Stanford

Manuel Rivas

Assistant Professor of Biomedical Data Science

NIH Biosketch available Online

Bio

ACADEMIC APPOINTMENTS

- Assistant Professor, Biomedical Data Science
- Member, Bio-X

HONORS AND AWARDS

- Clarendon Scholar, University of Oxford (2010-2015)
- Osler Award, University of Oxford (2010-2015)
- Gates Millenium Scholar, Bill & Melinda Gates Foundation (2004-2008)

PROFESSIONAL EDUCATION

- DPhil, University of Oxford , Clinical Medicine (2015)
- B.S., Massachusetts Institute of Technology , Mathematics (2008)

LINKS

- My Lab Site: http://med.stanford.edu/rivaslab

Teaching

COURSES

2018-19

- Workshop in Biostatistics: BIODS 260C, STATS 260C (Spr)

2017-18

- Topics in Biomedical Data Science: Large-scale inference: BIODS 215 (Win)
- Workshop in Biostatistics: BIODS 260C, STATS 260C (Spr)

2016-17

- Topics in Biomedical Data Science: Large-scale inference: BIODS 215 (Spr)
- Workshop in Biostatistics: BIODS 260C, STATS 260C (Spr)

STANFORD ADVISEES

Doctoral Dissertation Advisor (AC)

Yosuke Tanigawa, Guhan Venkataraman

Publications

PUBLICATIONS

- **Rare and common variant discovery in complex disease: the IBD case study.** *Human molecular genetics*
  Venkataraman, G. R., Rivas, M. A.
  2019

- **Phenome-wide Burden of Copy-Number Variation in the UK Biobank.** *American journal of human genetics*
  Aguirre, M., Rivas, M. A., Priest, J.
  2019

- **Opportunities and challenges for transcriptome-wide association studies** *NATURE GENETICS*
  Wainberg, M., Sinnott-Armstrong, N., Mancuso, N., Barbeira, A. N., Knowles, D. A., Golan, D., Ermel, R., Ruusalepp, A., Quertermous, T., Hao, K., Bjorkegren, J. M., Im, H., Pasaniuc, et al
  2019; 51 (4): 592–99

- **Significant shared heritability underlies suicide attempt and clinically predicted probability of attempting suicide.** *Molecular psychiatry*
  Ruderfer, D. M., Walsh, C. G., Aguirre, M. W., Tanigawa, Y., Ribeiro, J. D., Franklin, J. C., Rivas, M. A.
  2019

- **Global Biobank Engine: enabling genotype-phenotype browsing for biobank summary statistics.** *Bioinformatics (Oxford, England)*
  McInnes, G., Tanigawa, Y., DeBoever, C., Lavertu, A., Olivieri, J. E., Aguirre, M., Rivas, M. A.
  2018

- **Medical relevance of protein-truncating variants across 337,205 individuals in the UK Biobank study** *NATURE COMMUNICATIONS*
  DeBoever, C., Tanigawa, Y., Lindholm, M. E., McInnes, G., Lavertu, A., Ingelsson, E., Chang, C., Ashley, E. A., Bustamante, C. D., Daly, M. J., Rivas, M. A.
  2018; 9: 1612

- **Insights into the genetic epidemiology of Crohn's and rare diseases in the Ashkenazi Jewish population.** *PLoS genetics*
  Rivas, M. A., Avila, B. E., Koskela, J., Huang, H., Stevens, C., Pirinen, M., Haritunians, T., Neale, B. M., Kurki, M., Ganna, A., Graham, D., Glaser, B., Peter, et al
  2018; 14 (5): e1007329

- **DeepTag: inferring diagnoses from veterinary clinical notes.** *NPJ digital medicine*
  Nie, A., Zehnder, A., Page, R. L., Zhang, Y., Pineda, A. L., Rivas, M. A., Bustamante, C. D., Zou, J.
  2018; 1: 60

- **A protein-truncating R179X variant in RNF186 confers protection against ulcerative colitis** *NATURE COMMUNICATIONS*
  Rivas, M. A., Graham, D., Sulem, P., Stevens, C., Desch, A. N., Goyette, P., Gudbjartsson, D., Jonsdottir, I., Thorsteinsdottir, U., Degenhardt, F., Mucha, S., Kurki, M. I., Li, et al
  2016; 7

- **Discovery of rare variants for complex phenotypes** *HUMAN GENETICS*
  Kosmicki, J. A., Churchhouse, C. L., Rivas, M. A., Neale, B. M.
  2016; 135 (6): 625-634

- **Assessing allele-specific expression across multiple tissues from RNA-seq read data** *BIOINFORMATICS*
  Pirinen, M., Lappalainen, T., Zaitlen, N. A., Dermitzakis, E. T., Donnelly, P., McCarthy, M. I., Rivas, M. A.
  2015; 31 (15): 2497-2504

- **Effect of predicted protein-truncating genetic variants on the human transcriptome** *SCIENCE*
  Rivas, M. A., Pirinen, M., Conrad, D. F., Lek, M., Tsang, E. K., Karczewski, K. J., Maller, J. B., Kukurba, K. R., DeLuca, D. S., Fromer, M., Ferreira, P. G., Smith, K. S., Zhang, et al
  2015; 348 (6235): 666-669

- **The Power of Gene-Based Rare Variant Methods to Detect Disease-Associated Variation and Test Hypotheses About Complex Disease** *PLOS GENETICS*
  Moutsianas, L., Agarwala, V., Fuchsberger, C., Flannick, J., Rivas, M. A., Gaulton, K. J., Albers, P. K., McVean, G., Boehnke, M., Altshuler, D., McCarthy, M. I.
  2015; 11 (4)

- **Choice of transcripts and software has a large effect on variant annotation** *GENOME MEDICINE*

McCarthy, D. J., Humburg, P., Kanapin, A., Rivas, M. A., Gaulton, K., Cazier, J., Donnelly, P.
2014; 6

- **Assessing association between protein truncating variants and quantitative traits** *BIOINFORMATICS*
  Rivas, M. A., Pirinen, M., Neville, M. J., Gaulton, K. J., Moutsianas, L., Lindgren, C. M., Karpe, F., McCarthy, M. I., Donnelly, P.
  2013; 29 (19): 2419-2426

- **Transcriptome and genome sequencing uncovers functional variation in humans.** *Nature*
  Lappalainen, T., Sammeth, M., Friedländer, M. R., 't Hoen, P. A., Monlong, J., Rivas, M. A., Gonzàlez-Porta, M., Kurbatova, N., Griebel, T., Ferreira, P. G., Barann, M., Wieland, T., Greger, et al
  2013; 501 (7468): 506-511

- **Deep Resequencing of GWAS Loci Identifies Rare Variants in CARD9, IL23R and RNF186 That Are Associated with Ulcerative Colitis** *PLOS GENETICS*
  Beaudoin, M., Goyette, P., Boucher, G., Lo, K. S., Rivas, M. A., Stevens, C., Alikashani, A., Ladouceur, M., Ellinghaus, D., Torkvist, L., Goel, G., Lagace, C., Annese, et al
  2013; 9 (9)

- **A Flexible Approach for the Analysis of Rare Variants Allowing for a Mixture of Effects on Binary or Quantitative Traits** *PLOS GENETICS*
  Clarke, G. M., Rivas, M. A., Morris, A. P.
  2013; 9 (8)

- **Deep resequencing of GWAS loci identifies independent rare variants associated with inflammatory bowel disease** *NATURE GENETICS*
  Rivas, M. A., Beaudoin, M., Gardet, A., Stevens, C., Sharma, Y., Zhang, C. K., Boucher, G., Ripke, S., Ellinghaus, D., Burtt, N., Fennell, T., Kirby, A., Latiano, et al
  2011; 43 (11): 1066-U50

- **A framework for variation discovery and genotyping using next-generation DNA sequencing data** *NATURE GENETICS*
  DePristo, M. A., Banks, E., Poplin, R., Garimella, K. V., Maguire, J. R., Hartl, C., Philippakis, A. A., del Angel, G., Rivas, M. A., Hanna, M., McKenna, A., Fennell, T. J., Kernytsky, et al
  2011; 43 (5): 491-?

- **Testing for an Unusual Distribution of Rare Variants** *PLOS GENETICS*
  Neale, B. M., Rivas, M. A., Voight, B. F., Altshuler, D., Devlin, B., Orho-Melander, M., Kathiresan, S., Purcell, S. M., Roeder, K., Daly, M. J.
  2011; 7 (3)

- **Association of Genetic Variants in NUDT15 With Thiopurine-Induced Myelosuppression in Patients With Inflammatory Bowel Disease.** *JAMA*
  Walker, G. J., Harrison, J. W., Heap, G. A., Voskuil, M. D., Andersen, V., Anderson, C. A., Ananthakrishnan, A. N., Barrett, J. C., Beaugerie, L., Bewshea, C. M., Cole, A. T., Cummings, F. R., Daly, et al
  2019; 321 (8): 773–85

- **Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution.** *Nature genetics*
  Justice, A. E., Karaderi, T., Highland, H. M., Young, K. L., Graff, M., Lu, Y., Turcot, V., Auer, P. L., Fine, R. S., Guo, X., Schurmann, C., Lempradl, A., Marouli, et al
  2019

- **DeepTag: inferring diagnoses from veterinary clinical notes** *NPJ DIGITAL MEDICINE*
  Nie, A., Zehnder, A., Page, R. L., Zhang, Y., Pineda, A., Rivas, M. A., Bustamante, C. D., Zou, J.
  2018; 1

- **Base-specific mutational intolerance near splice sites clarifies the role of nonessential splice nucleotides** *GENOME RESEARCH*
  Zhang, S., Samocha, K. E., Rivas, M. A., Karczewski, K. J., Daly, E., Schmandt, B., Neale, B. M., MacArthur, D. G., Daly, M. J.
  2018; 28 (7): 968–74

- **Large-Scale Phenome-Wide Association Study of PCSK9 Variants Demonstrates Protection Against Ischemic Stroke** *CIRCULATION-GENOMIC AND PRECISION MEDICINE*
  Rao, A. S., Lindholm, D., Rivas, M. A., Knowles, J. W., Montgomery, S. B., Ingelsson, E.
  2018; 11 (7): e002162

- **Quantifying the Impact of Rare and Ultra-rare Coding Variation across the Phenotypic Spectrum.** *American journal of human genetics*
  Ganna, A., Satterstrom, F. K., Zekavat, S. M., Das, I., Kurki, M. I., Churchhouse, C., Alfoldi, J., Martin, A. R., Havulinna, A. S., Byrnes, A., Thompson, W. K., Nielsen, P. R., Karczewski, et al

2018

- **Genetic variants in cellular transport do not affect mesalamine response in ulcerative colitis** *PLOS ONE*
  Moran, C. J., Huang, H., Rivas, M., Kaplan, J. L., Daly, M. J., Winter, H. S.
  2018; 13 (3): e0192806

- **Sequence data and association statistics from 12,940 type 2 diabetes cases and controls (vol 4, 170179, 2017)** *SCIENTIFIC DATA*
  Flannick, J., Fuchsberger, C., Mahajan, A., Teslovich, T. M., Agarwala, V., Gaulton, K. J., Caulkins, L., Koesterer, R., Ma, C., Moutsianas, L., McCarthy, D. J., Rivas, M. A., Perry, et al
  2018; 5: 180002

- **Evaluating the contribution of rare variants to type 2 diabetes and related traits using pedigrees** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Jun, G., Manning, A., Almeida, M., Zawistowski, M., Wood, A. R., Teslovich, T. M., Fuchsberger, C., Feng, S., Cingolani, P., Gaulton, K. J., Dyer, T., Blackwell, T. W., Chen, et al
  2018; 115 (2): 379–84

- **Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity** *NATURE GENETICS*
  Turcot, V., Lu, Y., Highland, H. M., Schurmann, C., Justice, A. E., Fine, R. S., Bradfield, J. P., Esko, T., Giri, A., Graff, M., Guo, X., Hendricks, A. E., Karaderi, et al
  2018; 50 (1): 26-+

- **Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity.** *Nature genetics*
  Turcot, V., Lu, Y., Highland, H. M., Schurmann, C., Justice, A. E., Fine, R. S., Bradfield, J. P., Esko, T., Giri, A., Graff, M., Guo, X., Hendricks, A. E., Karaderi, et al
  2018; 50 (1): 26–41

- **Data Descriptor: Sequence data and association statistics from 12,940 type 2 diabetes cases and controls** *SCIENTIFIC DATA*
  Flannick, J., Fuchsberger, C., Mahajan, A., Teslovich, T. M., Agarwala, V., Gaulton, K. J., Caulkins, L., Koesterer, R., Ma, C., Moutsianas, L., McCarthy, D. J., Rivas, M. A., Perry, et al
  2017; 4: 170179

- **Large-scale GWAS identifies multiple loci for hand grip strength providing biological insights into muscular fitness** *NATURE COMMUNICATIONS*
  Willems, S. M., Wright, D. J., Day, F. R., Trajanoska, K., Joshi, P. K., Morris, J. A., Matteini, A. M., Garton, F. C., Grarup, N., Oskolkov, N., Thalamuthu, A., Mangino, M., Liu, et al
  2017; 8: 16015

- **Mosaic mutations in blood DNA sequence are associated with solid tumor cancers** *NPJ GENOMIC MEDICINE*
  Artomov, M., Rivas, M. A., Genovese, G., Daly, M. J.
  2017; 2: 22

- **biMM: Efficient estimation of genetic variances and covariances for cohorts with high-dimensional phenotype measurements.** *Bioinformatics*
  Pirinen, M., Benner, C., Marttinen, P., Järvelin, M., Rivas, M. A., Ripatti, S.
  2017

- **Variant Enriched in the Finnish Population is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk.** *Diabetes*
  Manning, A., Highland, H. M., Gasser, J., Sim, X., Tukiainen, T., Fontanillas, P., Grarup, N., Rivas, M. A., Mahajan, A., Locke, A. E., Cingolani, P., Pers, T. H., Viñuela, et al
  2017

- **Rare and low-frequency coding variants alter human adult height.** *Nature*
  Marouli, E., Graff, M., Medina-Gomez, C., Lo, K. S., Wood, A. R., Kjaer, T. R., Fine, R. S., Lu, Y., Schurmann, C., Highland, H. M., Rüeger, S., Thorleifsson, G., Justice, et al
  2017; 542 (7640): 186-190

- **Frameshift indels introduced by genome editing can lead to in-frame exon skipping.** *PloS one*
  Lalonde, S., Stone, O. A., Lessard, S., Lavertu, A., Desjardins, J., Beaudoin, M., Rivas, M., Stainier, D. Y., Lettre, G.
  2017; 12 (6)

- **Landscape of X chromosome inactivation across human tissues.** *Nature*
  Tukiainen, T., Villani, A. C., Yen, A., Rivas, M. A., Marshall, J. L., Satija, R., Aguirre, M., Gauthier, L., Fleharty, M., Kirby, A., Cummings, B. B., Castel, S. E., Karczewski, et al

2017; 550 (7675): 244–48

- **Analysis of protein-coding genetic variation in 60,706 humans** *NATURE*
  Lek, M., Karczewski, K. J., Minikel, E. V., Samocha, K. E., Banks, E., Fennell, T., O'Donnell-Luria, A. H., Ware, J. S., Hill, A. J., Cummings, B. B., Tukiainen, T., Birnbaum, D. P., Kosmicki, et al
  2016; 536 (7616): 285-?

- **The genetic architecture of type 2 diabetes** *NATURE*
  Fuchsberger, C., Flannick, J., Teslovich, T. M., Mahajan, A., Agarwala, V., Gaulton, K. J., Ma, C., Fontanillas, P., Moutsianas, L., McCarthy, D. J., Rivas, M. A., Perry, J. R., Sim, et al
  2016; 536 (7614): 41-?

- **A null mutation in ANGPTL8 does not associate with either plasma glucose or type 2 diabetes in humans** *BMC ENDOCRINE DISORDERS*
  Clapham, K. R., Chu, A. Y., Wessel, J., Natarajan, P., Flannick, J., Rivas, M. A., Sartori, S., Mehran, R., Baber, U., Fuster, V., Scott, R. A., Rader, D. J., Boehnke, et al
  2016; 16

- **A Frameshift in CSF2RB Predominant Among Ashkenazi Jews Increases Risk for Crohn's Disease and Reduces Monocyte Signaling via GM-CSF.** *Gastroenterology*
  Chuang, L. S., Villaverde, N., Hui, K. Y., Mortha, A., Rahman, A., Levine, A. P., Haritunians, T., Evelyn Ng, S. M., Zhang, W., Hsu, N. Y., Facey, J. A., Luong, T., Fernandez-Hernandez, et al
  2016

- **Sequence variation between 462 human individuals fine-tunes functional sites of RNA processing.** *Scientific reports*
  Ferreira, P. G., Oti, M., Barann, M., Wieland, T., Ezquina, S., Friedländer, M. R., Rivas, M. A., Esteve-Codina, A., Rosenstiel, P., Strom, T. M., Lappalainen, T., Guigó, R., Sammeth, et al
  2016; 6: 32406

- **TMEM258 Is a Component of the Oligosaccharyltransferase Complex Controlling ER Stress and Intestinal Inflammation.** *Cell reports*
  Graham, D. B., Lefkovith, A., Deelen, P., de Klein, N., Varma, M., Boroughs, A., Desch, A. N., Ng, A. C., Guzman, G., Schenone, M., Petersen, C. P., Bhan, A. K., Rivas, et al
  2016; 17 (11): 2955–65

- **A Protein Domain and Family Based Approach to Rare Variant Association Analysis.** *PloS one*
  Richardson, T. G., Shihab, H. A., Rivas, M. A., McCarthy, M. I., Campbell, C., Timpson, N. J., Gaunt, T. R.
  2016; 11 (4): e0153803

- **The landscape of genomic imprinting across diverse adult human tissues** *GENOME RESEARCH*
  Baran, Y., Subramaniam, M., Biton, A., Tukiainen, T., Tsang, E. K., Rivas, M. A., Pirinen, M., Gutierrez-Arcelus, M., Smith, K. S., Kukurba, K. R., Zhang, R., Eng, C., Torgerson, et al
  2015; 25 (7): 927-936

- **The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans** *SCIENCE*
  Ardlie, K. G., DeLuca, D. S., Segre, A. V., Sullivan, T. J., Young, T. R., Gelfand, E. T., Trowbridge, C. A., Maller, J. B., Tukiainen, T., Lek, M., Ward, L. D., Kheradpour, P., Iriarte, et al
  2015; 348 (6235): 648-660

- **Whole-genome sequencing to understand the genetic architecture of common gene expression and biomarker phenotypes** *HUMAN MOLECULAR GENETICS*
  Wood, A. R., Tuke, M. A., Nalls, M., Hernandez, D., Gibbs, J. R., Lin, H., Xu, C. S., Li, Q., Shen, J., Jun, G., Almeida, M., Tanaka, T., Perry, et al
  2015; 24 (5): 1504-1512

- **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

- **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

- **Identification and Functional Characterization of G6PC2 Coding Variants Influencing Glycemic Traits Define an Effector Transcript at the G6PC2-ABCB11 Locus** *PLOS GENETICS*

Mahajan, A., Sim, X., Ng, H. J., Manning, A., Rivas, M. A., Highland, H. M., Locke, A. E., Grarup, N., Im, H. K., Cingolani, P., Flannick, J., Fontanillas, P., Fuchsberger, et al

2015; 11 (1)

- **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

- **Transcriptome and genome sequencing uncovers functional variation in humans** *NATURE*

  Lappalainen, T., Sammeth, M., Friedlaender, M. R., 't Hoen, P. A., Monlong, J., Rivas, M. A., Gonzalez-Porta, M., Kurbatova, N., Griebel, T., Ferreira, P. G., Barann, M., Wieland, T., Greger, et al

  2013; 501 (7468): 506-511

- **Association Between Variants of PRDM1 and NDP52 and Crohn's Disease, Based on Exome Sequencing and Functional Studies** *GASTROENTEROLOGY*

  Ellinghaus, D., Zhang, H., Zeissig, S., Lipinski, S., Till, A., Jiang, T., Stade, B., Bromberg, Y., Ellinghaus, E., Keller, A., Rivas, M. A., Skieceviciene, J., Doncheva, et al

  2013; 145 (2): 339-347

- **Mosaic PPM1D mutations are associated with predisposition to breast and ovarian cancer.** *Nature*

  Ruark, E., Snape, K., Humburg, P., Loveday, C., Bajrami, I., Brough, R., Rodrigues, D. N., Renwick, A., Seal, S., Ramsay, E., Duarte, S. D., Rivas, M. A., Warren-Perry, et al

  2013; 493 (7432): 406-410

- **Mosaic PPM1D mutations are associated with predisposition to breast and ovarian cancer** *NATURE*

  Ruark, E., Snape, K., Humburg, P., Loveday, C., Bajrami, I., Brough, R., Rodrigues, D. N., Renwick, A., Seal, S., Ramsay, E., Duarte, S. D., Rivas, M. A., Warren-Perry, et al

  2013; 493 (7432): 406-U152

- **Rare, Low-Frequency, and Common Variants in the Protein-Coding Sequence of Biological Candidate Genes from GWASs Contribute to Risk of Rheumatoid Arthritis** *AMERICAN JOURNAL OF HUMAN GENETICS*

  Diogo, D., Kurreeman, F., Stahl, E. A., Liao, K. P., Gupta, N., Greenberg, J. D., Rivas, M. A., Hickey, B., Flannick, J., Thomson, B., Guiducci, C., Ripke, S., Adzhubey, et al

  2013; 92 (1): 15-27

- **Pooled DNA Resequencing of 68 Myocardial Infarction Candidate Genes in French Canadians** *CIRCULATION-CARDIOVASCULAR GENETICS*

  Beaudoin, M., Lo, K. S., N'Diaye, A., Rivas, M. A., Dube, M., Laplante, N., Phillips, M. S., Rioux, J. D., Tardif, J., Lettre, G.

  2012; 5 (5): 547-554

- **Genetic Adaptation of Fatty-Acid Metabolism: A Human-Specific Haplotype Increasing the Biosynthesis of Long-Chain Omega-3 and Omega-6 Fatty Acids** *AMERICAN JOURNAL OF HUMAN GENETICS*

  Ameur, A., Enroth, S., Johansson, A., Zaboli, G., Igl, W., Johansson, A. C., Rivas, M. A., Daly, M. J., Schmitz, G., Hicks, A. A., Meitinger, T., Feuk, L., Van Duijn, et al

  2012; 90 (5): 809-820

- **A map of human genome variation from population-scale sequencing** *NATURE*

  Altshuler, D., Durbin, R. M., Abecasis, G. R., Bentley, D. R., Chakravarti, A., Clark, A. G., Collins, F. S., De La Vega, F. M., Donnelly, P., Egholm, M., Flicek, P., Gabriel, S. B., Gibbs, et al

  2010; 467 (7319): 1061-1073

- **High-throughput, pooled sequencing identifies mutations in NUBPL and FOXRED1 in human complex I deficiency** *NATURE GENETICS*

  Calvo, S. E., Tucker, E. J., Compton, A. G., Kirby, D. M., Crawford, G., Burtt, N. P., Rivas, M., Guiducci, C., Bruno, D. L., Goldberger, O. A., Redman, M. C., Wiltshire, E., Wilson, et al

  2010; 42 (10): 851-?

- **Fine Mapping in 94 Inbred Mouse Strains Using a High-Density Haplotype Resource** *GENETICS*

  Kirby, A., Kang, H. M., Wade, C. M., Cotsapas, C., Kostem, E., Han, B., Furlotte, N., Kang, E. Y., Rivas, M., Bogue, M. A., Frazer, K. A., Johnson, F. M., Beilharz, et al

  2010; 185 (3): 1081-1095

- **Genetic Analysis of Human Traits In Vitro: Drug Response and Gene Expression in Lymphoblastoid Cell Lines** *PLOS GENETICS*

  Choy, E., Yelensky, R., Bonakdar, S., Plenge, R. M., Saxena, R., De Jager, P. L., Shaw, S. Y., Wolfish, C. S., Slavik, J. M., Cotsapas, C., Rivas, M., Dermitzakis, E. T., Cahir-McFarland, et al

2008; 4 (11)