

**Kirk E. Lohmueller, Ph.D.**

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**CURRICULUM VITAE**

**EDUCATION:**

- 2010**                      ***Ph.D. in Genetics***  
*Cornell University, Ithaca, NY*  
Focus on population genetics with a Biometry (Biostatistics) minor
- 2005**                      ***Bachelor of Science in Biology, (Magna Cum Laude)***  
*Georgetown University, Washington, DC*

**EMPLOYMENT:**

- July 2018-Present**      ***University of California, Los Angeles, CA***  
Associate Professor  
Department of Ecology and Evolutionary Biology  
Department of Human Genetics  
Member, Interdepartmental Program in Bioinformatics  
Member, Genetics & Genomics Home Area
- April 2013-June 2018** ***University of California, Los Angeles, CA***  
Assistant Professor  
Department of Ecology and Evolutionary Biology  
Member, Interdepartmental Program in Bioinformatics  
Member, Genetics & Genomics Home Area
- July 2015-June 2018** ***University of California, Los Angeles, CA***  
Assistant Professor  
Department of Human Genetics
- 2010-April 2013**        ***University of California, Berkeley, CA***  
Miller Research (Postdoctoral) Fellow

**PREVIOUS RESEARCH:**

- 2010-2013**                ***University of California, Berkeley, CA***  
Postdoctoral Researcher  
Advisor: Dr. Rasmus Nielsen  
Analysis of next-generation sequencing data to learn about demography and natural selection.
- 2005-2009**                ***Cornell University, Ithaca, NY***  
Graduate Student Research Assistant  
Advisors: Dr. Andy Clark & Dr. Carlos Bustamante

Research on human population genetics focusing on demographic history and natural selection.

- 2004-2005**                    **Georgetown University, Washington, DC**  
Undergraduate Research Assistant—Biology Department  
Advisor: Dr. John Braverman  
Statistical analyses on large genetic variation datasets.
- 2002-2004**                    **Georgetown University, Washington, DC**  
Undergraduate Research Assistant—Institute for Molecular and Human Genetics  
Advisor: Dr. Lee-Jun Wong  
Single nucleotide polymorphism (SNP) genotyping on human DNA samples.  
Extensively used PCR and electrophoresis.
- 1998-2001**                    **Whitehead/MIT Center for Genome Research, Cambridge MA**  
High School Student Research Assistant  
Advisor: Dr. Joel Hirschhorn  
Review and meta-analysis of genetic association studies.

**AWARDS AND HONORS:**

- 2019**                            **Department of Ecology & Evolutionary Biology Faculty Teaching Award**
- 2015**                            ***Selected as a Platform Session moderator for the American Society of Human Genetics annual meeting***
- 2015**                            ***UCLA Hellman Fellowship***
- 2014**                            ***Searle Scholar***
- 2014**                            ***Alfred P. Sloan Research Fellowship in Computational and Evolutionary Molecular Biology***
- 2010-2013**                    ***Miller Postdoctoral Research Fellowship, UC Berkeley***
- 2010**                            ***NIH Ruth Kirschstein National Research Service Award***  
(I used 6 months before switching to the Miller)
- 2010**                            ***NSF Postdoctoral Research Fellowship in Biology***  
(I was awarded, but I declined, this fellowship)
- 2010**                            ***Selected as a Platform Session moderator for the American Society of Human Genetics annual meeting***
- 2010**                            ***Trainee Research Semifinalist, American Society of Human Genetics***  
Awarded to top abstracts submitted for presentations at the 2010 meeting.
- 2005-06; 2007-09**           ***NSF Graduate Research Fellowship***
- 2005**                            ***Cornell Presidential Genomics Fellowship***  
(I was awarded, but I declined, this fellowship)

**2005** ***Chapman medal***  
 Awarded to the best senior thesis presentation in the Biology Department at Georgetown University.

**2004-2005** ***Barry Goldwater Scholarship***  
 Competitively awarded to students wishing to pursue careers in math and science.

**2001-2005** ***Georgetown-Hughes Undergraduate Research Scholarship***  
 An award from the Howard Hughes Medical Institute (through Georgetown University) to sponsor students' research during the summer.

**TEACHING:**

**2019** ***University of California, Los Angeles, CA***  
 EE BIOL 297: Population genomics of structural variants and transposable elements. Graduate seminar class (2 credits, Winter quarter).

**2018** ***University of California, Los Angeles, CA***  
 EE BIOL 297: Demystifying the Academic Job Talk. Graduate seminar class (2 credits, Winter quarter).

**2016** ***University of California, Los Angeles, CA***  
 EE BIOL 297: Coalescent Theory. Graduate seminar class (2 credits, Winter quarter).

**2014-2019 (annually)** ***University of California, Los Angeles, CA***  
 EE BIOL 135/235: Population Genetics. Upper-level undergraduate & graduate course. >50 students. (Spring quarter).

**2013-2018 (annually)** ***University of California, Los Angeles, CA***  
 EE BIOL M200A: Evolutionary Biology. Graduate introductory evolution class. Co-taught with Bob Wayne and Mike Alfaro. I taught the evolutionary genetics portion (Fall quarter).

**2013-2019 (annually)** ***University of California, Los Angeles, CA***  
 Quantitative skills bootcamp for incoming EEB graduate students. Co-taught with Jamie Lloyd-Smith and Mike Alfaro. Currently EEB 201 (2 day-workshop; Fall quarter).

**2013-2017 (annually)** ***California Criminalistics Institute, Los Angeles, CA***  
 R103: Population Genetics in Forensic DNA Analysis. Designed and taught a 3-day course on basic population genetics and statistics in forensic DNA analysis for DNA analysts from government forensic science laboratories.

**2013** ***University of California, Los Angeles, CA***  
 EE BIOL 297: The Neutral Theory of Molecular Evolution. Graduate seminar class (2 credits, Spring quarter).

**2013,2015,2019** ***California Criminalistics Institute, Richmond, CA***  
 R103: Population genetics in Forensic DNA Analysis. Designed and taught a 3-day course on basic population genetics and statistics in forensic DNA analysis for DNA analysts from government forensic science laboratories.

**2012** **University of California, Los Angeles, CA**  
 Gave two lectures on coalescent theory to the CS229: Current Topics in Bioinformatics course

**UNIVERSITY AND DEPARTMENTAL SERVICE:**

**2013-2019** **UCLA Legislative Assembly representative**, Department of Ecology and Evolutionary Biology

**2013-2016** **Member, Social Media Committee**, Department of Ecology and Evolutionary Biology

**2014-2017** **Member, Seminar Committee**, Department of Ecology and Evolutionary Biology

**2014-Present** **Member, Seminar Committee**, Interdepartmental Program in Bioinformatics

**2014-2017** **Member, Student Advising Committee**, Interdepartmental Program in Bioinformatics

**2015-Present** **Member, Executive Committee**, Genetics & Genomics Graduate Home Area

**2016** **Member, Faculty Search Committee**, Department of Human Genetics

**2016-2017** **Member, Department Chair Search Committee**, Department of Ecology and Evolutionary Biology

**2017-2018** **Chair, Population Genetics Faculty Search Committee**, Department of Ecology and Evolutionary Biology

**2017-2018** **Member, Graduate Admissions Committee**, Department of Ecology and Evolutionary Biology

**2017-Present** **Chair, Student Advising Committee**, Interdepartmental Program in Bioinformatics

**2018-2019** **Member, Personnel Committee**, Department of Ecology and Evolutionary Biology

**2018-2019** **Member, Departmental Awards Committee**, Department of Ecology and Evolutionary Biology

**2018-2019** **Member, Quantitative Biologist Faculty Search Committee**, Department of Ecology and Evolutionary Biology

**EDITORIAL ACTIVITIES:**

2019-Present Associate Editor, *Genome Biology and Evolution*

2017 Guest Editor for *PNAS*

2015 & 2017-2019 Guest Editor for *PLoS Genetics*

**OTHER PROFESSIONAL ACTIVITIES:**

- 2019 NIH F08 Fellowships: Genes, Genomes and Genetics ad hoc study section member
- 2019 Session chair, The Biology of Genomes, Cold Spring Harbor
- 2019 Walter Fitch Symposium Committee, Society of Molecular Biology and Evolution
- 2019 NIH Special Emphasis Panel, National Institute of General Medical Sciences (NIGMS), Maximizing Investigators' Research Award for Early Stage Investigators (R35) review
- 2018 Co-organizer of Population Genomics & the Microbiome, Computational Genomics Summer Institute, UCLA
- 2018 Session chair, Probabilistic Modeling in Genomics, Cold Spring Harbor
- 2018 Ad hoc grant reviewer, Swiss National Science Foundation
- 2018 Ad hoc grant reviewer, Bioinformatics and Computational Biology Competition, Génome Québec
- 2017 NIH Special Emphasis Panel, National Institute on Aging, The Dog Aging Project (U19) review
- 2017 & 2018 NIH Genetic Variation and Evolution (GVE) ad hoc study section member
- 2017 NIH Special Emphasis Panel, National Institute of General Medical Sciences (NIGMS), Pathway to Independence Award (K99/R00) review
- 2017 Panelist on the NSF Graduate Research Fellowship Program review panel
- 2016 & 2017 Program Committee member for the RECOMB 2016 Satellite Meeting on Computational Methods in Genetics.
- 2015 Organized a symposium (with Emilia Huerta-Sanchez, UC Merced) entitled "Reframing the demography vs. selection debate using 21st century models and data" at the annual Society of Molecular Biology and Evolution conference in Vienna.
- 2015 External review of a final grant report, National Institute of Justice, Forensic DNA Research and Development program.
- 2015 Taught a lesson on human evolution to high school students at UCLA for The Society of Asian Scientists and Engineer's White House Initiative.
- 2014 **Organized the Southern CALifornia Evolutionary Genetics & Genomics (SCALE) conference at UCLA.** This day-long conference brought together 89 students, postdocs and faculty from across Southern California to discuss evolutionary and population genetics. The meeting featured talks (mostly from students and postdocs), a poster session, and much informal discussion.

2014-2015	Ad hoc grant reviewer, NSF, Behavioral and Cognitive Sciences, Program of Archeology.
2014	Ad hoc grant reviewer, NSF, Division of Environment Biology, Program of Evolutionary Ecology.
2013	Taught an interactive lesson on forensic DNA typing to high school freshmen at Berkeley High School

**Invited reviewer for:** *Nature, Science, Nature Genetics, Nature Communications, Molecular Biology and Evolution, eLife, Proceedings of the National Academy of Sciences, Genome Research, American Journal of Human Genetics, Current Biology, Proceedings of the Royal Society B, PLoS Biology, PLoS Computational Biology, PLoS Genetics, PLoS ONE, Genome Biology, Trends in Genetics, Genome Biology and Evolution, Genetic Epidemiology, Molecular Ecology, Evolution, Genetica, Genetics, Genes, Human Molecular Genetics, Bioinformatics, BMC Medical Genetics, BMC Genomics, BMC Medical Genomics, European Journal of Human Genetics, Journal of Heredity, Trends in Molecular Medicine, Frontiers in Evolutionary and Population Genetics, Evolution Letters, Ecology & Evolution (reviewed 13-16 manuscripts annually since 2013).*

#### STUDENT AND POSTDOC MENTORING:

2019-Present	<b>Xinjun Zhang</b> (Postdoc)
2019-Present	<b>Gustavo Barroso</b> (Postdoc)
2015-Present	<b>Annabel Beichman</b> (PhD student, Ecology and Evolutionary Biology; joint with Bob Wayne)
2016-Present	<b>Jazlyn Mooney</b> (PhD student, Genetics & Genomics)
2017-Present	<b>Arun Durvasula</b> (PhD student, Genetics & Genomics; joint with Sriram Sankararaman)
2017-Present	<b>Jesse Garcia</b> (PhD student, Bioinformatics)
2018-Present	<b>Chris Kyriazis</b> (PhD student, Ecology and Evolutionary Biology; joint with Bob Wayne)
2018-Present	<b>Pooneh Kalhori</b> (Undergraduate student)
2019-Present	<b>Abigail Yohannes</b> (Undergraduate student)
2013-2016	<b>Diego Ortega Del Vecchio</b> (PhD student, Bioinformatics; joint with John Novembre); currently an Assistant Professor at the National Autonomous University of Mexico
2015-2018	<b>Tanya Phung</b> (PhD student, Bioinformatics); currently a postdoc with Melissa Wilson at Arizona State University
2013-2018	<b>Bernard Kim</b> (PhD student, Ecology and Evolutionary Biology); currently a postdoc with Dmitri Petrov at Stanford University
2013-2015	<b>Charleston Chiang</b> (Postdoc, NIH NRSA Postdoctoral Fellowship; joint with John Novembre); currently Assistant Professor at USC
2013-2018	<b>Clare Marsden</b> (Postdoc & then Assistant Project Scientist, UCLA Computational Biology Initiative Postdoctoral Fellowship); currently a forensic DNA analyst at LAPD Crime Lab.
2014-2018	<b>Christian Huber</b> (Postdoc); currently a Discovery Early Career Award (DECRA) recipient at the Australian Centre of Ancient DNA at the University of Adelaide
2014-2018	<b>Ying Zhen</b> (Postdoc; joint with Tom Smith & then Assistant Project Scientist, UCLA Computational Biology Initiative Postdoctoral Fellowship); currently an Assistant Professor, Westlake University, Hangzhou, China
2017-2018	<b>Eduardo Amorim</b> (Postdoc)
2014-2015	<b>Amy Chow</b> (Undergraduate student); currently a mechanical engineering MS student at San Diego State University
Fall 2014	<b>Tanya Phung</b> (Bioinformatics rotation student)

Spring 2014	<b>Megan Roytman</b> (Bioinformatics rotation student)
Fall 2015	<b>Jazlyn Mooney</b> (Genetics & Genomics rotation student)
Fall 2016	<b>Arun Durvasula</b> (Genetics & Genomics rotation student)
2016-2017	<b>Jesse Garcia</b> (Undergraduate student in the Bruins-in-Genomics Summer program)
Spring 2017	<b>James Perez</b> (Bioinformatics rotation student)
2017-2018	<b>Norris Khoo</b> (Undergraduate student in the Bruins-in-Genomics Summer program); currently in MS program in Computer Science at USC
Summer 2019	<b>Miguel Guardado</b> (Undergraduate student in the Bruins-in-Genomics Summer program)
Summer 2019	<b>Jonathan Mah</b> (Undergraduate student in the Bruins-in-Genomics Summer program)
2012-2013	<b>Mingze He</b> (Visiting student from BGI, Shenzhen, China; joint with Rasmus Nielsen and Emilia-Huerta Sanchez); currently a graduate student at Iowa State University
Summer 2010	<b>Alison Feder</b> (Summer undergraduate student); currently a Miller Postdoctoral Fellow at UC Berkeley

## GRADUATE COMMITTEES:

### PhD Committee member for:

Monique Ambrose, 2013-2018 (Ecology and Evolutionary Biology)  
 Kelly Barr, 2017-Present (Ecology and Evolutionary Biology)  
 Cliff Boldridge, 2017-Present (Biochemistry, Molecular and Structural Biology)  
 Rob Brown, 2014-2017 (Bioinformatics)  
 Daniel Chavez, 2018-Present (Ecology and Evolutionary Biology)  
 Tina DelCarpio, 2018-Present (Ecology and Evolutionary Biology)  
 Madza Farias-Virgens, 2018-Present (Integrative Biology & Physiology)  
 Meixi Lin, 2019-Present (Ecology and Evolutionary Biology)  
 Evan McCartney-Melstad, 2013-2016 (Ecology and Evolutionary Biology)  
 Sergio Morales, 2015-2016 (Ecology and Evolutionary Biology)  
 Kevin Neal, 2014-2019 (Ecology and Evolutionary Biology)  
 Scott O'Donnell, 2016-Present (Ecology and Evolutionary Biology)  
 Allison Fritts-Penniman, 2013-2016 (Ecology and Evolutionary Biology)  
 Gabriela Pinho, 2015-Present (Ecology and Evolutionary Biology)  
 Jacqueline Robinson, 2013-2017 (Ecology and Evolutionary Biology)  
 Megan Roytman, 2016-2018 (Bioinformatics)  
 Jaleal Sanjak, 2015-2017 (Ecology and Evolution at UC Irvine)  
 Rena Schweizer, 2013-2015 (Ecology and Evolutionary Biology)  
 Sarah Spendlove, 2019-Present (Bioinformatics)  
 Adriana Sperlea, 2016-Present (Bioinformatics)  
 Stephanie Steele, 2015-2017 (Ecology and Evolutionary Biology)  
 Erin Toffelmier, 2013-Present (Ecology and Evolutionary Biology)  
 Rachel Turba, 2017-Present (Ecology and Evolutionary Biology)  
 Camille Yabut, 2013-2014 (Ecology and Evolutionary Biology)

### PhD Guidance Committee member for:

Kelly Barr, 2016-2017 (Ecology and Evolutionary Biology)  
 Annabel Beichman, 2013-2014 (Ecology and Evolutionary Biology)  
 Joey Curti, 2019-Present (Ecology and Evolutionary Biology)  
 Tina DelCarpio, 2017-2018 (Ecology and Evolutionary Biology)  
 Emma Fox, 2017-2018 (Ecology and Evolutionary Biology)  
 Camille Gaynus, 2014-2015 (Ecology and Evolutionary Biology)  
 Audra Huffmeyer, 2015-2016 (Ecology and Evolutionary Biology)  
 Chris Kyriazis, 2017-2018 (Ecology and Evolutionary Biology)  
 Natalie Lozano, 2017-2018 (Ecology and Evolutionary Biology)  
 Alayna Mead, 2018-2019 (Ecology and Evolutionary Biology)

Kevin Neal, 2013-2014 (Ecology and Evolutionary Biology)  
 Scott O'Donnell, 2015-2016 (Ecology and Evolutionary Biology)  
 Gabriela Pinho, 2014-2015 (Ecology and Evolutionary Biology)  
 Celine Snedden, 2018-2019 (Ecology and Evolutionary Biology)

**MS Committee member for:**

Jessica Arriens, 2016-2018 (Ecology and Evolutionary Biology)  
 Clive L. F. Lau, 2016-2017 (Ecology and Evolutionary Biology)  
 Sara Makanani, 2018-Present (Ecology and Evolutionary Biology)  
 Alayna Mead, 2015-2017 (Ecology and Evolutionary Biology)

**RESEARCH FUNDING:****Ongoing:**

**Source:** NIH/NIGMS R35GM119856 (PI: K. Lohmueller)  
**Title:** Population genomics of the selective effects of new mutations  
**Period:** 9/01/16-5/31/21  
**Direct costs to KL:** \$1,013,625

**Source:** NIH/NIEHS R21ES031000 (PIs: K. Lamia, Scripps; K. Lohmueller)  
**Title:** Quantifying the impact of circadian disruption on genome stability  
**Period:** 8/15/19-7/31/21  
**Total direct costs:** \$275,000 (\$102,596 direct to KL)

**Source:** NIH/NHGRI R01HG009120-01A1 (PI: B. Pasaniuc, UCLA)  
**Title:** Integrative approaches for mapping the genetic risk of complex traits  
**Period:** 3/01/17-3/1/22  
**Role:** co-Investigator  
**Direct costs to KL:** \$72,230

**Source:** NSF DEB 1556705 (PI: R. Wayne, UCLA)  
**Title:** SG: Selection in bottlenecked populations  
**Period:** 04/01/16-03/31/19 (in NCE till 3/31/20)  
**Role:** co-PI  
**Direct costs to UCLA:** \$97,308

**Completed:**

**Source:** Alfred P. Sloan Foundation (PI: K. Lohmueller)  
**Title:** Research Fellowship in Computational & Evolutionary Molecular Biology  
**Period:** 9/15/14-9/14/16 (NCE till 9/14/18)  
**Total Direct costs:** \$50,000

**Source:** Searle Scholars Program (PI: K. Lohmueller)  
**Title:** Why does natural selection vary across species?  
**Period:** 7/01/14-6/30/17 (NCE till 6/30/18)  
**Total Direct costs:** \$300,000

**Source:** NIJ 2013-DN-BX-K029 (PI: K. Lohmueller; co-PI: K. Inman, CalState East Bay)  
**Title:** Advancing probabilistic approaches to interpreting low-template DNA profiles and mixtures: Developing theory, implementing practice  
**Period:** 1/01/14-3/31/17  
**Direct costs to KL:** \$162,782



**Source:** UCLA Hellman Fellowship (PI: K. Lohmueller)  
**Title:** Population genomic signatures of mutagenic recombination  
**Period:** 7/01/15-6/30/16  
**Total Direct costs:** \$21,608

**Source:** NIH/NHGRI R01HG007089 (PI: J. Novembre, University of Chicago)  
**Title:** Haplotype-based analysis methods for population genomics  
**Period:** 3/01/13-6/30/16  
**Role:** co-Investigator  
**Direct costs to UCLA:** \$182,542

**Source:** Miller Research Institute, UC Berkeley (PI: K. Lohmueller)  
**Title:** Understanding our evolutionary past through the study of human genetic variation  
**Period:** 7/01/10-3/31/13  
**Total Direct costs:** \$201,000

**Source:** NIH/NHGRI 1F32HG005308 (PI: K. Lohmueller)  
**Title:** Population genetics of deleterious polymorphism in human populations  
**Period:** 1/01/10-6/30/10  
**Total Direct costs:** \$18,684

#### PUBLICATIONS:

1. Huber CD, Kim BY, **Lohmueller KE**. Population genetic models of GERP scores suggest pervasive turnover of constrained sites across mammalian evolution, Submitted. doi: <https://doi.org/10.1101/836858>
2. Durvasula A, **Lohmueller KE**. Negative selection on complex traits limits genetic risk prediction accuracy between populations, Submitted. doi: <http://dx.doi.org/10.1101/721936>
3. Ortega-Del Vecchyo D, **Lohmueller KE**, Novembre J. Haplotype-based inference of the distribution of fitness effects, Submitted. doi: <https://doi.org/10.1101/770966>
4. Grujic O, Phung TN, Kwon SB, Arneson A, Lee Y, **Lohmueller KE**, Ernst J. Identification and characterization of constrained non-exonic bases lacking predictive epigenomic and transcription factor binding annotations, Submitted. doi: <https://doi.org/10.1101/722876>
5. Kyriazis CC, Wayne RK, **Lohmueller KE**. High genetic diversity can contribute to extinction in small populations, Submitted. doi: <https://doi.org/10.1101/678524>
6. Zhen Y, Huber CD, Davies RW, **Lohmueller KE**. Stronger and higher proportion of beneficial amino acid changing mutations in humans compared to mice and flies, Submitted. doi: <https://doi.org/10.1101/427583>
7. Buckleton JS, **Lohmueller KE**, Inman K, Cheng K, Curran JM, Pugh SN, Bright JA, Taylor DA. Testing whether stutter and low-level DNA peaks are additive. *Forensic Sci Int Genet*, 2019; 43:102166.
8. Sura SA, Smith LL, Ambrose MR, Amorim CEG, Beichman AC, Gomez ACR, Juhn M, Kandlikar GS, Miller JS, Mooney J, Mummah RO, **Lohmueller KE**, Lloyd-Smith JO. Ten simple rules for giving an effective academic job talk. *PLoS Comput Biol*, 2019; 15:e1007163.
9. Beichman A, Koepfli KP, Li G; Murphy W, Dobrynin P, Kilver S, Tinker MT; Murray MJ, Johnson J, Lindblad-Toh K, Karlsson EK, **Lohmueller KE\***, Wayne RK\*. Aquatic adaptation and depleted

- diversity: a deep dive into the genomes of the sea otter (*Enhydra lutris*) and giant otter (*Pteronura brasiliensis*), *Mol Bio Evol*, 2019; 36:2631-2655. (**\*Contributed equally**).
10. Phung TN, Wayne RK, Wilson MA\*, **Lohmueller KE\***. Complex patterns of sex-biased demography in canines. *Proc Royal Soc B*, 2019; 286:20181976. (**\*Contributed equally**).
  11. Robinson JA, Räikkönen J, Vucetich LM, Vucetich JA, Hedrick PW, Peterson RO, **Lohmueller KE\***, Wayne RK\*. Genomic signatures of extensive inbreeding in Isle Royale wolves, a population on the threshold of extinction. *Sci Adv*, 2019; 5(5):eaau0757. (**\*Contributed equally**).
  12. Mooney JA, Huber CD, Service S, Sul JH, Marsden CD, Zhang Z, Sabatti C, Ruiz-Linares A, Bedoy G, Costa Rica/Colombia Consortium for Genetic Investigation of Bipolar Endophenotypes, Freimer N, **Lohmueller KE**. Understanding the hidden complexity of Latin American population isolates. *Am J Hum Genet*, 2018; 103:707-726.
  13. Robinson JA, Brown C, Kim BY, **Lohmueller KE\***, Wayne RK\*. Purging of strongly deleterious mutations explains long-term persistence and absence of inbreeding depression in island foxes. *Current Biology*, 2018; 28: 3487-94. (**\*Contributed equally**).
  14. Kim BY, Huber CD, **Lohmueller KE**. Deleterious variation mimics signatures of genomic incompatibility and adaptive introgression. *PLoS Genetics* 2018; 14 e1007741.
  15. Kim BY, Wei X, Fitz-Gibbon S, **Lohmueller KE**, Ortego J, Gugger PF, Sork VL. RADseq data reveal pervasive, but not promiscuous, ancient introgression within Californian white oak species (*Quercus: Fagaceae*). *Mol Ecol*, 2018; 27: 4556-4571.
  16. Beichman AC, Huerta-Sanchez E, and **Lohmueller KE**. Using genomic data to infer historic population dynamics of non-model organisms, *Annu Rev Ecol Evol Syst*, 2018; 49: 433-456.
  17. vonHoldt BM, Kartzinel RY, Huber CD, Le Underwood V, Zhen Y, Ruegg K, **Lohmueller KE**, Smith TB. Growth factor gene *IGF1* is associated with bill size in the black-bellied seedcracker *Pyrenestes ostrinus*. *Nat Commun*, 2018; 9: 4855.
  18. Huber CD, Durvasula A, Hancock AM, **Lohmueller KE**. Gene expression drives the evolution of dominance, *Nat Commun*, 2018; 9: 2750.
  19. Chiang CWK, Marcus JH, Sidore C, Biddanda A, Al-Asadi H, Zoledziewska M, Pitzalis M, Busonero F, Maschio A, Pistis G, Steri M, Angius A, **Lohmueller KE**, Abecasis GR, Schlessinger D, Cucca F, and Novembre J. Genomic history of the Sardinian population, *Nat Genet*, 2018; 50: 1426-1434.
  20. Schweizer RM, Durvasula A, Smith J, Vohr SH, Stahler DR, Galaverni M, Thalmann O, Smith DW, Randi E, Ostrander EA, Green RE, **Lohmueller KE**, Novembre J, Wayne RK. Natural selection and origin of a melanistic allele in North American gray wolves, *Mol Bio Evol*, 2018; 35:1190-1209.
  21. Beichman A, Phung TN, **Lohmueller KE**. Comparison of single genome and allele frequency data reveals discordant human demographic histories, *G3: Genes, Genomes and Genetics*, 2017; 7:3605-3620.
  22. Zhen Y, Harrigan RJ, Ruegg KC, Anderson EC, Ng TC, Lao S, **Lohmueller KE**, and Smith TB. Genomic divergence across ecological gradients in the Central African rainforest songbird (*Andropadus virens*), *Mol Ecol*, 2017; 26:4966-4977.
  23. Huber CD, Kim B, Marsden CD, **Lohmueller KE**. Determining the factors driving selective effects of new nonsynonymous mutations, *Proc Natl Acad Sci USA*, 2017; 114:4465-470.
  24. Kim BY, Huber CD, **Lohmueller KE**. Inference of the distribution of selection coefficients for new nonsynonymous mutations using large samples, *Genetics*, 2017; 206:345-361.

25. Pedersen CET, **Lohmueller KE**, Grarup N, Bjerregaard P, Hansen T, Siegismund HR, Moltke I, Albrechtsen A. The effect of an extreme and prolonged population bottleneck on patterns of deleterious variation: insights from the Greenlandic Inuit, *Genetics*, 2017; 205:787-801.
26. Ortega-Del Vecchyo D, Marsden CD, and **Lohmueller KE**. PReFerSim: Fast simulation of demography and selection under the Poisson Random Field model, *Bionformatics*, 2016; 32:3516-3518.
27. Freedman AH\*, **Lohmueller KE\***, Wayne RK\*, Evolutionary history, selective sweeps and deleterious variation in the dog, *Annu Rev Ecol Evol Syst*, 2016; 47:73-96. (\***Contributed equally**).
28. Phung TN, Huber CD, **Lohmueller KE**. Determining the effect of natural selection on linked neutral divergence across species, *PLoS Genetics*, 2016; 12: e1006199.
29. Robinson JA, Ortega-Del Vecchyo D, Fan Z, Kim BY, vonHoldt BM, Marsden CD, **Lohmueller KE\***, Wayne RK\*. Genomic flatlining in the endangered island fox (*Urocyon littoralis*), *Current Biology*, 2016; 26:1183-9. (\***Contributed equally**).
30. Huber CD, **Lohmueller KE**. Population genetic tests of neutral evolution. In: Kliman, R.M. (ed.), *Encyclopedia of Evolutionary Biology*. vol. 3, pp. 112–118. Oxford: Academic Press.
31. Marsden CD, Ortega-Del Vecchyo D, O'Brien DP, Taylor JF, Ramirez O, Vilà C, Marques-Bonet T, Schnabel RD, Wayne RK, **Lohmueller KE**. Bottlenecks and selective sweeps during domestication have increased deleterious genetic variation in dogs, *Proc Natl Acad Sci USA*, 2016; 113:152-7.
32. Marsden CD, Rudin N, Inman K, **Lohmueller KE**. An assessment of the information content of likelihood ratios derived from complex mixtures. *Forensic Sci Int Genet*, 2016; 22:64-72.
33. Haned H, Gill P, **Lohmueller K**, Inman K, Rudin N. Validation of probabilistic genotyping software for use in forensic DNA casework: Definitions and illustrations. *Sci Justice*, 2016; 56(2):104-8.
34. Brown R, Lee H, Eskin A, Kichaev G, **Lohmueller KE**, Reversade B, Nelson SF, Pasaniuc B. Leveraging ancestry to improve causal variant identification in exome sequencing for monogenic disorders. *Eur J Hum Genet*, 2016; 24:113-9.
35. Inman K, Rudin N, Cheng K, Robinson C, Kirschner A, Inman-Semerau L, **Lohmueller KE**. Lab Retriever: a software tool for calculating likelihood ratios incorporating a probability of drop-out for forensic DNA profiles, *BMC Bioinformatics*, 2015; 16: 298.
36. Zoledziwska M\*, Sidore C\*, Chiang CWK\*, Sanna S\*, Mulas A, Steri M, Busonero F, Marcus JH, Marongiu M, Maschio A, Ortega del Vecchyo D, Floris M, Meloni A, Delitala A, Concas MP, Murgia F, Biniino G, Vaccargiu S, Nagaraja R, **Lohmueller KE**, UK10K Consortium, Timpson NJ, Soranzo N, Tachmazidou I, Dedoussis G, Zeggini E, The Understanding Society Scientific Group, Uzzau S, Jones C, Lyons R, Angius A, Abecasis GR\*\*, Novembre J\*\*, Schlessinger D\*\*, Cucca F\*\*. Major height reducing variants and selection for short stature on the island of Sardinia, *Nat Genet*, 2015, 47: 1352-6.
37. Rohlf RV, Aguiar VR, **Lohmueller KE**, Castro AM, Ferreira AC, Almeida VC, Louro ID, Nielsen R. Fitting the Balding-Nichols model to forensic databases. *Forensic Sci Int Genet*, 2015; 19: 86-91.
38. Kim BY, **Lohmueller KE**. Selection and reduced population size cannot explain higher amounts of Neanderthal ancestry in East Asian than European human populations, *Am J Hum Genet*, 2015; 96: 454-61.
39. **Lohmueller KE**. The distribution of deleterious genetic variation in human populations, *Curr Opin Genet Dev* 2014; 29: 139-146.

40. **Lohmueller KE**. On the origin of Peter Rabbit, *Science* 2014; 345: 1000-10001.
41. DeGiorgio M, **Lohmueller KE**, Nielsen R. A model-based approach for identifying signatures of balancing selection in genetic data, *PLoS Genetics* 2014; 10: e1004561.
42. Ko A, Cantor RM, Weissglas-Volkov D, Nikkola E, Linga Reddy PVM, Sinsheimer JS, Pasaniuc B, Brown R, Alvarez M, Rodriguez A, Rodriguez-Guillen R, Bautista IC, Arellano-Campos O, Muñoz-Hernández LL, Salomaa V, Kaprio J, Jula A, Jauhiainen M, Heliövaara M, Raitakari O, Lehtimäki T, Eriksson JG, Perola M, **Lohmueller KE**, Rodriguez-Torres M, Riba L, Tusie-Luna T, Aguilar-Salinas CA, Pajukanta P. Amerindian-specific regions under positive selection harbor new lipid variants in Latinos. *Nat Commun* 2014; 5: 3983.
43. **Lohmueller KE**. The impact of population demography and selection on the genetic architecture of complex traits. *PLoS Genetics* 2014; 10: e1004379.
44. **Lohmueller KE**, Rudin N, Inman K. Analysis of allelic drop-out using the Identifiler® and PowerPlex® 16 forensic STR typing systems. *Forensic Sci Int Genet* 2014; 12C:1-11.
45. Wilson Sayres M, **Lohmueller KE**, Nielsen R. Natural selection reduced diversity on human Y chromosomes. *PLoS Genetics* 2014; 10: e1004064.
46. **Lohmueller KE\***, Sparsø T\*, Li Q, Andersson E, Korneliussen T, Albrechtsen A, Banasik K, Grarup N, Hallgrimsdottir I, Kiil K, Kilpeläinen T, Krarup N, Pers T, Sanchez G, Jørgensen T, Sandbæk A, Lauritzen T, Kristiansen K, Brunak S, Li Y, Hansen T, Wang J, Nielsen R, Pedersen O. Whole exome sequencing of 2,000 Danish individuals and the role of low-frequency coding variants in type 2 diabetes. *Am J Hum Genet* 2013; 93:1072-1086. (**\*Contributed equally**).
47. **Lohmueller KE**, Rudin N. Calculating the weight of evidence in low-template forensic DNA casework. *Journal of Forensic Sciences*, 2013; 58 Suppl 1:S243-9.
48. Rasmussen M\*, Guo X\*, Wang Y\*, **Lohmueller KE\***, and 54 additional co-authors. Aboriginal Australian genomic sequence obtained from hundred-year-old lock of hair reveals separate human dispersals into Asia. *Science* 2011; 334:94-98 (**\*Contributed equally**).
49. **Lohmueller KE**, Albrechtsen A, Li Y, Kim SY, Korneliussen T, Vinckenbosch N, Tian G, Huerta-Sanchez E, Feder A, Grarup N, Jørgensen T, Jiang T, Witte DR, Sandbæk A, Hellmann I, Lauritzen T, Hansen T, Pedersen O, Wang J, Nielsen R. Natural selection affects multiple aspects of genetic variation at putatively neutral sites across the human genome. *PLoS Genetics* 2011; 7:e1002326.
50. Kim SY, **Lohmueller KE**, Albrechtsen A, Li Y, Korneliussen T, Tian G, Grarup N, Jiang T, Andersen G, Witt D, Jorgensen T, Hansen T, Pedersen O, Wang J, Nielsen R. Estimation of allele frequency and association mapping using next-generation sequencing data. *BMC Bioinformatics* 2011; 12:231.
51. **Lohmueller KE**, Bustamante CD, Clark AG. Detecting directional selection in the presence of recent admixture in African Americans. *Genetics* 2011; 187:823-835.
52. Boyko A, Quignon P, Li L, Schoenebeck J, Degenhardt JD, **Lohmueller KE**, et al. A simple genetic architecture underlies quantitative traits in dogs, *PLoS Biology* 2010; 8:e1000451.
53. **Lohmueller KE**, Bustamante CD, Clark AG. The effect of recent admixture on inference of ancient population history. *Genetics* 2010; 185:611-622.
54. **Lohmueller KE**, Degenhardt JD, Keinan A. (Letter to the Editor) Sex-averaged recombination and mutation rates: A comment on Labuda et al., *Am J Hum Genet* 2010; 86:978-980.
55. **Lohmueller KE**. (Letter to the Editor) Graydon et al. provide no new evidence that forensic STR loci are functional. *Forensic Sci Int Genet* 2010; 4:273-274.

56. vonHoldt BM, Pollinger JP, **Lohmueller KE**, et al. Genome-wide SNP and haplotype analysis reveals a rich history underlying dog domestication. *Nature* 2010; 464:898-902.
57. Wall JD, **Lohmueller KE**, Plagnol V. Detecting ancient admixture and estimating demographic parameters in multiple human populations. *Mol Biol Evol* 2009; 26:1823-1827.
58. **Lohmueller KE**, Bustamante CD, Clark AG. Methods for human demographic inference using haplotype patterns from genome-wide SNP data. *Genetics* 2009; 182:217-231.
59. Auton A, Bryc K, Boyko AR, **Lohmueller KE**, Novembre J, Reynolds A, Indap A, Wright MH, Degenhardt J, Gutenkunst RN, King KS, Nelson MR, Bustamante CD. Global distribution of genomic diversity underscores rich complex history of continental human populations. *Genome Research* 2009; 19:795-803.
60. Boyko AR, Williamson SH, Indap AR, Degenhardt JD, Hernandez RD, **Lohmueller KE**, Adams MD, Schmidt A, Sninsky JJ, Sunyaev SR, White TJ, Nielsen R, Clark AG, Bustamante CD. Assessing the evolutionary impact of amino acid mutations in the human genome. *PLoS Genetics* 2008; 4:e1000083.
61. **Lohmueller KE**, Indap AR, Schmidt S, Boyko AR, Hernandez RD, Hubisz MJ, Sninsky JJ, White TJ, Sunyaev SR, Nielsen R, Clark AG, Bustamante CD. Proportionally more deleterious genetic variation in European than in African populations. *Nature* 2008; 451:994-997.
62. Olshen AB, Gold B, **Lohmueller KE**, Struewing JP, Satagopan J, Stefanov SA, Eskin E, Kirchhoff T, Lautenberger JA, Klein RJ, Friedman E, Norton L, Ellis NA, Viale A, Lee CS, Borgen PI, Clark AG, Offit K, Boyd J. Analysis of genetic variation in Ashkenazi Jews by high density SNP genotyping. *BMC Genetics* 2008; 9:14.
63. **Lohmueller KE**, Mauney MM, Reich DE, Braverman JM. Variants associated with common disease are not unusually differentiated in frequency across populations. *Am J Hum Genet* 2006; 78:130-136.
64. **Lohmueller KE**, Wong LJC, Mauney MM, Jiang L, Felder RA, Jose PA, Williams SM. Patterns of genetic variation in the hypertension candidate gene *GRK4*: ethnic variation and haplotype structure. *Ann Hum Genet* 2006; 70:27-41.
65. Patterson N, Hattangadi N, Lane B, **Lohmueller KE**, Hafler DA, Oksenberg JR, Hauser SL, Smith MW, O'Brien SJ, Altshuler D, Daly MJ, Reich D. Methods for high-density admixture mapping of disease genes. *Am J Hum Genet* 2004; 74:979-1000.
66. **Lohmueller KE**, Pierce CL, Pike M, Lander ES, Hirschhorn JN. Meta-analysis of genetic association studies supports a contribution of common variants to susceptibility to common disease. *Nat Genet* 2003; 33:177-182.
67. Hirschhorn JN, **Lohmueller K**, Byrne E, Hirschhorn K. A comprehensive review of genetic association studies. *Genet Med* 2002; 2:45-61.

#### INVITED PRESENTATIONS AND SEMINARS:

##### 2019

- Seminar for the Medical and Population Genetics group, UCSD, San Diego, CA, October 2019
- Invited presentation at the Discovery Research Investigating Founder Population Traits (DRIFT) Consortium (sponsored by Regeneron), Houston, TX, October 2019.
- Seminar for the Vienna Graduate School of Population Genetics, Vienna, Austria, June 2019.
- Seminar for the International Laboratory for Human Genome Research, National Autonomous University of Mexico, Queretaro, Mexico, May 2019.

- Invited presentation at the Biology of Genomes meeting, Cold Spring Harbor, NY, May 2019.
- Seminar for the Institute of Ecology & Evolution at the University of Oregon, Eugene, OR, April 2019.
- Seminar for the Medical and Population Genetics (MPG) group at the Broad Institute, Cambridge, MA, March 2019.
- Presentation and workshop leader at the UCLA La Kretz Workshop in Conservation Genomics, March 2019.
- Invited presentation at the “The Role of Genomics and Metagenomics in Human Health: Recent Developments in Statistical and Computational Methods”, Banff International Research Station for Mathematical Innovation and Discovery (BIRS), Banff, Alberta, Canada, February 2019.

## 2018

- Invited presentation at the Probabilistic Modeling in Genomics meeting, Cold Spring Harbor, NY, November 2018. (T. Phung from my lab presented instead)
- Invited presentation at the PopSim meeting, Cold Spring Harbor, NY, November 2018.
- Seminar for the Department of Ecology and Evolutionary Biology at Princeton University, Princeton, NJ, September 2018.
- Invited presentation for the UCLA Computational Genomics Summer Institute, University of California, Los Angeles, CA, July 2018.
- Invited presentation at the SMBE Satellite Meeting on Modern Methods for the Study of Ancient DNA, Providence, RI, April 2018.
- Presentation and workshop leader at the UCLA La Kretz Workshop in Conservation Genomics, March 2018.
- Seminar at the Ecology, Evolution, and Behavioral Seminar Series at the University of Minnesota, St. Paul, MN, March 2018.

## 2017

- Invited presentation for the UCLA Computational Genomics Summer Institute, University of California, Los Angeles, CA, July 2017.
- Invited presentation at the Society of Molecular Biology and Evolution, Austin, TX, July 2017.
- Invited presentation at the Searle Scholars Annual Meeting, Chicago, IL, April 2017.
- Presentation and workshop leader at the UCLA La Kretz Workshop in Conservation Genomics, March 2017.
- Seminar at Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, February 2017.
- Seminar for the Department of Genome Sciences, University of Washington, Seattle, WA, February 2017.
- Seminar for the Department of Biology, Washington University, St. Louis, MO, January 2017.
- Seminar for the Department of Ecology and Evolution, University of Chicago, Chicago, IL, January 2017.
- Seminar for the Duke Center for Genomic and Computational Biology, Duke University, Durham, NC, January 2017.

## 2016

- Invited presentation for the UCLA Computational Genomics Summer Institute, University of California, Los Angeles, CA, August 2016.
- Invited presentation for the UCLA Computational Genomics Summer Institute, University of California, Los Angeles, CA, July 2016.
- Seminar at the College of Life Sciences, Sichuan University, Chengdu, China, June 2016.

- Seminar at the Institute of Zoology, Chinese Academy of Sciences, Beijing, China, June 2016.
- Invited presentation at the Dog10k Genomes Consortium meeting, Beijing, China, June 2016.
- Presentation and workshop leader at the UCLA La Kretz Workshop in Conservation Genomics, March 2016.
- Seminar at the Max Plank Institute for Evolutionary Anthropology, Leipzig, Germany, March 2016.
- Seminar for the Bioinformatics and Genomics graduate program, Penn State University, State College, PA, February 2016.
- Seminar for the Department of Preventative Medicine, University of Southern California, Los Angeles, CA, January 2016.

#### **2015**

- Seminar at the University of Bristol. Bristol, UK, October 2015.
- Invited presentation at the “Hidden Complexities in Complex Traits and Genome-wide Association” workshop, Royal Statistical Society, London, UK, October 2015.
- Seminar for the Department of Statistics, University of California, Los Angeles, CA, June 2015.
- Presentation and workshop leader at the UCLA La Kretz Workshop in Conservation Genomics, March 2015.

#### **2014**

- Workshop presenter at the 25th International Symposium on Human Identification, Phoenix, AZ, September 2014.
- Invited talk for Principals in Population Genetics: A coalescence of community to celebrate Andy Clark, Cornell University, Ithaca, NY, July 2014.
- Presentation and workshop leader at the UCLA La Kretz Workshop in Conservation Genomics, March 2014.
- Seminar for the Center for Behavior, Evolution, and Culture, University of California, Los Angeles, CA, February 2014.
- Invited talk at the Collaborative Fund in Biodiversity and Environment Workshop on Population / Genomics Data Analysis, University of Southern California, Los Angeles, CA, January 2014.

#### **2013**

- Seminar for the Molecular and Computational Biology Program, University of Southern California, Los Angeles, CA, November 2013.
- Seminar for the Department of Biomathematics Seminar Series, University of California, Los Angeles, CA, October 2013.
- Invited talk at the Southern California Evolutionary Genetics & Genomics meeting, University of California, Irvine, CA, September 2013.
- Seminar for the Bioinformatics Interdepartmental Ph.D. Program Seminar Series, University of California, Los Angeles, CA, April 2013.
- Presentation and workshop leader at the UCLA La Kretz Workshop in Conservation Genomics, March 2013.

#### **Before 2013**

- Seminar for the Department of Molecular and Cellular Biology, University of California, Berkeley, CA, March 2012.
- Seminar for the Bioinformatics Interdepartmental Ph.D. Program Seminar Series, University of California, Los Angeles, CA, February 2012.

- Seminar for the Department of Biology, Dartmouth College, Hanover, NH, February 2012.
- Seminar for the Department of Human Evolutionary Biology, Harvard University, February 2012.
- Seminar for the Department of Biology, University of Maryland, February 2012.
- Seminar for the Department of Biological Statistics and Computational Biology, Cornell University, Ithaca, NY, January 2012.
- Seminar for the Center for Complex Biological Systems, University of California, Irvine, CA, January 2012.
- Seminar for the Department of Genetics, Stanford University, Palo Alto, CA, January 2012.
- Seminar for the Department of Medicine & Lung Biology Center, University of California, San Francisco, CA, November 2011.
- Seminar for the Department of Biological Sciences, University of Southern California, Los Angeles, CA, November 2011.
- Seminar for the Bioinformatics Interdepartmental Ph.D. Program Seminar Series, University of California, Los Angeles, CA, May 2011.
- Seminar for the Mathematical and Computational Biology Seminar Series, University of California, Berkeley, CA, April 2011.
- Seminar for the Department of Genetics, Harvard Medical School, Boston, MA, January 2011.
- Seminar for the Ecology and Evolution Colloquium at San Francisco State University, San Francisco, CA, November 2010.

#### **SELECT CONFERENCE PRESENTATIONS AND OTHER SEMINARS:**

##### **2019**

- Platform presentation, Society of Molecular Biology and Evolution, Manchester, UK, July 2019.

##### **2018**

- Platform presentation, Evolution, Montpellier, France, August, 2018. (C. Huber from my lab presented instead)
- Platform presentation, Society of Molecular Biology and Evolution, Yokohama, Japan, July 2018.
- Lightning talk, Population, Evolutionary, and Quantitative Genetics Conference, Madison, WI, May 2018

##### **2017**

- Platform presentation, Evolution, Portland, OR, June 2017

##### **2015**

- Platform presentation, Society of Molecular Biology and Evolution, Vienna, Austria, July 2015.
- Platform presentation, Plant & Animal Genome XXIII conference, San Diego, CA, January 2015.

##### **2013**

- Workshop at the 24th International Symposium on Human Identification, Atlanta, GA, October 2013.
- Platform presentation, Society of Molecular Biology and Evolution conference, Chicago, IL, July 2013.
- Workshop, AAFS, Washington D.C., February 2013.
- Platform presentation at the Bay Area Population Genomics conference, Palo Alto, CA, February 2013.



### Before 2013

- Platform presentation at the California Association of Criminalists Northern Study Group meeting, Hayward, CA, May 2012.
- Platform presentation at the California Association of Criminalists meeting, Bakersfield, CA, May 2012.
- Platform presentation at the DNA workshop during the California Association of Criminalists meeting, Sacramento, CA, October 2011.
- Platform presentation, The 12th International Meeting on Human Genome Variation and Complex Genome Analysis (HGV2011), Berkeley, CA, September 2011.
- Platform presentation, Abstract A143, American Academy of Forensic Sciences, Chicago, February 2011.
- Platform presentation, Abstract 21, American Society of Human Genetics, Washington, DC, November 2010.
- Platform presentation at the DNA workshop during the California Association of Criminalists meeting, Oakland, CA, October 2010.
- Seminar at Georgetown University, Washington, DC, October 2009.
- Seminar at Oxford University, Oxford, UK, February 2009.
- Seminar at Harvard University, Boston, MA, February 2009.
- Seminar at the University of California, San Francisco, CA, January 2009.
- Seminar at the University of California, Berkeley, CA, January 2009.
- Platform presentation, Abstract 127, American Society of Human Genetics, Philadelphia, PA, 2008.
- Platform presentation, Abstract 270, The Biology of Genomes, Cold Spring Harbor, 2007.
- Platform presentation, Abstract 150, American Society of Human Genetics, Toronto, 2004.

### MEDIA COVERAGE:

1. Pennisi, E. July 19, 2019. "Genomics guides help for dwindling species." *Science* <https://science.sciencemag.org/content/365/6450/210>
2. Zhang, S. July 1, 2019. "A surprising idea about the risks of extinction." *The Atlantic* <https://www.theatlantic.com/science/archive/2019/07/isle-royale-wolves-and-risks-extinction/593020/>
3. Bhanoo, S.N. December 21, 2015. "Domesticated dogs lag in reproduction." *The New York Times* [http://www.nytimes.com/2015/12/22/science/domesticated-dogs-lag-in-reproduction.html?\\_r=1](http://www.nytimes.com/2015/12/22/science/domesticated-dogs-lag-in-reproduction.html?_r=1)
4. Taylor, A.P. December 21, 2015. "Domestication's downsides for dogs." *The Scientist* <http://www.the-scientist.com/?articles.view/articleNo/44889/title/Domestication-s-Downsides-for-Dogs/>
5. Griffiths, S. December 21, 2015. "Domestication and NOT inbreeding may be to blame for canine diseases: Humans caused genetic changes in the animals as they became our pets." *The Daily Mail* <http://www.dailymail.co.uk/sciencetech/article-3369151/Domestication-NOT-inbreeding-blame-canine-diseases-Humans-caused-genetic-changes-animals-pets.html>
6. Kaplan, K. December 22, 2015. "Dog domestication saddled man's best friend with defective genes, study says." *Los Angeles Times* <http://touch.latimes.com/#section/-1/article/p2p-85380285/>
7. Zimmer, C. February 19, 2015. "A new theory on how Neanderthal DNA spread in Asia." *The New York Times* [http://www.nytimes.com/2015/02/20/science/a-new-theory-on-how-neanderthal-dna-spread-in-asia.html?\\_r=0](http://www.nytimes.com/2015/02/20/science/a-new-theory-on-how-neanderthal-dna-spread-in-asia.html?_r=0)

8. Winsor, M. February 19, 2015. "Neanderthal DNA by race: Asians have closer link from multiple breeding events, Sstudies say." *International Business Times* <http://www.ibtimes.com/neanderthal-dna-race-asians-have-closer-link-multiple-breeding-events-studies-say-1822230>
9. Gray, R. February 13, 2015. "Neanderthals interbred for longer with East Asian humans, DNA reveals." *The Daily Mail* <http://www.dailymail.co.uk/sciencetech/article-2952418/Neanderthals-interbred-longer-modern-humans-east-Asia-DNA-reveals.html>
10. Anderson, A. February 12, 2015. "Papers support possibility of second wave of Neanderthal admixture with East Asian ancestors." *GenomeWeb* <https://www.genomeweb.com/genetic-research/papers-support-possibility-second-wave-neanderthal-admixture-east-asian-ancestors>
11. Perlman, D. September 23, 2011. "Hair DNA reveals 2 migration waves out of Africa." *The San Francisco Chronicle* <http://www.sfgate.com/science/article/Hair-DNA-reveals-2-migration-waves-out-of-Africa-2309028.php>