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)

Nikhil Milind, Courtney Smith

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*
  Wang, H., Choi, Y., Tayo, B., Wang, X., Morris, N., Zhang, X., Broeckel, U., Hanis, C., Kardia, S., Redline, S., Cooper, R. S., Tang, H., Zhu, et al
  2017; 41 (2): 122-135

- **Genome-wide Trans-ethnic Meta-analysis Identifies Seven Genetic Loci Influencing Erythrocyte Traits and a Role for RBPMS in Erythropoiesis** *AMERICAN JOURNAL OF HUMAN GENETICS*
  van Rooij, F. A., Qayyum, R., Smith, A. V., Zhou, Y., Trompet, S., Tanaka, T., Keller, M. F., Chang, L., Schmidt, H., Yang, M., Chen, M., Hayes, J., Johnson, et al
  2017; 100 (1): 51–63

- **Leveraging Multi-ethnic Evidence for Risk Assessment of Quantitative Traits in Minority Populations.** *American journal of human genetics*
  Coram, M. A., Fang, H. n., Candille, S. I., Assimes, T. L., Tang, H. n.
  2017; 101 (2): 218–26

- **Dynamic landscape and regulation of RNA editing in mammals.** *Nature*
  Tan, M. H., Li, Q. n., Shanmugam, R. n., Piskol, R. n., Kohler, J. n., Young, A. N., Liu, K. I., Zhang, R. n., Ramaswami, G. n., Ariyoshi, K. n., Gupte, A. n., Keegan, L. P., George, et al
  2017; 550 (7675): 249–54

- **Landscape of X chromosome inactivation across human tissues.** *Nature*
  Tukiainen, T. n., Villani, A. C., Yen, A. n., Rivas, M. A., Marshall, J. L., Satija, R. n., Aguirre, M. n., Gauthier, L. n., Fleharty, M. n., Kirby, A. n., Cummings, B. B., Castel, S. E., Karczewski, et al
  2017; 550 (7675): 244–48

- **Enhancing GTEx by bridging the gaps between genotype, gene expression, and disease.** *Nature genetics*
  2017; 49 (12): 1664–70

- **The impact of rare variation on gene expression across tissues.** *Nature*
  Li, X. n., Kim, Y. n., Tsang, E. K., Davis, J. R., Damani, F. N., Chiang, C. n., Hess, G. T., Zappala, Z. n., Strober, B. J., Scott, A. J., Li, A. n., Ganna, A. n., Bassik, et al
  2017; 550 (7675): 239–43

- **Genetic effects on gene expression across human tissues.** *Nature*
  Battle, A. n., Brown, C. D., Engelhardt, B. E., Montgomery, S. B.
  2017; 550 (7675): 204–13

- **Gene by Environment Investigation of Incident Lung Cancer Risk in African-Americans.** *EBioMedicine*
  David, S. P., Wang, A., Kapphahn, K., Hedlin, H., Desai, M., Henderson, M., Yang, L., Walsh, K. M., Schwartz, A. G., Wiencke, J. K., Spitz, M. R., Wenzlaff, A. S., Wrensch, et al
  2016; 4: 153-161

- **Meta-analysis of lipid-traits in Hispanics identifies novel loci, population-specific effects, and tissue-specific enrichment of eQTLs** *SCIENTIFIC REPORTS*
  Below, J. E., Parra, E. J., Gamazon, E. R., Torres, J., Krithika, S., Candille, S., Lu, Y., Manichakul, A., Peralta-Romero, J., Duan, Q., Li, Y., Morris, A. P., Gottesman, et al
  2016; 6

- **Meta-analysis of lipid-traits in Hispanics identifies novel loci, population-specific effects, and tissue-specific enrichment of eQTLs.** *Scientific reports*
  Below, J. E., Parra, E. J., Gamazon, E. R., Torres, J., Krithika, S., Candille, S., Lu, Y., Manichakul, A., Peralta-Romero, J., Duan, Q., Li, Y., Morris, A. P., Gottesman, et al
  2016; 6: 19429

- **PREMIX: PRivacy-preserving EstiMation of Individual admiXture.** *AMIA ... Annual Symposium proceedings. AMIA Symposium*
  Chen, F., Dow, M., Ding, S., Lu, Y., Jiang, X., Tang, H., Wang, S.
  2016; 2016: 1747-1755

- **PLOS Genetics Data Sharing Policy: In Pursuit of Functional Utility** *PLOS GENETICS*
  Barsh, G. S., Cooper, G. M., Copenhaver, G. P., Gibson, G., McCarthy, M. I., Tang, H., Williams, S. M.
  2015; 11 (12): e1005716

- **Integrative analysis of RNA, translation, and protein levels reveals distinct regulatory variation across humans** *GENOME RESEARCH*
  Cenik, C., Cenik, E. S., Byeon, G. W., Grubert, F., Candille, S. I., Spacek, D., Alsallakh, B., Tilgner, H., Araya, C. L., Tang, H., Ricci, E., Snyder, M. P.
  2015; 25 (11): 1610-1621

- **Characterizing Race/Ethnicity and Genetic Ancestry for 100,000 Subjects in the Genetic Epidemiology Research on Adult Health and Aging (GERA) Cohort.** *Genetics*
  Banda, Y., Kvale, M. N., Hoffmann, T. J., Hesselson, S. E., Ranatunga, D., Tang, H., Sabatti, C., Croen, L. A., Dispensa, B. P., Henderson, M., Iribarren, C., Jorgenson, E., Kushi, et al
  2015; 200 (4): 1285-1295

- **Characterizing Race/Ethnicity and Genetic Ancestry for 100,000 Subjects in the Genetic Epidemiology Research on Adult Health and Aging (GERA) Cohort** *GENETICS*
  Banda, Y., Kvale, M. N., Hoffmann, T. J., Hesselson, S. E., Ranatunga, D., Tang, H., Sabatti, C., Croen, L. A., Dispensa, B. P., Henderson, M., Iribarren, C., Jorgenson, E., Kushi, et al

2015; 200 (4): 1285-?

- **Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction.** *Nature*
  Do, R., Stitziel, N. O., Won, H., Jørgensen, A. B., Duga, S., Angelica Merlini, P., Kiezun, A., Farrall, M., Goel, A., Zuk, O., Guella, I., Asselta, R., Lange, et al
  2015; 518 (7537): 102-106

- **Variants for HDL-C, LDL-C, and Triglycerides Identified from Admixture Mapping and Fine-Mapping Analysis in African American Families** *CIRCULATION-CARDIOVASCULAR GENETICS*
  Shetty, P. B., Tang, H., Feng, T., Tayo, B., Morrison, A. C., Kardia, S. L., Hanis, C. L., Arnett, D. K., Hunt, S. C., Boerwinkle, E., Rao, D. C., Cooper, R. S., Risch, et al
  2015; 8 (1): 106-U206

- **Trans-ethnic meta-analysis of white blood cell phenotypes** *HUMAN MOLECULAR GENETICS*
  Keller, M. F., Reiner, A. P., Okada, Y., van Rooij, F. A., Johnson, A. D., Chen, M., Smith, A. V., Morris, A. P., Tanaka, T., Ferrucci, L., Zonderman, A. B., Lettre, G., Harris, et al
  2014; 23 (25): 6944–60

- **Genome-wide association and admixture analysis of glaucoma in the Women's Health Initiative** *HUMAN MOLECULAR GENETICS*
  Hoffmann, T. J., Tang, H., Thornton, T. A., Caan, B., Haan, M., Millen, A. E., Thomas, F., Risch, N.
  2014; 23 (24): 6634-6643

- **Leveraging population admixture to characterize the heritability of complex traits** *NATURE GENETICS*
  Zaitlen, N., Pasaniuc, B., Sankararaman, S., Bhatia, G., Zhang, J., Gusev, A., Young, T., Tandon, A., Pollack, S., Vilhjalmsson, B. J., Assimes, T. L., Berndt, S. I., Blot, et al
  2014; 46 (12): 1356-1362

- **Leveraging population admixture to characterize the heritability of complex traits.** *Nature genetics*
  Zaitlen, N., Pasaniuc, B., Sankararaman, S., Bhatia, G., Zhang, J., Gusev, A., Young, T., Tandon, A., Pollack, S., Vilhjálmsson, B. J., Assimes, T. L., Berndt, S. I., Blot, et al
  2014; 46 (12): 1356-1362

- **The Association of the Vanin-1 N131S Variant with Blood Pressure Is Mediated by Endoplasmic Reticulum-Associated Degradation and Loss of Function** *PLOS GENETICS*
  Wang, Y., Tayo, B. O., Bandyopadhyay, A., Wang, H., Feng, T., Franceschini, N., Tang, H., Gao, J., Sung, Y. J., Elston, R. C., Williams, S. M., Cooper, R. S., Mu, et al
  2014; 10 (9)

- **The association of the vanin-1 N131S variant with blood pressure is mediated by endoplasmic reticulum-associated degradation and loss of function.** *PLoS genetics*
  Wang, Y. J., Tayo, B. O., Bandyopadhyay, A., Wang, H., Feng, T., Franceschini, N., Tang, H., Gao, J., Sung, Y. J., Elston, R. C., Williams, S. M., Cooper, R. S., Mu, et al
  2014; 10 (9): e1004641

- **Modeling 3D facial shape from DNA.** *PLoS genetics*
  Claes, P., Liberton, D. K., Daniels, K., Rosana, K. M., Quillen, E. E., Pearson, L. N., McEvoy, B., Bauchet, M., Zaidi, A. A., Yao, W., Tang, H., Barsh, G. S., Absher, et al
  2014; 10 (3)

- **Modeling 3D Facial Shape from DNA.** *PLoS genetics*
  Claes, P., Liberton, D. K., Daniels, K., Rosana, K. M., Quillen, E. E., Pearson, L. N., McEvoy, B., Bauchet, M., Zaidi, A. A., Yao, W., Tang, H., Barsh, G. S., Absher, et al
  2014; 10 (3)

- **Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol.** *American journal of human genetics*
  Lange, L. A., Hu, Y., Zhang, H., Xue, C., Schmidt, E. M., Tang, Z., Bizon, C., Lange, E. M., Smith, J. D., Turner, E. H., Jun, G., Kang, H. M., Peloso, et al
  2014; 94 (2): 233-245

- **A Variational Bayes Discrete Mixture Test for Rare Variant Association** *GENETIC EPIDEMIOLOGY*

Logsdon, B. A., Dai, J. Y., Auer, P. L., Johnsen, J. M., Ganesh, S. K., Smith, N. L., Wilson, J. G., Tracy, R. P., Lange, L. A., Jiao, S., Rich, S. S., Lettre, G., Carlson, et al

2014; 38 (1): 21-30

- **ACCURATE CONSTRUCTION OF LONG RANGE HAPLOTYPE IN UNRELATED INDIVIDUALS** *STATISTICA SINICA*

  Johnson, N. A., London, S. J., Romieu, I., Wong, W. H., Tang, H.

  2013; 23 (4): 1441-1461

- **Multiethnic Meta-Analysis of Genome-Wide Association Studies in > 100 000 Subjects Identifies 23 FibrinogenAssociated Loci but No Strong Evidence of a Causal Association Between Circulating Fibrinogen and Cardiovascular Disease** *CIRCULATION*

  Sabater-Lleal, M., Huang, J., Chasman, D., Naitza, S., Dehghan, A., Johnson, A. D., Teumer, A., Reiner, A. P., Folkersen, L., Basu, S., Rudnicka, A. R., Trompet, S., Malarstig, et al

  2013; 128 (12): 1310-1324

- **Genome-wide Association Analysis of Blood-Pressure Traits in African-Ancestry Individuals Reveals Common Associated Genes in African and Non-African Populations** *AMERICAN JOURNAL OF HUMAN GENETICS*

  Franceschini, N., Fox, E., Zhang, Z., Edwards, T. L., Nalls, M. A., Sung, Y. J., Tayo, B. O., Sun, Y. V., Gottesman, O., Adeyemo, A., Johnson, A. D., Young, J. H., Rice, et al

  2013; 93 (3): 545-554

- **African American race but not genome-wide ancestry is negatively associated with atrial fibrillation among postmenopausal women in the Women's Health Initiative.** *American heart journal*

  Perez, M. V., Hoffmann, T. J., Tang, H., Thornton, T., Stefanick, M. L., Larson, J. C., Kooperberg, C., Reiner, A. P., Caan, B., Iribarren, C., Risch, N.

  2013; 166 (3): 566-572

- **African American race but not genome-wide ancestry is negatively associated with atrial fibrillation among postmenopausal women in the Women's Health Initiative.** *American heart journal*

  Perez, M. V., Hoffmann, T. J., Tang, H., Thornton, T., Stefanick, M. L., Larson, J. C., Kooperberg, C., Reiner, A. P., Caan, B., Iribarren, C., Risch, N.

  2013; 166 (3): 566-572 e1

- **Variation and genetic control of protein abundance in humans** *NATURE*

  Wu, L., Candille, S. I., Choi, Y., Xie, D., Jiang, L., Li-Pook-Than, J., Tang, H., Snyder, M.

  2013; 499 (7456): 79-82

- **Genome-wide association analysis of red blood cell traits in African Americans: the COGENT Network** *HUMAN MOLECULAR GENETICS*

  Chen, Z., Tang, H., Qayyum, R., Schick, U. M., Nalls, M. A., Handsaker, R., Li, J., Lu, Y., Yanek, L. R., Keating, B., Meng, Y., van Rooij, F. J., Okada, et al

  2013; 22 (12): 2529-2538

- **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

- **Association of DXA-derived Bone Mineral Density and Fat Mass With African Ancestry** *JOURNAL OF CLINICAL ENDOCRINOLOGY & METABOLISM*

  Ochs-Balcom, H. M., Preus, L., Wactawski-Wende, J., Nie, J., Johnson, N. A., Zakharia, F., Tang, H., Carlson, C., Carty, C., Chen, Z., Hoffman, T., Hutter, C. M., Jackson, et al

  2013; 98 (4): E713-E717

- **ACCURATE CONSTRUCTION OF LONG RANGE HAPLOTYPE IN UNRELATED INDIVIDUALS.** *Statistica Sinica*

  Johnson, N. A., London, S. J., Romieu, I., Wong, W. H., Tang, H.

  2013; 23: 1441-1461

- **Imputation of Exome Sequence Variants into Population-Based Samples and Blood-Cell-Trait-Associated Loci in African Americans: NHLBI GO Exome Sequencing Project** *AMERICAN JOURNAL OF HUMAN GENETICS*

  Auer, P. L., Johnsen, J. M., Johnson, A. D., Logsdon, B. A., Lange, L. A., Nalls, M. A., Zhang, G., Franceschini, N., Fox, K., Lange, E. M., Rich, S. S., O'Donnell, C. J., Jackson, et al

  2012; 91 (5): 794-808

- **Genome-Wide Association Studies of Quantitatively Measured Skin, Hair, and Eye Pigmentation in Four European Populations** *PLOS ONE*

Candille, S. I., Absher, D. M., Beleza, S., Bauchet, M., McEvoy, B., Garrison, N. A., Li, J. Z., Myers, R. M., Barsh, G. S., Tang, H., Shriver, M. D.
2012; 7 (10)

- **Variants in CXADR and F2RL1 are associated with blood pressure and obesity in African-Americans in regions identified through admixture mapping** *JOURNAL OF HYPERTENSION*
  Shetty, P. B., Tang, H., Tayo, B. O., Morrison, A. C., Hanis, C. L., Rao, D. C., Young, J. H., Fox, E. R., Boerwinkle, E., Cooper, R. S., Risch, N. J., Zhu, X.
  2012; 30 (10): 1970-1976

- **Genome-wide Association and Population Genetic Analysis of C-Reactive Protein in African American and Hispanic American Women** *AMERICAN JOURNAL OF HUMAN GENETICS*
  Reiner, A. P., Beleza, S., Franceschini, N., Auer, P. L., Robinson, J. G., Kooperberg, C., Peters, U., Tang, H.
  2012; 91 (3): 502-512

- **Estimating Kinship in Admixed Populations** *AMERICAN JOURNAL OF HUMAN GENETICS*
  Thornton, T., Tang, H., Hoffmann, T. J., Ochs-Balcom, H. M., Caan, B. J., Risch, N.
  2012; 91 (1): 122-138

- **Personal Omics Profiling Reveals Dynamic Molecular and Medical Phenotypes** *CELL*
  Chen, R., Mias, G. I., Li-Pook-Than, J., Jiang, L., Lam, H. Y., Chen, R., Miriami, E., Karczewski, K. J., Hariharan, M., Dewey, F. E., Cheng, Y., Clark, M. J., Im, et al
  2012; 148 (6): 1293-1307

- **Human genetic variation altering anthrax toxin sensitivity** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Martchenko, M., Candille, S. I., Tang, H., Cohen, S. N.
  2012; 109 (8): 2972-2977

- **Genome-wide association study of body height in African Americans: the Women's Health Initiative SNP Health Association Resource (SHARe)** *HUMAN MOLECULAR GENETICS*
  Carty, C. L., Johnson, N. A., Hutter, C. M., Reiner, A. P., Peters, U., Tang, H., Kooperberg, C.
  2012; 21 (3): 711-720

- **Genome-Wide Association Study of White Blood Cell Count in 16,388 African Americans: the Continental Origins and Genetic Epidemiology Network (COGENT)** *PLOS GENETICS*
  Reiner, A. P., Lettre, G., Nalls, M. A., Ganesh, S. K., Mathias, R., Austin, M. A., Dean, E., Arepalli, S., Britton, A., Chen, Z., Couper, D., Curb, J. D., Eaton, et al
  2011; 7 (6)

- **Joint Testing of Genotype and Ancestry Association in Admixed Families** *GENETIC EPIDEMIOLOGY*
  Tang, H., Siegmund, D. O., Johnson, N. A., Romieu, I., London, S. J.
  2010; 34 (8): 783-791

- **Lack of Association Between the Trp719Arg Polymorphism in Kinesin-Like Protein-6 and Coronary Artery Disease in 19 Case-Control Studies** *JOURNAL OF THE AMERICAN COLLEGE OF CARDIOLOGY*
  Assimes, T. L., Holm, H., Kathiresan, S., Reilly, M. P., Thorleifsson, G., Voight, B. F., Erdmann, J., Willenborg, C., Vaidya, D., Xie, C., Patterson, C. C., Morgan, T. M., Burnett, et al
  2010; 56 (19): 1552-1563

- **Detecting Genomic Aberrations Using Products in a Multiscale Analysis** *BIOMETRICS*
  Yu, X., Randolph, T. W., Tang, H., Hsu, L.
  2010; 66 (3): 684-693

- **Genome-Wide Association Study Implicates Chromosome 9q21.31 as a Susceptibility Locus for Asthma in Mexican Children** *PLOS GENETICS*
  Hancock, D. B., Romieu, I., Shi, M., Sienra-Monge, J., Wu, H., Chiu, G. Y., Li, H., Estela del Rio-Navarro, B., Willis-Owens, S. A., Weiss, S. T., Raby, B. A., Gao, H., Eng, et al
  2009; 5 (8)

- **Admixture mapping of quantitative trait loci for blood lipids in African-Americans** *HUMAN MOLECULAR GENETICS*
  Basu, A., Tang, H., Lewis, C. E., North, K., Curb, J. D., Quertermous, T., Mosley, T. H., Boerwinkle, E., Zhu, X., Risch, N. J.

2009; 18 (11): 2091-2098

- **Admixture Mapping of Quantitative Trait Loci for BMI in African Americans: Evidence for Loci on Chromosomes 3q, 5q, and 15q** *OBESITY*
  Basu, A., Tang, H., Arnett, D., Gu, C. C., Mosley, T., Kardia, S., Luke, A., Tayo, B., Cooper, R., Zhu, X., Risch, N.
  2009; 17 (6): 1226-1231

- **Molecular and Evolutionary History of Melanism in North American Gray Wolves** *SCIENCE*
  Anderson, T. M., vonHoldt, B. M., Candille, S. I., Musiani, M., Greco, C., Stahler, D. R., Smith, D. W., Padhukasahasram, B., Randi, E., Leonard, J. A., Bustamante, C. D., Ostrander, E. A., Tang, et al
  2009; 323 (5919): 1339-1343

- **Characterizing the admixed African ancestry of African Americans** *GENOME BIOLOGY*
  Zakharia, F., Basu, A., Absher, D., Assimes, T. L., Go, A. S., Hlatky, M. A., Iribarren, C., Knowles, J. W., Li, J., Narasimhan, B., Sidney, S., Southwick, A., Myers, et al
  2009; 10 (12)

- **Worldwide patterns of haplotype diversity at 9p21.3, a locus associated with type 2 diabetes and coronary heart disease** *GENOME MEDICINE*
  Silander, K., Tang, H., Myles, S., Jakkula, E., Timpson, N. J., Cavalli-Sforza, L., Peltonen, L.
  2009; 1

- **Genome-wide distribution of ancestry in Mexican Americans** *HUMAN GENETICS*
  Basu, A., Tang, H., Zhu, X., Gu, C. C., Hanis, C., Boerwinkle, E., Risch, N.
  2008; 124 (3): 207-214

- **Susceptibility locus for clinical and subclinical coronary artery disease at chromosome 9p21 in the multi-ethnic ADVANCE study** *HUMAN MOLECULAR GENETICS*
  Assimes, T. L., Knowles, J. W., Basu, A., Iribarren, C., Southwick, A., Tang, H., Absher, D., Li, J., Fair, J. M., Rubin, G. D., Sidney, S., Fortmann, S. P., Go, et al
  2008; 17 (15): 2320-2328

- **Admixture Mapping and the Role of Population Structure for Localizing Disease Genes** *GENETIC DISSECTION OF COMPLEX TRAITS, 2ND EDITION*
  Zhu, X., Tang, H., Risch, N.
  2008; 60: 547-569

- **IMPROVING POPULATION-SPECIFIC ALLELE FREQUENCY ESTIMATES BY ADAPTING SUPPLEMENTAL DATA: AN EMPIRICAL BAYES APPROACH.** *The annals of applied statistics*
  Coram, M., Tang, H.
  2007; 1 (2): 459-479

- **IMPROVING POPULATION-SPECIFIC ALLELE FREQUENCY ESTIMATES BY ADAPTING SUPPLEMENTAL DATA: AN EMPIRICAL BAYES APPROACH** *ANNALS OF APPLIED STATISTICS*
  Coram, M., Tang, H.
  2007; 1 (2): 459-479

- **Recent genetic selection in the ancestral admixture of Puerto Ricans** *AMERICAN JOURNAL OF HUMAN GENETICS*
  Tang, H., Choudhry, S., Mei, R., Morgan, M., Rodriguez-Cintron, W., Burchard, E. G., Risch, N. J.
  2007; 81 (3): 626-633

- **A statistical method for chromatographic alignment of LC-MS data** *BIOSTATISTICS*
  Wang, P., Tang, H., Fitzgibbon, M. P., McIntosh, M., Coram, M., Zhang, H., Yi, E., Aebersold, R.
  2007; 8 (2): 357-367

- **Reduced selection leads to accelerated gene loss in Shigella** *GENOME BIOLOGY*
  Hershberg, R., Tang, H., Petrov, D. A.
  2007; 8 (8)

- **Combining multiple family-based association studies.** *BMC proceedings*
  Tang, H., Peng, J., Wang, P., Coram, M., Hsu, L.
  2007; 1: S162-?

- **Ancestry-environment interactions and asthma risk among Puerto Ricans** *AMERICAN JOURNAL OF RESPIRATORY AND CRITICAL CARE MEDICINE*
  Choudhry, S., Burchard, E. G., Borrell, L. N., Tang, H., Gomez, I., Naqvi, M., Nazario, S., Torres, A., Casal, J., Martinez-Cruzado, J. C., Ziv, E., Avila, P. C., Rodriguez-Cintron, et al
  2006; 174 (10): 1086-1091

- **A classical likelihood based approach for admixture mapping using EM algorithm** *HUMAN GENETICS*
  Zhu, X., Zhang, S., Tang, H., Cooper, R.
  2006; 120 (3): 431-445

- **Genomewide evolutionary rates in laboratory and wild yeast** *GENETICS*
  Ronald, J., Tang, H., Brem, R. B.
  2006; 174 (1): 541-544

- **Population stratification confounds genetic association studies among Latinos** *HUMAN GENETICS*
  Choudhry, S., Coyle, N. E., Tang, H., Salari, K., Lind, D., Clark, S. L., Tsai, H. J., Naqvi, M., Phong, A., Ung, N., Matallana, H., Avila, P. C., Casal, et al
  2006; 118 (5): 652-664

- **Locally weighted transmission/disequilibrium test for genetic association analysis** *14th Genetic Analysis Workshop*
  Hsu, L., Yu, X. S., Houwing-Duistermaat, J. J., Uh, H. W., El Galta, R., Lebrec, J. J., Tang, H.
  BIOMED CENTRAL LTD.2005

- **A newly discovered founder population: the Roma/Gypsies** *BIOESSAYS*
  Kaaydjieva, L., Morar, B., Chaix, R., Tang, H.
  2005; 27 (10): 1084-1094

- **Genetic admixture and asthma-related phenotypes in Mexican American and Puerto Rican asthmatics** *GENETIC EPIDEMIOLOGY*
  Salari, K., Choudhry, S., Tang, H., Naqvi, M., Lind, D., Avila, P. C., Coyle, N. E., Ung, N., Nazario, S., Casal, J., Torres-Palacios, A., Clark, S., Phong, et al
  2005; 29 (1): 76-86

- **Estimation of individual admixture: Analytical and study design considerations** *GENETIC EPIDEMIOLOGY*
  Tang, H., Peng, J., Wang, P., Risch, N. J.
  2005; 28 (4): 289-301

- **Genetic structure, self-identified race/ethnicity, and confounding in case-control association studies** *AMERICAN JOURNAL OF HUMAN GENETICS*
  Tang, H., Quertermous, T., Rodriguez, B., Kardia, S. L., Zhu, X. F., Brown, A., Pankow, J. S., Province, M. A., Hunt, S. C., Boerwinkle, E., Schork, N. J., Risch, N. J.
  2005; 76 (2): 268-275

- **Admixture mapping for hypertension loci with genome-scan markers** *NATURE GENETICS*
  Zhu, X. F., Luke, A., Cooper, R. S., Quertermous, T., Hanis, C., Mosley, T., Gu, C. C., Tang, H., Rao, D. C., Risch, N., Weder, A.
  2005; 37 (2): 177-181

- **Ethnicity and human genetic linkage maps** *AMERICAN JOURNAL OF HUMAN GENETICS*
  Jorgenson, E., Tang, H., Gadde, M., Province, M., Leppert, M., Kardia, S., Schork, N., Cooper, R., Rao, D. C., Boerwinkle, E., Risch, N.
  2005; 76 (2): 276-290

- **Partial deficiency of the C-terminal-domain phosphatase of RNA polymerase II is associated with congenital cataracts facial dysmorphism neuropathy syndrome** *NATURE GENETICS*
  Varon, R., Gooding, R., Steglich, C., Marns, L., Tang, H., Angelicheva, D., Yong, K. K., Ambrugger, P., Reinhold, A., Morar, B., Baas, F., Kwa, M., Tournev, et al
  2003; 35 (2): 185-189

- **Geographic distribution of disease mutations in the Ashkenazi Jewish population supports genetic drift over selection** *AMERICAN JOURNAL OF HUMAN GENETICS*
  Risch, N., Tang, H., Katzenstein, H., Ekstein, J.
  2003; 72 (4): 812-822

- **Categorization of humans in biomedical research: genes, race and disease.** *Genome biology*
  Risch, N., Burchard, E., Ziv, E., Tang, H.
  2002; 3 (7): comment2007-?
- **Frequentist estimation of coalescence times from nucleotide sequence data using a tree-based partition** *GENETICS*
  Tang, H., Siegmund, D. O., Shen, P. D., Oefner, P. J., Feldman, M. W.
  2002; 161 (1): 447-459
- **Geographic distribution of three Tay-Sachs mutations in Ashkenazim supports drift over selection.**
  Risch, N. J., Tang, H., Katzenstein, H., Ekstein, J.
  CELL PRESS.2001: 180–80
- **Locating regions of differential variability in DNA and protein sequences** *GENETICS*
  Tang, H., Lewontin, R. C.
  1999; 153 (1): 485-495