- 5.) Population Management Using Genetics (ROH). NAPRRS-NSIF Joint Conference. Chicago IL, December 1-3, 2017.
- 4.) How Many Generations of Genotyped Animals Do We Need? DNA Technology in Beef Cattle. Meat Animal Research Center, Clay Center, NE, October 16-17, 2017.
- 3.) Utilizing genomic information to manage the diversity and minimize the unfavorable effects of inbreeding in livestock populations. DNA Technology in Beef Cattle. Meat Animal Research Center, Clay Center, NE, October 16-17, 2017.
- 2.) Computational Aspects of Characterizing Genomic Inbreeding in Livestock. Breeding and Genetics Symposium: Inbreeding in the Genomics Era. ADSA Annual Meeting. Pittsburgh, Pennsylvania, June 25-28, 2017.
- 1.) The Use of Genomic Information to Manage populations at the Genomic Level. North Carolina State Swine Research Day. May 12, 2015.

SOFTWARE

Geno-Diver: A genetic simulation program that is able to simulate quantitative and/or fitness characters.

Unfavorable Haplotype Finder: Software that identify haplotypes contained within a run of homozygosity (ROH) that give rise to an unfavorable phenotype.

ROH Calculation: Software that calculates whether a SNP is in a run-of-homozygosity of a specified length.

ROH Relationship Matrix: Software that calculates a run-of-homozygosity based relationship matrix.