

JONATHAN K. PRITCHARD
CURRICULUM VITAE

Professor, Departments of Biology and Genetics
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CV version: November 2019

Education

- 1989–1994 B.Sc., Biology and Mathematics
Pennsylvania State University
- 1994–1998 Ph.D., Biology
Stanford University
Advised by Marcus Feldman
- 1998–2001 Postdoctoral Fellow, Statistics
University of Oxford
Advised by Peter Donnelly

Employment History

- 2013–Present Professor, Departments of Genetics and Biology, Stanford University
- 2008–2019 Investigator, Howard Hughes Medical Institute
- 2006–2013 Professor, Department of Human Genetics, The University of Chicago
- 2001–2005 Assistant Professor, Department of Human Genetics, The University of Chicago

Awards and honors

- 2019 Fabio Frassetto International Prize in Physical Anthropology from the Lincean Academy of Italy
- 2016 Review of Pritchard et al. (2000) in the Classic Papers series for the centennial year of *Genetics* by John Novembre (PMID 27729489). P. et al. has now been cited >26,000 times (G Scholar)
- 2015 Kistler Prize in Population Genetics and Society
- 2013 Selected as a Fellow of the American Academy of Arts and Sciences
- 2013 Edward Novitski Prize from the Genetics Society of America; this award recognizes “creativity and intellectual ingenuity in the solution of significant problems in genetics”
- 2013 Outstanding Alumni Award, Eberly College of Science, Penn State University
- 2013 *Best postdoc talk* award to my postdoc S. Gopalakrishnan; Am. Soc. Hum Genet. meeting
- 2008 Selected as an investigator of the Howard Hughes Medical Institute
- 2007 *Best postdoc talk* award to my postdoc Graham Coop; Am. Soc. Hum. Genet. meeting.
- 2006 *Best Ph.D thesis award* to my student Ben Voight (for U of C Biological Sciences Division)
- 2006 New York Times front page news article on Voight et al paper on natural selection

- 2004 Selected Packard Fellow
- 2004 Selected Alfred P. Sloan Fellow
- 2003 Lancet's *Paper of the Year* (for any biomedical journal) was awarded to the paper of Rosenberg, Pritchard et al. (Science 2002) on human population structure (editorial in Lancet 362:2101-2103).
- 2002 Mitchell Prize from the American Statistical Association and the International Society of Bayesian Analysis, presented annually for "an outstanding paper describing how a Bayesian analysis has solved an important applied problem."
- 1994-1998 Howard Hughes Medical Institute Predoctoral Fellowship
- 1994 McCoy Award, given to the Penn State Outstanding Scholar-Athlete
- 1992 Stecker Award, given to a Penn State undergraduate in Mathematics
- 1989-1993 Penn State Braddock Scholarship and Academic Excellence Scholarship

Selected Professional Activities

- 2018–present SAB/advisor: Calico, Precise.ly, Inari
- 2017–present Co-Director: Stanford Center for Computational, Evolutionary and Human Genomics
- 2017–present External Advisory Board to Wellcome Trust Sanger Institute
- 2017 Lead organizing cmte for "Human Evolution: fossils, archaeology, and genomics" meeting, Hinxton, UK
- 2016–2020 NHGRI (NIH) Council Member
- 2016–2018 Lead organizing committee for "Biology of Genomes" meeting, Cold Spring Harbor
- 2015–present Science Magazine Board of Reviewing Editors
- 2014–present Frequent guest editor for PLOS Genetics
- 2013 Scientific Advisory Board, Cellular Genomics Program, Wellcome Trust Sanger Institute
- 2012–present Editorial Board: Current Biology
- 2008–2012 Associate Editor: Molecular Biology and Evolution
- 2006–2016 23andMe, SAB
- 2006–2014 Associate Editor: PLOS Genetics

Research Support [as PI]

- 2016-2019 RO1 HG008140: "Integration of functional data and GWAS to elucidate genetic basis of diseases"
- 2017-2020 UO1 HG009431: "Decoding the regulatory architecture of the human genome across cell types, individuals and disease."

Previous grants/fellowships:

- 2008-2019 Investigator, Howard Hughes Medical Institute.
- 2014-2017 RO1 ES025009: "Computational methods for modeling lineage-specific gene regulation." Administrative supplement for 2016-2017.
- 2012-2016 UO1 HG007036: "Genetic and epigenetic controls of gene regulation." Includes administrative supplement for 2015-2016.
- 2010-2013 RO1 MH090951: "Statistical analysis of gene expression quantitative trait loci (eQTL)." Includes administrative supplement for 2012-2013.
- 2008-2016 RO1 MH084703: "Analysis and interpretation of DNA sequence data in association studies."
- 2003-2008 RO1 HG002772: "Linkage Disequilibrium Methods for Complex Trait Mapping."
- 2004–2009 Packard Foundation Fellowship: "Population genetics of genomic rearrangements."

2004-2006 Sloan Foundation Fellowship
 1999-2003 Burroughs-Wellcome Fund Hitchings-Elion Postdoc-Faculty Award
 "Population structure and linkage disequilibrium in association mapping."
 1998 NIH (NRSA) 3-year Postdoctoral Award (replaced by BWF award)
 "The impact of population history on association mapping."
 1994-1998 Howard Hughes Medical Institute Predoctoral Fellowship
 1994 NSF Predoctoral Fellowship (declined)
 1989-1993 Penn State Braddock Scholarship (four-year full-tuition award)
 1989-1993 Penn State Academic Excellence Scholarship

Graduate Student/Postdoc Mentoring:

2019–Present Hakhamanesh Mostafavi (postdoc)
 2019–Present Clemens Weiss (postdoc)
 2019–Present Jeff Spence (postdoc)
 2019–Present Sahin Naqvi (postdoc; joint with Joanna Wysocka)
 2019–Present Shaila Musharoff (postdoc)
 2018–Present Yuval Simons (postdoc)
 2018–Present Jake Freimer (postdoc; joint with Alex Marson)
 2018–Present Hanna Ollila (postdoc)
 2016–Present Harold Pimentel (postdoc)
 2015–Present Ziyue Gao (postdoc)

2019–Present Alyssa Fortier (PhD student, Biology)
 2019–Present Roshni Patel (PhD student, Genetics)
 2018–Present Adele Xu (MSTP; primary lab Maria Barna)
 2017–present Hannah Moots (PhD student, Archaeology)
 2017–present Margaret Antonio (PhD student, BMI)
 2017–present Nasa Sinnott-Armstrong (PhD student, Genetics)

Previous Postdocs:

2015–2018 David Knowles (postdoc); joint w/ Sylvia Plevritis; now asst prof, NY Genome Center/ Columbia
 2014–2018 Eilon Sharon (postdoc); joint with Hunter Fraser; now staff scientist, Insitro
 2012–2018 Yair Field (postdoc; now staff scientist, Illumina)
 2015–2017 Kelley Harris (postdoc; now assistant professor, U Washington)
 2012–2017 Xun Lan (postdoc; now assistant professor, Tsinghua University)
 2014–2017 Yang Li (postdoc; now assistant professor, U Chicago)
 2014–2017 Anand Bhaskar (postdoc); now data scientist, Facebook
 2011–2016 Anil Raj (postdoc); now staff scientist, Calico
 2014–2016 David Golan (postdoc); cofounder of Viz.ai
 2014–2015 Audrey Fu (visiting postdoc); now assistant professor, Univ of Idaho
 2014–2015 Towfique Raj (visiting postdoc); now assistant professor, Mt Sinai
 2014–2015 Kyle Gaulton (visiting postdoc); now assistant professor, UCSD
 2010–2015 Graham McVicker (postdoc); now assistant professor, Salk Institute
 2013–2014 Alexis Battle (postdoc); now associate professor, Johns Hopkins
 2011–2014 Stoyan Georgiev (postdoc); now data scientist, Google
 2011–2013 Zia Khan (postdoc; joint with Y Gilad); assistant professor, University of Maryland; now Genentech
 2011–2013 Shyam Gopalakrishnan (postdoc; joint with Abe Palmer); now researcher U Copenhagen
 2012–2013 Allegra Petti (postdoc; joint with Y Gilad); now staff scientist, Wash U St Louis

2009–2012 Roger Pique-Regi (postdoc); now associate professor, Wayne State, MI
 2008–2011 Daniel Gaffney (postdoc); now group leader, Sanger Institute, UK
 2009–2011 Pall Melsted (postdoc); now assistant professor, University of Iceland
 2009–2011 Ying Wang (postdoc); now junior faculty, Beijing Institute of Genomics
 2008–2009 Jordana Bell (postdoc); now Senior Lecturer, Kings College London
 2006–2007 Jean-Baptiste Veyrieras (postdoc); now group leader at bioMerieux
 2004–2008 Graham Coop (postdoc); now professor, U. of California, Davis
 2001–2005 Sebastian Zöllner (postdoc); now professor, Biostatistics, U. of Michigan
 2002–2004 Giovanni Montana (postdoc); now professor of Biostatistics, Imperial College London
 2002–2003 Jeffrey Wall (postdoc); now professor of Epidemiology and Biostats, UCSF

Previous PhD Students:

2015–2019 Jessica Ribado (PhD student, Genetics; joint w/ Ami Bhatt; now PD at Centers for Disease Modeling)
 2015–2019 Evan Boyle (PhD student, Genetics; joint with Will Greenleaf; now postdoc with Gene Yeo, UCSD)
 2014–2019 Diego Calderon (PhD student, BMI; now postdoc with Trapnell/Shendure at U Washington)
 2014–2019 Emily Glassberg (PhD student, Biology; now at Boston Consulting Group)
 2014–2018 Arbel Harpak (PhD student, Biology; postdoc with Molly Przeworski, Columbia)
 2014–2018 Natalie Telis (PhD student, BMI; staff scientist at Ancestry)
 2011–2015 Bryce van de Geijn (PhD student, Chicago GGSB); postdoc with Alkes Price, Harvard SPH
 2014–2015 Cristina Pop (PhD, CS with Daphne Koller; mentored by me 2014-5); data scientist at Google
 2011–2014 Paul Grabowski (PhD student, Ecology and Evolution; joint with J. Borevitz); postdoc at USDA
 2012–2013 Carolyn Jumper (PhD student, Human Genetics); switched to Cox lab due to Stanford move
 2012–2013 Michael Turchin (PhD student, Human Genetics); switched to Stephens lab due to Stanford move
 2008–2012 Jack Degner (PhD, GGSB); postdoc with Eileen Furlong, EMBL; now Senior Scientist at AbbVie
 2007–2011 Joseph Pickrell (PhD, Human Genetics); postdoc with David Reich, Harvard;
 asst prof NY Genome Center/Columbia Univ; now founder/CEO of GenCove
 2004–2008 Sridhar Kudaravalli (PhD, Human Genetics, 2008)
 2004–2008 Su Yeon Kim (PhD, Statistics, 2008; joint with P. McCullagh)
 postdoc with Rasmus Nielsen, Terry Speed at UC Berkeley; now Bioinformatician Veracyte
 2004–2006 Daniel Davison (PhD, Comm Ev. Biol., 2006; joint with S. Hackett)
 postdoc in Statistics with Peter Donnelly, U. of Oxford; now at Counsyl
 2003–2007 Donald Conrad (PhD, Human Genetics, 2008)
 postdoc with Matt Hurles, Sanger Institute; now assoc. prof. Wash U.
 2002–2006 Benjamin Voight (PhD, Human Genetics, 2006; joint with N. Cox)
 postdoc with Mark Daly, Broad Institute; now assoc. prof., Univ of Pennsylvania

Selected other lab members:

2001–2007 Ben Lehmann (programmer); now PhD student in astrophysics, UCSC
 2011-2012 Andy Dahl (Honors Thesis, Statistics); DPhil student, Oxford; PD UCSF; now asst Prof U Chicago
 2006–2008 Melissa Hubisz (M.S., Human Genetics); PhD student, Cornell; staff scientist Cornell
 2001–2007 Xiaoquan William Wen (programmer); now Associate Professor Biostatistics, Michigan

Publications

- [1] S Catania, PA Dumesic, H Pimentel, A Nasif, CI Stoddard, JE Burke, JK Diedrich, S Cook, T Shea, E Geinger, [5 others], JK Pritchard, and HD Madhani. Evolutionary persistence of DNA methylation for millions of years after ancient loss of a de novo methyltransferase. *bioRxiv*, page 149385, 2019.
- [2] N Sinnott-Armstrong, Y Tanigawa, D Amar, NJ Mars, M Aguirre, GR Venkataraman, M Wainberg, HM Ollila, JP Pirruccello, J Qian, [8 others], JK Pritchard, MJ Daly, and MA Rivas. Genetics of 38 blood and urine biomarkers in the UK Biobank. *BioRxiv*, page 660506, 2019.
- [3] H Mostafavi, A Harpak, D Conley, JK Pritchard, and M Przeworski. Variable prediction accuracy of polygenic scores within an ancestry group. *BioRxiv*, page 629949, 2019.
- [4] ML Antonio, Z Gao, HM Moots, M Lucci, F Candilio, S Sawyer, V Oberreiter, D Calderon, K Devitofranceschi, RC Aikens, S Aneli, F Bartoli, A Bedini, O Cheronet, DJ Cotter, DM Fernandes, G Gasperetti, R Grifoni, A Guidi, F La Pastina, E Loreti, D Manacorda, G Matullo, S Morretta, A Nava, NV Fiocchi, F Nomi, C Pavolini, M Pentiricci, P Pergola, M Piranomonte, R Schmidt, G Spinola, A Spertuti, M Rubini, L Bondioli, A Coppa, R Pinhasi, and JK. Pritchard. Ancient Rome: A genetic crossroads of Europe and the Mediterranean. *Science*, 366(6466):708–714, 2019.
- [5] D Calderon, MLT Nguyen, A Mezger, A Kathiria, F Müller, V Nguyen, N Lescano, B Wu, J Trombetta, JV Ribado, DA Knowles, Z Gao, F Blaesche, AV Parent, TD Burt, MS Anderson, LA Criswell, WJ Greenleaf, A Marson, and JK. Pritchard. Landscape of stimulation-responsive chromatin across diverse human immune cells. *Nature Genetics*, pages 1–12, 2019.
- [6] N Telis, EC Glassberg, JK Pritchard, and C Gunter. Public discussion affects question asking at academic conferences. *The American Journal of Human Genetics*, 2019.
- [7] X Liu, YI Li, and JK Pritchard. Trans effects on gene expression can drive omnigenic inheritance. *Cell*, 177(4):1022–1034, 2019.
- [8] MC Stahlschmidt, TC Collin, DM Fernandes, G Bar-Oz, A Belfer-Cohen, Z Gao, N Jakeli, Z Matskevich, T Meshveliani, JK Pritchard, F McDermott, and R Pinhasi. Ancient mammalian and plant DNA from late Quaternary stalagmite layers at Solkoto Cave, Georgia. *Scientific Reports*, 9(1):6628, 2019.
- [9] JJ Berg, A Harpak, N Sinnott-Armstrong, Anja M Joergensen, H Mostafavi, Y Field, EA Boyle, X Zhang, F Racimo, JK Pritchard, and Coop G. Reduced signal for polygenic adaptation of height in UK Biobank. *ELife*, 8:e39725, 2019.
- [10] NA Rosenberg, MD Edge, JK Pritchard, and MW Feldman. Interpreting polygenic scores, polygenic adaptation, and human phenotypic differences. *Evolution, medicine, and public health*, 2019(1):26–34, 2019.
- [11] EC Glassberg, Z Gao, A Harpak, X Lan, and JK Pritchard. Evidence for weak selective constraint on human gene expression. *Genetics*, 211(2):757–772, 2019.
- [12] EA Boyle, JK Pritchard, and WJ Greenleaf. High-resolution mapping of cancer cell networks using co-functional interactions. *Molecular Systems Biology*, 14(12), 2018.
- [13] H Ollila, E Sharon, L Lin, N Sinnott-Armstrong, A Ambati, RP Hillary, O Jolanki, J Faraco, M Einen, G Luo, et al. Narcolepsy risk loci are enriched in immune cells and suggest autoimmune modulation of the t cell receptor repertoire. *bioRxiv*, page 373555, 2018.
- [14] P Desai, N Telis, B Lehmann, K Bettinger, JK Pritchard, and S Datta. Scireader*: A cloud-based recommender system for biomedical literature. *bioRxiv*, page 333922, 2018.

- [15] E Sharon, S-AA Chen, NM Khosla, JD Smith, JK Pritchard, and HB Fraser. Functional genetic variants revealed by massively parallel precise genome editing. *Cell*, 175(2):544–557, 2018.
- [16] SH Wang, CJ Hsiao, Z Khan, and JK Pritchard. Post-translational buffering leads to convergent protein expression levels between primates. *Genome Biology*, 19(1):83, 2018.
- [17] DA Knowles, CK Burrows, JD Blischak, KM Patterson, DJ Serie, N Norton, C Ober, JK Pritchard, and Y Gilad. Determining the genetic basis of anthracycline-cardiotoxicity by molecular response QTL mapping in induced cardiomyocytes. *eLife*, 7, 2018.
- [18] R Yamamoto, AC Wilkinson, J Ooehara, X Lan, C-Y Lai, Y Nakauchi, JK Pritchard, and H Nakauchi. Large-scale clonal analysis resolves aging of the mouse hematopoietic stem cell compartment. *Cell Stem Cell*, 22(4):600–607, 2018.
- [19] D Sparvoli, E Richardson, H Osakada, X Lan, M Iwamoto, GR Bowman, C Kontur, WA Bourland, DH Lynn, JK Pritchard, T Haraguchi, JB Dacks, and Turkewitz AP. Remodeling the Specificity of an Endosomal CORVET Tether Underlies Formation of Regulated Secretory Vesicles in the Ciliate *Tetrahymena thermophila*. *Current Biology*, 28(5):697–710, 2018.
- [20] YI Li, DA Knowles, J Humphrey, AN Barbeira, SP Dickinson, HK Im, and JK Pritchard. Annotation-free quantification of RNA splicing using LeafCutter. *Nature Genetics*, 50(1):151, 2018.
- [21] NE Banovich, YI Li, A Raj, MC Ward, P Greenside, D Calderon, PY Tung, JE Burnett, M Myrthil, SM Thomas, CK Burrows, I Gallego Romero, BJ Pavlovic, A Kundaje, JK Pritchard, and Y Gilad. Impact of regulatory variation across human iPSCs and differentiated cells. *Genome Research*, 28(1):122–131, 2018.
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- [23] D Calderon, A Bhaskar, DA Knowles, D Golan, T Raj, A Fu, and JK Pritchard. Inferring relevant cell types for complex traits using single-cell gene expression. *The American Journal of Human Genetics*, 101(5):686–699, 2017.
- [24] E Sharon, H Shi, S Kharbanda, W Koh, LR Martin, KK Khush, H Valentine, JK Pritchard, and I De Vlaminck. Quantification of transplant-derived circulating cell-free DNA in absence of a donor genotype. *PLoS Computational Biology*, 13(8):e1005629, 2017.
- [25] EA Boyle, YI Li, and JK Pritchard. The omnigenic model: Response from the authors. *Journal of Psychiatry and Brain Science*, 2(5):S8, 2017.
- [26] EA Boyle, YI Li, and JK Pritchard. An expanded view of complex traits: From polygenic to omnigenic. *Cell*, 169(7):1177–1186, 2017.
- [27] K Harris and JK Pritchard. Rapid evolution of the human mutation spectrum. *eLife*, 6:e24284, 2017.
- [28] R Nielsen, JM Akey, M Jakobsson, JK Pritchard, S Tishkoff, and E Willerslev. Tracing the peopling of the world through genomics. *Nature*, 541(7637):302–310, 2017.
- [29] PY Tung, JD Blischak, CJ Hsiao, DA Knowles, JE Burnett, JK Pritchard, and Y Gilad. Batch effects and the effective design of single-cell gene expression studies. *Scientific Reports*, 7, 2017.
- [30] A Harpak, A Bhaskar, and JK Pritchard. Mutation rate variation is a primary determinant of the distribution of allele frequencies in humans. *PLoS Genetics*, 12(12):e1006489, 2016.

- [31] N Telis, BV Lehmann, MW Feldman, and JK Pritchard. A bibliometric history of the journal *Genetics*. *Genetics*, 204(4):1337–1342, 2016.
- [32] Y Field, EA Boyle, N Telis, Z Gao, KJ Gaulton, D Golan, L Yengo, G Rocheleau, P Froguel, MI McCarthy, and JK Pritchard. Detection of human adaptation during the past 2,000 years. *Science*, 354:760–764, 2016.
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- [34] E Sharon, LV Sibener, A Battle, HB Fraser, KC Garcia, and JK Pritchard. Genetic variation in MHC proteins is associated with T cell receptor expression biases. *Nature Genetics*, 2016.
- [35] CC Parker, S Gopalakrishnan, P Carbonetto, NM Gonzales, E Leung, YJ Park, E Aryee, J Davis, DA Blizard, CL Ackert-Bicknell, LA, JK Pritchard, and Palmer AA. Genome-wide association study of behavioral, physiological and gene expression traits in outbred CFW mice. *Nature Genetics*, 2016.
- [36] C Kontur, S Kumar, X Lan, JK Pritchard, and AP Turkewitz. Whole genome sequencing identifies a novel factor required for secretory granule maturation in *Tetrahymena thermophila*. *G3*, 6:2505–2516, 2016.
- [37] A Raj, SH Wang, H Shim, A Harpak, YI Li, B Engelmann, M Stephens, Y Gilad, and JK Pritchard. Thousands of novel translated open reading frames in humans inferred by ribosome footprint profiling. *eLife*, 5:e13328, 2016.
- [38] X Lan and JK Pritchard. Coregulation of tandem duplicate genes slows evolution of subfunctionalization in mammals. *Science*, 352(6288):1009–1013, 2016.
- [39] YI Li, B van de Geijn, A Raj, DA Knowles, AA Petti, D Golan, Y Gilad, and JK Pritchard. RNA splicing is a primary link between genetic variation and disease. *Science*, 352(6285):600–604, 2016.
- [40] CK Burrows, NE Banovich, BJ Pavlovic, K Patterson, I Gallego Romero, JK Pritchard, and Y Gilad. Genetic variation, not cell type of origin, underlies the majority of identifiable regulatory differences in iPSCs. *PLoS Genet*, 12(1):e1005793, 2016.
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- [44] Grubert F, Zaugg JB, Kasowski M, Ursu O, Spacek DV, Martin AR, Greenside P, Srivas R, Phanstiel DH, Pekowska A, Heidari N, Euskirchen G, Huber W, Pritchard JK, Bustamante CD, Steinmetz LM, Kundaje A, and Snyder M. Genetic control of chromatin states in humans involves local and distal chromosomal interactions. *Cell*, 162(5):1051–1065, 2015.
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- [47] AA Pai, JK Pritchard, and Y Gilad. The genetic and mechanistic basis for variation in gene regulation. *PLOS Genetics*, 11(1):e1004857, 2015.
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- [51] A Raj, M Stephens, and JK Pritchard. Variational inference of population structure in large SNP datasets. *Genetics*, 197:573–589, 2014.
- [52] DA Cusanovich, B Pavlovic, JK Pritchard, and Y Gilad. The functional consequences of variation in transcription factor binding. *PLoS Genetics*, 10(3):e1004226, 2014.
- [53] C Jeong, G Alkorta-Aranburu, B Basnyat, M Neupane, DB Witonsky, JK Pritchard, CM Beall, and A Di Rienzo. Admixture facilitates genetic adaptations to high altitude in Tibet. *Nature Communications*, 5:3281, 2014.
- [54] YB Simons, MC Turchin, JK Pritchard, and G Sella. The deleterious mutation load is insensitive to recent population history. *Nature Genetics*, 46:220–224, 2014.
- [55] N Nalabothula, G McVicker, J Maiorano, R Martin, JK Pritchard, and YN Fondufe-Mittendorf. The chromatin architectural proteins HMGD1 and H1 bind reciprocally and have opposite effects on chromatin structure and gene regulation. *BMC Genomics*, 15(1):92, 2014.
- [56] E Birney and JK Pritchard. Archaic humans: Four makes a party. *Nature*, 505:32–34, 2014.
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- [59] G Alkorta-Aranburu, CM Beall, DB Witonsky, A Gebremedhin, JK Pritchard, and A Di Rienzo. The genetic architecture of adaptations to high altitude in Ethiopia. *PLoS Genetics*, 8(12):e1003110, 2012.
- [60] DJ Gaffney, G McVicker, AA Pai, YN Fondufe-Mittendorf, N Lewellen, K Michelini, J Widom, Y Gilad, and JK Pritchard. Controls of nucleosome positioning in the human genome. *PLOS Genetics*, 8(11):e1003036, 2012.
- [61] JK Pickrell and JK Pritchard. Inference of population splits and mixtures from genome-wide allele frequency data. *PLOS Genetics*, 8(11):e1002967, 2012.

- [62] AA Pai, CE Cain, O Mizrahi-Man, S De Leon, N Lewellen, J-B Veyrieras, JF Degner, DJ Gaffney, JK Pickrell, M Stephens, JK Pritchard, and Y Gilad. The contribution of RNA decay quantitative trait loci to inter-individual variation in steady-state gene expression levels. *PLoS Genetics*, 8(10):e1003000, 2012.
- [63] J.R. Ecker, W.A. Bickmore, I. Barroso, J.K. Pritchard, Y. Gilad, and E. Segal. Genomics: ENCODE explained. *Nature*, 489(7414):52–55, 2012.
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- [65] JK Pickrell, Y Gilad, and JK Pritchard. Comment on “Widespread RNA and DNA sequence differences in the human transcriptome”. *Science*, 335(6074):1302–1302, 2012.
- [66] JM Zullo, IA Demarco, R Piqué-Regi, DJ Gaffney, CB Epstein, CJ Spooner, TR Luperchio, BE Bernstein, JK Pritchard, KL Reddy, and H Singh. DNA sequence-dependent compartmentalization and silencing of chromatin at the nuclear lamina. *Cell*, 149(7):1474–1487, 2012.
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