JONATHAN K. PRITCHARD

Bing Professor of Population Studies
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CV version: December 2022

Employment History

2020–Present	Bing Professor of Population Studies
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

Education

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

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 ∼35,000 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

2021–present	Co-Director of Graduate Studies, Dept of Biology, Stanford
2018–present	SAB: NY Genome Center; Company SABs: Calico, Inari, Relation Therapeutics
2017–present	Co-Director: Stanford Center for Computational, Evolutionary and Human Genomics
2017–2021	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
2015–2022	Science Magazine Board of Reviewing Editors
2014–2016	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 only]

2020-2024	RO1 HG011432: "New methods for constructing and evaluating polygenic scores."
2016-2024	RO1 HG008140: "Integration of functional data and GWAS to elucidate genetic basis of diseases"

Previous grants/fellowships:

2017-2020	UO1 HG009431: "Decoding the regulatory architecture of the human genome across cell types, individuals and disease." [Supplement to 2021]
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	U01 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

Mentoring:

2022–Present	Ronghui Zhu (postdoc; joint with Alex Marson)
2021–Present	Mineto Ota (postdoc; joint with Aviv Regev)
2021–Present	Romain Lopez (postdoc; joint with Aviv Regev)
2021–Present	Josh Weinstock (postdoc; joint with Alexis Battle)
2020–Present	Daphna Rothschild (postdoc; joint with Maria Barna)
2019–Present	Hakhamanesh Mostafavi (postdoc)
2019–Present	Clemens Weiss (postdoc)
2019–Present	Jeff Spence (postdoc)
2019–Present	Sahin Naqvi (postdoc; joint with Joanna Wysocka)
2018–Present	Yuval Simons (postdoc)

2022–Present	Alvina Adimoelja (PhD student, Genetics; joint with Christina Curtis)
2022–Present	Jon Judd (PhD student, Genetics; joint with John Witte, Linda Kachuri)
2022–Present	Tony Zeng (PhD student, Genetics; joint with Jesse Engreitz)
2022–Present	Wilder Wohns (MD student)
2020–Present	Courtney Smith (MSTP student, Genetics)
2020–Present	Matthew Aguirre (PhD student, BMI)
2019–Present	Alyssa Fortier (PhD student, Biology)
2019–Present	Roshni Patel (PhD student, Genetics)

Previous Postdocs:

2019–2022	Shaila Musharoff (postdoc); now Assistant Professor, Cornell
2018–2022	Jake Freimer (postdoc; joint with Alex Marson); now staff scientist at Genentech
2018–2019	Hanna Ollila (postdoc); now Group Leader, University of Helsinki
2016–2020	Harold Pimentel (postdoc); now Assistant Professor, UCLA
2015–2020	Ziyue Gao (postdoc); now Assistant Professor, Univ Pennsylvania
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 Assoc Prof, 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); G.L. at Sanger Institute; now head of Cellular Genetics, Genomics PLC
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:

2018–Present Adele Xu (MSTP; primary lab Maria Barna); now MD student
2017–present Margaret Antonio (PhD student, BMI); now staff scientist at Grail
2017–present Nasa Sinnott-Armstrong (PhD student, Genetics); now Asst Prof, Fred Hutch
2017–2021 Hannah Moots (PhD student, Archaeology; now postdoc at U Chicago)
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:

2016–2017 Ben Lehmann (programmer); PhD in astrophysics UCSC, now Postdoc MIT

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] R Lopez, N Tagasovska, S Ra, K Cho, JK Pritchard, and A Regev. Learning causal representations of single cells via sparse mechanism shift modeling. *arXiv preprint arXiv:2211.03553*, 2022.

[2] Jazlyn A Mooney, Lily Agranat-Tamir, Jonathan K Pritchard, and Noah A Rosenberg. On the number of genealogical ancestors tracing to the source groups of an admixed population. *arXiv preprint arXiv:2210.12306*, 2022.

[3] CJ Smith, N Sinnott-Armstrong, A Cichońska, H Julkunen, EB Fauman, P Würtz, and JK Pritchard. Integrative analysis of metabolite GWAS illuminates the molecular basis of pleiotropy and genetic correlation. *Elife*, 11:e79348, 2022.

[4] Q Li, MJ Gloudemans, JM Geisinger, B Fan, F Aguet, T Sun, G Ramaswami, YI Li, J-B Ma, JK Pritchard, Montgomery SB, and Li JB. RNA editing underlies genetic risk of common inflammatory diseases. *Nature*, 608:1–9, 2022.

[5] JW Freimer, O Shaked, S Naqvi, N Sinnott-Armstrong, A Kathiria, CM Garrido, AF Chen, JT Cortez, WJ Greenleaf, JK Pritchard, and A Marson. Systematic discovery and perturbation of regulatory genes in human T cells reveals the architecture of immune networks. *Nature Genetics*, 54(8):1133–1144, 2022.

[6] RA Patel, SA Musharoff, JP Spence, H Pimentel, C Tcheandjieu, H Mostafavi, Nasa Sinnott-Armstrong, [17 others], and Pritchard JK. Genetic interactions drive heterogeneity in causal variant effect sizes for gene expression and complex traits. *The American Journal of Human Genetics*, 109(7):1286–1297, 2022.

[7] R Lopez, J-C Hütter, JK Pritchard, and A Regev. Large-scale differentiable causal discovery of factor graphs. *arXiv preprint arXiv:2206.07824*, 2022.

[8] YB Simons, H Mostafavi, CJ Smith, JK Pritchard, and G Sella. Simple scaling laws control the genetic architectures of human complex traits. *bioRxiv*, 2022.

[9] AL Fortier and JK Pritchard. Ancient trans-species polymorphism at the major histocompatibility complex in primates. *bioRxiv*, 2022.

[10] S Naqvi, S Kim, H Hoskens, H Matthews, RA Spritz, OD Klein, B Hallgrimsson, T Swigut, P Claes, JK Pritchard, and Wysocka J. Precise modulation of transcription factor levels reveals drivers of dosage sensitivity. *bioRxiv*, 2022.

[11] ML Antonio, CL Weiß, Z Gao, S Sawyer, [95 others], and Pritchard JK. Stable population structure in Europe since the Iron Age, despite high mobility. *bioRxiv*, 2022.

[12] H Mostafavi, JP Spence, S Naqvi, and JK Pritchard. Limited overlap of eQTLs and GWAS hits due to systematic differences in discovery. *bioRxiv*, 2022.

[13] AF Xu, R Molinuevo, E Fazzari, H Tom, Z Zhang, J Menendez, KM Casey, D Ruggero, L Hinck, JK Pritchard, and Barna M. Subfunctionalized expression drives evolutionary retention of ribosomal protein paralogs in vertebrates. *bioRxiv*, 2022.

[14] DG Ashbrook, T Sasani, M Maksimov, MH Gunturkun, N Ma, F Villani, Y Ren, D Rothschild, H Chen, L Lu, [4 others], Pritchard JK, Palmer AA, and Williams RW. Private and sub-family specific mutations of founder haplotypes in the BXD family reveal phenotypic consequences relevant to health and disease. *bioRxiv*, 2022.

[15] JP Spence, N Sinnott-Armstrong, T Assimes, and JK Pritchard. A flexible modeling and inference framework for estimating variant effect sizes from GWAS summary statistics. *bioRxiv*, 2022.

[16] Y Simons, O Naret, J Fellay, and JK Pritchard. Is competition for cellular resources a driver of complex trait heritability? *bioRxiv*, 2022.

[17] HM Moots, ML Antonio, S Sawyer, JP Spence, [20 others], JK Pritchard, and R Pinhasi. A Genetic History of Continuity and Mobility in the Iron Age Central Mediterranean. *bioRxiv*, 2022.

[18] TA Sasani, DG Ashbrook, AC Beichman, L Lu, AA Palmer, RW Williams, JK Pritchard, and K Harris. A natural mutator allele shapes mutation spectrum variation in mice. *Nature*, 605(7910):497–502, 2022.

[19] Sahin Naqvi, Yoeri Sleyp, Hanne Hoskens, Karlijne Indencleef, Jeffrey P Spence, [9 others], Jonathan K Pritchard, S Sunaert, H Peeters, J Wysocka, and P Claes. Shared heritability of human face and brain shape. *Nature Genetics*, 53:1–10, 2021.

[20] N Sinnott-Armstrong, S Naqvi, M Rivas, and JK Pritchard. GWAS of three molecular traits highlights core genes and pathways alongside a highly polygenic background. *Elife*, 10:e58615, 2021.

[21] N Sinnott-Armstrong, IS Sousa, S Laber, E Rendina-Ruedy, SEN Dankel, T Ferreira, G Mellgren, D Karasik, M Rivas, JK Pritchard, [9 others], and M Claussnitzer. A regulatory variant at 3q21.1 confers an increased pleiotropic risk for hyperglycemia and altered bone mineral density. *Cell Metabolism*, 33(3):615–628, 2021.

[22] N Sinnott-Armstrong, Y Tanigawa, D Amar, N Mars, C Benner, M Aguirre, GR Venkataraman, M Wainberg, HM Ollila, T Kiiskinen, JP Pirruccello, J Qian, [8 others], JK Pritchard, MJ Daly, and MA Rivas. Genetics of 35 blood and urine biomarkers in the UK Biobank. *Nature Genetics*, 53(2):185–194, 2021.

[23] S Catania, PA Dumesic, H Pimentel, A Nasif, CI Stoddard, JE Burke, JK Diedrich, S Cook, T Shea, E Geinger, Lintner R, Yates JR 3rd, Hajkova P, GJ Narlikar, CA Cuomo, JK Pritchard, and HD. Madhani. Evolutionary persistence of DNA methylation for millions of years after ancient loss of a de novo methyltransferase. *Cell*, 2020.

[24] H Mostafavi, A Harpak, I Agarwal, D Conley, JK Pritchard, and M Przeworski. Variable prediction accuracy of polygenic scores within an ancestry group. *Elife*, 9:e48376, 2020.

[25] AE Trevino, N Sinnott-Armstrong, J Andersen, S-J Yoon, N Huber, JK Pritchard, HY Chang, WJ Greenleaf, and SP Pasca. Chromatin accessibility dynamics in a model of human forebrain development. *Science*, 367(6476), 2020.

[26] 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 Sperduti, 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.

[27] 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 Blaeschke, 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.

[28] N Telis, EC Glassberg, JK Pritchard, and C Gunter. Public discussion affects question asking at academic conferences. *The American Journal of Human Genetics*, 2019.

[29] X Liu, YI Li, and JK Pritchard. Trans effects on gene expression can drive omnigenic inheritance. *Cell*, 177(4):1022–1034, 2019.

[30] 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 Solkota Cave, Georgia. *Scientific Reports*, 9(1):6628, 2019.

[31] 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.

[32] 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.

[33] 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.

[34] EA Boyle, JK Pritchard, and WJ Greenleaf. High-resolution mapping of cancer cell networks using co-functional interactions. *Molecular Systems Biology*, 14(12), 2018.

[35] 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.

[36] 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.

[37] 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.

[38] 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.

[39] 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.

[40] 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.

[41] 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.

[42] 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.

[43] 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.

[44] A Harpak, X Lan, Z Gao, and JK Pritchard. Frequent non-allelic gene conversion on the human lineage and its effect on the divergence of gene duplicates. *Proceedings of the National Academy of Sciences*, 114(48):12779–12784, 2017.

[45] 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.

[46] E Sharon, H Shi, S Kharbanda, W Koh, LR Martin, KK Khush, H Valantine, 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.

[47] EA Boyle, YI Li, and JK Pritchard. The omnigenic model: Response from the authors. *Journal of Psychiatry and Brain Science*, 2(5):S8, 2017.

[48] EA Boyle, YI Li, and JK Pritchard. An expanded view of complex traits: From polygenic to omnigenic. *Cell*, 169(7):1177–1186, 2017.

[49] K Harris and JK Pritchard. Rapid evolution of the human mutation spectrum. *eLife*, 6:e24284, 2017.

[50] 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.

[51] 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.

[52] 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.

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[55] MR Corces, JD Buenrostro, B Wu, PG Greenside, SM Chan, JL Koenig, MP Snyder, JK Pritchard, A Kundaje, WJ Greenleaf, R Majeti, and Chang HY. Lineage-specific and single-cell chromatin accessibility charts human hematopoiesis and leukemia evolution. *Nature Genetics*, 2016.

[56] 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.

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[58] 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.

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