Stanford



Hua Tang

Professor of Genetics and, by courtesy, of Statistics

NIH Biosketch available Online Curriculum Vitae available Online

Bio

BIO

Dr. Tang received her PhD in Statistics, with a minor in Genetics, from Stanford University in 2002. From 2002 to 2006, she was on faculty in the PHS division at the Fred Hutchinson Cancer Research Center. Dr. Tang joined the Stanford Genetics Department in 2007. The goals of her research are to better understand the evolutionary forces that have shaped the pattern of genetic variation in humans, as well as to elucidate the genetic architecture of complex traits and diseases in the context of human evolution.

ACADEMIC APPOINTMENTS

- Professor, Genetics
- Professor (By courtesy), Statistics
- Member, Bio-X
- Member, Stanford Cancer Institute
- Member, Wu Tsai Neurosciences Institute

PROFESSIONAL EDUCATION

- AB, Harvard and Radcliffe College , Biology (1997)
- PhD, Stanford University , Statistics (minor Genetics) (2002)

LINKS

- Tang Lab Website: http://med.stanford.edu/tanglab/

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

Research in our laboratory develops and applies statistical methods for analyzing patterns of human genetic variation, which underlie the phenotypic diversity of our species. We are collaborating on various genome-wide studies focusing on stratified or recently admixed populations. These studies offer unique opportunities to elucidate the evolutionary forces that have shaped the patterns of genetic variation in humans, to uncover the genetic basis of complex traits, and to shed light on the mechanisms that lead to diverse phenotypes and disparate disease risks among populations.

Teaching

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Peter Gerlach, Matt Grieshop, Nikhil Milind, Courtney Smith, Julie F. Wang

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biomedical Data Science (PhD Program)
- Genetics (PhD Program)

Publications

PUBLICATIONS

- **Harmonizing Genetic Ancestry and Self-identified Race/Ethnicity in Genome-wide Association Studies.** *American journal of human genetics*
  Fang, H. n., Hui, Q. n., Lynch, J. n., Honerlaw, J. n., Assimes, T. L., Huang, J. n., Vujkovic, M. n., Damrauer, S. M., Pyarajan, S. n., Gaziano, J. M., DuVall, S. L., O'Donnell, C. J., Cho, et al
  2019

- **Leveraging Multi-ethnic Evidence for Mapping Complex Traits in Minority Populations: An Empirical Bayes Approach** *AMERICAN JOURNAL OF HUMAN GENETICS*
  Coram, M. A., Candille, S. I., Duan, Q., Chan, K. H., Li, Y., Kooperberg, C., Reiner, A. P., Tang, H.
  2015; 96 (5): 740-752

- **Genome-wide characterization of shared and distinct genetic components that influence blood lipid levels in ethnically diverse human populations.** *American journal of human genetics*
  Coram, M. A., Duan, Q., Hoffmann, T. J., Thornton, T., Knowles, J. W., Johnson, N. A., Ochs-Balcom, H. M., Donlon, T. A., Martin, L. W., Eaton, C. B., Robinson, J. G., Risch, N. J., Zhu, et al
  2013; 92 (6): 904-916

- **Genetic Architecture of Skin and Eye Color in an African-European Admixed Population** *PLOS GENETICS*
  Beleza, S., Johnson, N. A., Candille, S. I., Absher, D. M., Coram, M. A., Lopes, J., Campos, J., Araujo, I. I., Anderson, T. M., Vilhjalmsson, B. J., Nordborg, M., Correia e Silva, A., Shriver, et al
  2013; 9 (3)

- **Ancestral Components of Admixed Genomes in a Mexican Cohort** *PLOS GENETICS*
  Johnson, N. A., Coram, M. A., Shriver, M. D., Romieu, I., Barsh, G. S., London, S. J., Tang, H.
  2011; 7 (12)

- **Worldwide human relationships inferred from genome-wide patterns of variation** *SCIENCE*
  Li, J. Z., Absher, D. M., Tang, H., Southwick, A. M., Casto, A. M., Ramachandran, S., Cann, H. M., Barsh, G. S., Feldman, M., Cavalli-Sforza, L. L., Myers, R. M.
  2008; 319 (5866): 1100-1104

- **Reconstructing genetic ancestry blocks in admixed individuals** *AMERICAN JOURNAL OF HUMAN GENETICS*
  Tang, H., Coram, M., Wang, P., Zhu, X., Risch, N.
  2006; 79 (1): 1-12

- **Rare variant contribution to the heritability of coronary artery disease.** *Nature communications*
  Rocheleau, G., Clarke, S. L., Auguste, G., Hasbani, N. R., Morrison, A. C., Heath, A. S., Bielak, L. F., Iyer, K. R., Young, E. P., Stitziel, N. O., Jun, G., Laurie, C., Broome, et al
  2024; 15 (1): 8741

- **Proteome-wide association study using cis and trans variants and applied to blood cell and lipid-related traits in the Women's Health Initiative study.** *Genetic epidemiology*
  Chen, B. D., Lee, C., Tapia, A. L., Reiner, A. P., Tang, H., Kooperberg, C., Manson, J. E., Li, Y., Raffield, L. M.
  2024

- **In silico identification of putative causal genetic variants.** *bioRxiv : the preprint server for biology*
  He, Z., Chu, B., Yang, J., Gu, J., Chen, Z., Liu, L., Morrison, T., Belloy, M. E., Qi, X., Hejazi, N., Mathur, M., Le Guen, Y., Tang, et al
  2024

- **A computational framework for the inference of protein complex remodeling from whole-proteome measurements.** *Nature methods*
  Buljan, M., Banaei-Esfahani, A., Blattmann, P., Meier-Abt, F., Shao, W., Vitek, O., Tang, H., Aebersold, R.

2023

- **Improving genetic risk prediction across diverse population by disentangling ancestry representations.** *Communications biology*
  Gyawali, P. K., Le Guen, Y., Liu, X., Belloy, M. E., Tang, H., Zou, J., He, Z.
  2023; 6 (1): 964
- **Differences in the Circulating Proteome in Individuals with versus without Sickle Cell Trait.** *Clinical journal of the American Society of Nephrology : CJASN*
  Cai, Y., Franceschini, N., Surapaneni, A., Garrett, M. E., Tahir, U. A., Hsu, L., Telen, M. J., Yu, B., Tang, H., Li, Y., Liu, S., Gerszten, R. E., Coresh, et al
  2023
- **Genomics and phenomics of body mass index reveals a complex disease network.** *Nature communications*
  Huang, J., Huffman, J. E., Huang, Y., Do Valle, Í., Assimes, T. L., Raghavan, S., Voight, B. F., Liu, C., Barabási, A. L., Huang, R. D., Hui, Q., Nguyen, X. T., Ho, et al
  2022; 13 (1): 7973
- **Implicating genes, pleiotropy, and sexual dimorphism at blood lipid loci through multi-ancestry meta-analysis.** *Genome biology*
  Kanoni, S., Graham, S. E., Wang, Y., Surakka, I., Ramdas, S., Zhu, X., Clarke, S. L., Bhatti, K. F., Vedantam, S., Winkler, T. W., Locke, A. E., Marouli, E., Zajac, et al
  2022; 23 (1): 268
- **Powerful, scalable and resource-efficient meta-analysis of rare variant associations in large whole genome sequencing studies.** *Nature genetics*
  Li, X., Quick, C., Zhou, H., Gaynor, S. M., Liu, Y., Chen, H., Selvaraj, M. S., Sun, R., Dey, R., Arnett, D. K., Bielak, L. F., Bis, J. C., Blangero, et al
  2022
- **Whole genome sequencing identifies structural variants contributing to hematologic traits in the NHLBI TOPMed program.** *Nature communications*
  Wheeler, M. M., Stilp, A. M., Rao, S., Halldórsson, B. V., Beyter, D., Wen, J., Mihkaylova, A. V., McHugh, C. P., Lane, J., Jiang, M. Z., Raffield, L. M., Jun, G., Sedlazeck, et al
  2022; 13 (1): 7592
- **GhostKnockoff inference empowers identification of putative causal variants in genome-wide association studies.** *Nature communications*
  He, Z., Liu, L., Belloy, M. E., Le Guen, Y., Sossin, A., Liu, X., Qi, X., Ma, S., Gyawali, P. K., Wyss-Coray, T., Tang, H., Sabatti, C., Candes, et al
  2022; 13 (1): 7209
- **A framework for detecting noncoding rare-variant associations of large-scale whole-genome sequencing studies.** *Nature methods*
  Li, Z., Li, X., Zhou, H., Gaynor, S. M., Selvaraj, M. S., Arapoglou, T., Quick, C., Liu, Y., Chen, H., Sun, R., Dey, R., Arnett, D. K., Auer, et al
  2022
- **A Prism Vote method for individualized risk prediction of traits in genotype data of Multi-population.** *PLoS genetics*
  Xia, X., Zhang, Y., Sun, R., Wei, Y., Li, Q., Chong, M. K., Wu, W. K., Zee, B. C., Tang, H., Wang, M. H.
  2022; 18 (10): e1010443
- **A saturated map of common genetic variants associated with human height.** *Nature*
  Yengo, L., Vedantam, S., Marouli, E., Sidorenko, J., Bartell, E., Sakaue, S., Graff, M., Eliasen, A. U., Jiang, Y., Raghavan, S., Miao, J., Arias, J. D., Graham, et al
  2022
- **Transcriptome variation in human tissues revealed by long-read sequencing.** *Nature*
  Glinos, D. A., Garborcauskas, G., Hoffman, P., Ehsan, N., Jiang, L., Gokden, A., Dai, X., Aguet, F., Brown, K. L., Garimella, K., Bowers, T., Costello, M., Ardlie, et al
  2022
- **Large-scale genome-wide association study of coronary artery disease in genetically diverse populations.** *Nature medicine*
  Tcheandjieu, C., Zhu, X., Hilliard, A. T., Clarke, S. L., Napolioni, V., Ma, S., Lee, K. M., Fang, H., Chen, F., Lu, Y., Tsao, N. L., Raghavan, S., Koyama, et al
  2022
- **Sex-biased admixture and assortative mating shape genetic variation and influence demographic inference in admixed Cabo Verdeans.** *G3 (Bethesda, Md.)*

Korunes, K. L., Soares-Souza, G. B., Bobrek, K., Tang, H., Araujo, I. I., Goldberg, A., Beleza, S.
2022

- **Robust Identification of Temporal Biomarkers in Longitudinal Omics Studies.** *Bioinformatics (Oxford, England)*
  Metwally, A. A., Zhang, T., Wu, S., Kellogg, R., Zhou, W., Contrepois, K., Tang, H., Snyder, M.
  2022

- **Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data.** *Nature genetics*
  Wainschtein, P., Jain, D., Zheng, Z., TOPMed Anthropometry Working Group, NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium, Cupples, L. A., Shadyab, A. H., McKnight, B., Shoemaker, B. M., Mitchell, B. D., Psaty, B. M., Kooperberg, C., Liu, C., Albert, et al
  2022

- **Rare transmission of commensal and pathogenic bacteria in the gut microbiome of hospitalized adults.** *Nature communications*
  Siranosian, B. A., Brooks, E. F., Andermann, T., Rezvani, A. R., Banaei, N., Tang, H., Bhatt, A. S.
  1800; 13 (1): 586

- **Whole genome sequence analysis of platelet traits in the NHLBI trans-omics for precision medicine initiative.** *Human molecular genetics*
  Little, A., Hu, Y., Sun, Q., Jain, D., Broome, J., Chen, M., Thibord, F., McHugh, C., Surendran, P., Blackwell, T. W., Brody, J. A., Bhan, A., Chami, et al
  2021

- **Advances and challenges in quantitative delineation of the genetic architecture of complex traits.** *Quantitative biology (Beijing, China)*
  Tang, H., He, Z.
  2021; 9 (2): 168-184

- **Advances and challenges in quantitative delineation of the genetic architecture of complex traits** *QUANTITATIVE BIOLOGY*
  Tang, H., He, Z.
  2021; 9 (2): 168-184

- **Identification of putative causal loci in whole-genome sequencing data via knockoff statistics.** *Nature communications*
  He, Z., Liu, L., Wang, C., Le Guen, Y., Lee, J., Gogarten, S., Lu, F., Montgomery, S., Tang, H., Silverman, E. K., Cho, M. H., Greicius, M., Ionita-Laza, et al
  2021; 12 (1): 3152

- **Genetic and non-genetic factors affecting the expression of COVID-19-relevant genes in the large airway epithelium.** *Genome medicine*
  Kasela, S., Ortega, V. E., Martorella, M., Garudadri, S., Nguyen, J., Ampleford, E., Pasanen, A., Nerella, S., Buschur, K. L., Barjaktarevic, I. Z., Barr, R. G., Bleecker, E. R., Bowler, et al
  2021; 13 (1): 66

- **Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program.** *American journal of human genetics*
  Hu, Y., Stilp, A. M., McHugh, C. P., Rao, S., Jai, D., Zheng, X., Lane, J., Meric de Bellefon, S., Raffield, L. M., Chen, M., Yanek, L. R., Wheeler, M., Yao, et al
  2021

- **Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease.** *Cell*
  de Goede, O. M., Nachun, D. C., Ferraro, N. M., Gloudemans, M. J., Rao, A. S., Smail, C., Eulalio, T. Y., Aguet, F., Ng, B., Xu, J., Barbeira, A. N., Castel, S. E., Kim-Hellmuth, et al
  2021

- **Functional and structural basis of extreme conservation in vertebrate 5' untranslated regions.** *Nature genetics*
  Byeon, G. W., Cenik, E. S., Jiang, L., Tang, H., Das, R., Barna, M.
  2021

- **Inherited causes of clonal haematopoiesis in 97,691 whole genomes (vol 586 , pg 763, 2020)** *NATURE*
  Bick, A. G., Weinstock, J. S., Nandakumar, S. K., Fulco, C. P., Bao, E. L., Zekavat, S. M., Szeto, M. D., Liao, X., Leventhal, M. J., Nasser, J., Chang, K., Laurie, C., Burugula, et al
  2021; 591 (7851): E27

- **Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program.** *Nature*
  Taliun, D., Harris, D. N., Kessler, M. D., Carlson, J., Szpiech, Z. A., Torres, R., Taliun, S. A., Corvelo, A., Gogarten, S. M., Kang, H. M., Pitsillides, A. N., LeFaive, J., Lee, et al

2021; 590 (7845): 290–99

- **Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices.** *Nature communications*
  Natarajan, P., Pampana, A., Graham, S. E., Ruotsalainen, S. E., Perry, J. A., de Vries, P. S., Broome, J. G., Pirruccello, J. P., Honigberg, M. C., Aragam, K., Wolford, B., Brody, J. A., Antonacci-Fulton, et al
  2021; 12 (1): 2182

- **Genome-wide analysis of common and rare variants via multiple knockoffs at biobank scale, with an application to Alzheimer disease genetics.** *American journal of human genetics*
  He, Z., Le Guen, Y., Liu, L., Lee, J., Ma, S., Yang, A. C., Liu, X., Rutledge, J., Losada, P. M., Song, B., Belloy, M. E., Butler, R. R., Longo, et al
  2021

- **Whole-genome sequencing in diverse subjects identifies genetic correlates of leukocyte traits: The NHLBI TOPMed program.** *American journal of human genetics*
  Mikhaylova, A. V., McHugh, C. P., Polfus, L. M., Raffield, L. M., Boorgula, M. P., Blackwell, T. W., Brody, J. A., Broome, J., Chami, N., Chen, M. H., Conomos, M. P., Cox, C., Curran, et al
  2021

- **Inherited causes of clonal haematopoiesis in 97,691 whole genomes.** *Nature*
  Bick, A. G., Weinstock, J. S., Nandakumar, S. K., Fulco, C. P., Bao, E. L., Zekavat, S. M., Szeto, M. D., Liao, X., Leventhal, M. J., Nasser, J., Chang, K., Laurie, C., Burugula, et al
  2020

- **The GTEx Consortium atlas of genetic regulatory effects across human tissues** *SCIENCE*
  Aguet, F., Barbeira, A. N., Bonazzola, R., Brown, A., Castel, S. E., Jo, B., Kasela, S., Kim-Hellmuth, S., Liang, Y., Parsana, P., Flynn, E., Fresard, L., Gamazon, et al
  2020; 369 (6509): 1318-+

- **The Polygenic and Monogenic Basis of Blood Traits and Diseases.** *Cell*
  Vuckovic, D., Bao, E. L., Akbari, P., Lareau, C. A., Mousas, A., Jiang, T., Chen, M., Raffield, L. M., Tardaguila, M., Huffman, J. E., Ritchie, S. C., Megy, K., Ponstingl, et al
  2020; 182 (5): 1214

- **Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations.** *Cell*
  Chen, M., Raffield, L. M., Mousas, A., Sakaue, S., Huffman, J. E., Moscati, A., Trivedi, B., Jiang, T., Akbari, P., Vuckovic, D., Bao, E. L., Zhong, X., Manansala, et al
  2020; 182 (5): 1198

- **Genome-Wide Gene-Diabetes and Gene-Obesity Interaction Scan in 8,255 Cases and 11,900 Controls from PanScan and PanC4 Consortia.** *Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology*
  Tang, H., Jiang, L., Stolzenberg-Solomon, R. Z., Arslan, A. A., Beane Freeman, L. E., Bracci, P. M., Brennan, P., Canzian, F., Du, M., Gallinger, S., Giles, G. G., Goodman, P. J., Kooperberg, et al
  2020; 29 (9): 1784–91

- **Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale.** *Nature genetics*
  Li, X., Li, Z., Zhou, H., Gaynor, S. M., Liu, Y., Chen, H., Sun, R., Dey, R., Arnett, D. K., Aslibekyan, S., Ballantyne, C. M., Bielak, L. F., Blangero, et al
  2020

- **Detecting fitness epistasis in recently admixed populations with genome-wide data.** *BMC genomics*
  Ni, X. n., Zhou, M. n., Wang, H. n., He, K. Y., Broeckel, U. n., Hanis, C. n., Kardia, S. n., Redline, S. n., Cooper, R. S., Tang, H. n., Zhu, X. n.
  2020; 21 (1): 476

- **A Quantitative Proteome Map of the Human Body.** *Cell*
  Jiang, L. n., Wang, M. n., Lin, S. n., Jian, R. n., Li, X. n., Chan, J. n., Dong, G. n., Fang, H. n., Robinson, A. E., Snyder, M. P.
  2020

- **RobNorm: Model-Based Robust Normalization Method for Labeled Quantitative Mass Spectrometry Proteomics Data.** *Bioinformatics (Oxford, England)*
  Wang, M. n., Jiang, L. n., Jian, R. n., Chan, J. Y., Liu, Q. n., Snyder, M. P., Tang, H. n.

2020

- **Whole Genome Sequencing Identifies CRISPLD2 as a Lung Function Gene in Children With Asthma** *CHEST*
  Kachroo, P., Hecker, J., Chawes, B. L., Ahluwalia, T. S., Cho, M. H., Qiao, D., Kelly, R. S., Chu, S. H., Virkud, Y. V., Huang, M., Barnes, K. C., Burchard, E. G., Eng, et al
  2019; 156 (6): 1068–79

- **A multi-ancestry genome-wide study incorporating gene-smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure.** *Human molecular genetics*
  Sung, Y. J., de Las Fuentes, L., Winkler, T. W., Chasman, D. I., Bentley, A. R., Kraja, A. T., Ntalla, I., Warren, H. R., Guo, X., Schwander, K., Manning, A. K., Brown, M. R., Aschard, et al
  2019

- **Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids.** *Nature genetics*
  Bentley, A. R., Sung, Y. J., Brown, M. R., Winkler, T. W., Kraja, A. T., Ntalla, I., Schwander, K., Chasman, D. I., Lim, E., Deng, X., Guo, X., Liu, J., Lu, et al
  2019; 51 (4): 636-648

- **Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids** *NATURE GENETICS*
  Bentley, A. R., Sung, Y. J., Brown, M. R., Winkler, T. W., Kraja, A. T., Ntalla, I., Schwander, K., Chasman, D., Lim, E., Deng, X., Guo, X., Liu, J., Lu, et al
  2019; 51 (4): 636-+

- **Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity** *NATURE COMMUNICATIONS*
  Kilpelainen, T. O., Bentley, A. R., Noordam, R., Sung, Y., Schwander, K., Winkler, T. W., Jakupovic, H., Chasman, D. I., Manning, A., Ntalla, I., Aschard, H., Brown, M. R., de las Fuentes, et al
  2019; 10

- **Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity.** *Nature communications*
  Kilpelainen, T. O., Bentley, A. R., Noordam, R., Sung, Y. J., Schwander, K., Winkler, T. W., Jakupovic, H., Chasman, D. I., Manning, A., Ntalla, I., Aschard, H., Brown, M. R., de Las Fuentes, et al
  2019; 10 (1): 376

- **Evaluating the strength of genetic results: Risks and responsibilities.** *PLoS genetics*
  Barsh, G. S., Cooper, G. M., Copenhaver, G. P., Sirugo, G. n., Tang, H. n., Williams, S. M.
  2019; 15 (10): e1008437

- **Association of APOL1 Risk Alleles with Cardiovascular Disease in African Americans in the Million Veteran Program.** *Circulation*
  Bick, A. G., Akwo, E. n., Robinson-Cohen, C. n., Lee, K. n., Lynch, J. n., Assimes, T. L., DuVall, S. n., Edwards, T. n., Fang, H. n., Freiberg, S. M., Giri, A. n., Huffman, J. E., Huang, et al
  2019

- **Doubling down on forensic twin studies.** *PLoS genetics*
  Copenhaver, G. P., Weir, B., Rothstein, M., Tang, H., Williams, S. M., Barsh, G. S.
  2018; 14 (12): e1007831

- **Genetics of blood lipids among similar to 300,000 multi-ethnic participants of the Million Veteran Program** *NATURE GENETICS*
  Klarin, D., Damrauer, S. M., Cho, K., Sun, Y., Teslovich, T. M., Honerlaw, J., Gagnon, D. R., Du Vall, S. L., Li, J., Peloso, G. M., Chaffin, M., Small, A. M., Huang, et al
  2018; 50 (11): 1514-+

- **Genetics of blood lipids among ~300,000 multi-ethnic participants of the Million Veteran Program.** *Nature genetics*
  Klarin, D., Damrauer, S. M., Cho, K., Sun, Y. V., Teslovich, T. M., Honerlaw, J., Gagnon, D. R., DuVall, S. L., Li, J., Peloso, G. M., Chaffin, M., Small, A. M., Huang, et al
  2018

- **Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries** *PLOS ONE*
  Feitosa, M. F., Kraja, A. T., Chasman, D. I., Sung, Y. J., Winkler, T. W., Ntalla, I., Guo, X., Franceschini, N., Cheng, C., Sim, X., Vojinovic, D., Marten, J., Musani, et al

2018; 13 (6): e0198166

- **A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure** *AMERICAN JOURNAL OF HUMAN GENETICS*
  Sung, Y. J., Winkler, T. W., de las Fuentes, L., Bentley, A. R., Brown, M. R., Kraja, A. T., Schwander, K., Ntalla, I., Guo, X., Franceschini, N., Lu, Y., Cheng, C., Sim, et al
  2018; 102 (3): 375–400
- **Exome-wide association study of plasma lipids in > 300,000 individuals** *NATURE GENETICS*
  Liu, D. J., Peloso, G. M., Yu, H., Butterworth, A. S., Wang, X., Mahajan, A., Saleheen, D., Emdin, C., Alam, D., Alves, A., Amouyel, P., Di Angelantonio, E., Arveiler, et al
  2017; 49 (12): 1758-+
- **Skin color variation in Africa.** *Science (New York, N.Y.)*
  Tang, H., Barsh, G. S.
  2017; 358 (6365): 867-868
- **Trans-ancestry Fine Mapping and Molecular Assays Identify Regulatory Variants at the ANGPTL8 HDL-C GWAS Locus.** *G3 (Bethesda, Md.)*
  Cannon, M. E., Duan, Q., Wu, Y., Zeynalzadeh, M., Xu, Z., Kangas, A. J., Soininen, P., Ala-Korpela, M., Civelek, M., Lusis, A. J., Kuusisto, J., Collins, F. S., Boehnke, et al
  2017; 7 (9): 3217-3227
- **Genome-Wide Association Study of Blood Pressure Traits by Hispanic/Latino Background: the Hispanic Community Health Study/Study of Latinos** *SCIENTIFIC REPORTS*
  Sofer, T., Wong, Q., Hartwig, F. P., Taylor, K., Warren, H. R., Evangelou, E., Cabrera, C. P., Levy, D., Kramer, H., Lange, L. A., Horta, B. L., Kerr, K. F., Reiner, et al
  2017; 7: 10348
- **Joint genotype- and ancestry-based genome-wide association studies in admixed populations** *GENETIC EPIDEMIOLOGY*
  Szulc, P., Bogdan, M., Frommlet, F., Tang, H.
  2017; 41 (6): 555–66
- **Inference on the Genetic Basis of Eye and Skin Color in an Admixed Population via Bayesian Linear Mixed Models.** *Genetics*
  Lloyd-Jones, L. R., Robinson, M. R., Moser, G., Zeng, J., Beleza, S., Barsh, G. S., Tang, H., Visscher, P. M.
  2017; 206 (2): 1113-1126
- **A Poisson Log-Normal Model for Constructing Gene Covariation Network Using RNA-seq Data.** *Journal of computational biology : a journal of computational molecular cell biology*
  Choi, Y., Coram, M., Peng, J., Tang, H.
  2017
- **Single-trait and multi-trait genome-wide association analyses identify novel loci for blood pressure in African-ancestry populations.** *PLoS genetics*
  Liang, J., Le, T. H., Edwards, D. R., Tayo, B. O., Gaulton, K. J., Smith, J. A., Lu, Y., Jensen, R. A., Chen, G., Yanek, L. R., Schwander, K., Tajuddin, S. M., Sofer, et al
  2017; 13 (5)
- **Genome-wide survey in African Americans demonstrates potential epistasis of fitness in the human genome.** *Genetic epidemiology*
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