

Curriculum Vitae

Yen-Yi Ho

Office Address

University of South Carolina,
209G LeConte College
1523 Greene Street,
Columbia, SC 29208
Phone: 803-777-5163
Email: Hoyen@stat.sc.edu
Website: <http://People.stat.sc.edu/hoyen/>

Education

- 2009 Ph.D., Biostatistics, Johns Hopkins University,
*Thesis Title: Gene Association Networks and Higher-Order Interactions:
Algorithms and Statistical Models.*
Committee: Dr. Giovanni Parmigiani (Advisor), Dr. Leslie Cope,
Dr. Pien-Chien Huang, Dr. Thomas Louis
- 2001 M.S., Epidemiology, National Taiwan University
Committee: Dr. Wen-Chung Lee (Advisor), Dr. Wei J Chen,
Dr. Chuhsing Kate Hsiao, Dr. Chien-Jen Chen
- 1999 B.S., Double Major in Medical Technology & Public Health,
National Taiwan University

Employment

- Aug 2016 – Present Assistant Professor, Department of Statistics, College of Arts and Sciences,
University of South Carolina
- 2011 – 2016 Assistant Professor, Division of Biostatistics, School of Public Health,
University of Minnesota
- 2011 – 2016 Faculty, Biostatistics and Bioinformatics Shared Resource
Masonic Cancer Center, University of Minnesota
- 2009 – 2011 Postdoctoral Research Fellow
McKusick-Nathans Institute of Genetic Medicine
Johns Hopkins University School of Medicine
- 2006 – 2007 Statistical Consultant, Biostatistics Consulting Center
Department of Biostatistics, Johns Hopkins University
- 2005 – 2009 Statistical Consultant, School of Nursing
Johns Hopkins University
- 2001 – 2003 Research Associate, Bioresource Collection and Research Center
Hsinchu, Taiwan

Honors and Awards

- 2017 ASA/Kutner Travel Award
 2003 – 2005 Government Funded Scholarship for Studying Abroad,
 Taiwanese Ministry of Education
 1999 Research Creativity Award, National Science Council, Taiwan
 Awarded for Outstanding Undergraduate Research

Teaching Experience

- 2011 – 2016 Member, Statistical Genetics and Bioinformatics Curriculum Committee
 Division of Biostatistics, University of Minnesota
 2012 – 2016 Instructor, Statistics for Human Genetics and Molecular Biology (PUBH7445)
 Division of Biostatistics, University of Minnesota
 Fall 2016 Instructor, Elementary Statistics for the Biological and Life Sciences (STAT205)
 Department of Statistics, University of South Carolina
 Spring 2017 – 2020 Instructor, Introduction to Analysis of Genomic Data Using R (STAT599)
 Department of Biological Sciences, University of South Carolina
 Fall 2017 – Present Instructor, Data Analysis I (STAT704)
 Department of Statistics, University of South Carolina
 Fall 2017 – Present Introduction to Biostatistics (BMSC700, Guest Lecture)
 School of Medicine, University of South Carolina
 Spring 2019 Instructor, Data Analysis II (STAT705)
 Department of Statistics, University of South Carolina
 Spring 2021 Instructor, Genomic Data Science (STAT588/BIOL588)

Professional Memberships and Service

- American Statistical Association
 Institute of Mathematical Statistics
 Referee, American Journal of Epidemiology (2014)
 Referee, Turkish Journal of Medical Sciences (2015)
 Referee, PLOS ONE (2016)
 Member, Cancer Protocol Review Committee,
 Masonic Cancer Center, University of Minnesota (2011–2015)
 Referee, PLOS Computational Biology (2017)
 Referee, Nucleic Acids Research (2017)
 Reviewer, ASPIRE II Grant Review Committee (April 2018)
 Member, Department of Statistics PhD Qualifying Exam Committee (May 2018, May 2019)
 Referee, Journal of Gerontology: Biological Sciences (2018)
 Referee, Journal of the Royal Statistical Society C (2018)
 Referee, BMC Bioinformatics (2018)
 Referee, Journal of the Royal Statistical Society C (2019)
 Referee, Drug and Alcohol Dependence (2020)
 Referee, BMC Bioinformatics (2020)

Software

1. **Ho, Y.-Y.** (2009). LiquidAssociation: R/Bioconductor package for estimating liquid association using the conditional normal model. Available at <http://www.bioconductor.org>
2. Gunderson, T.* (2014). fastLiquidAssociation: R/Bioconductor package for exploring liquid association on a genome-wide scale. Available at <http://www.bioconductor.org>. * Package was developed under Ho's supervision as the author's thesis advisor.
3. Yang, Z.* (2020) ZENCO: Modeling Dynamic Correlation in Zero-Inflated Count Data. Available at <https://github.com/zheny714/ZENCO>. * Package was developed under Ho's supervision as the author's thesis advisor.

Publications

* indicates methodological contribution.

1. Chen, W.J., Liu P.-H., **Ho Y.-Y.**, and Chien, K.-L., et al. (2003). Sibling recurrence risk ratio analysis of the metabolic syndrome and its components over time. *BMC Genetics* **4**, S33-S28.
- 2.* Lee, W.-C., **Ho Y.-Y.** (2003). Potential for gene-gene confounding bias in case-parental control studies. *Annals of Epidemiology* **13**, 261-266.
- 3.* **Ho Y.-Y.**, Cope L., Dettling M., and Parmigiani G. (2007). Statistical methods for identifying differentially expressed gene combinations. In: Ochs M.F. (eds) *Gene Function Analysis. Methods in Molecular Biology* **408**, 171-191. Humana Press.
- 4.* **Ho Y.-Y.**, Parmigiani, G., Louis, T.A., Cope, L.M. (2010). Modeling liquid association. *Biometrics* **67**, 133-141. doi: 10.1111/j.1541-0420.2010.01440.x.
5. Jiang, Q., **Ho Y.-Y.**, Hao L, Nichols Berrios C, Chakravarti, A. (2011). Copy number variants in candidate genes are genetic modifiers of Hirschsprung disease. *PLoS One* **6**, e21219.
6. **Ho Y.-Y.**, Matteini A.M., Beamer B., and Fried L., et al. (2011). Exploring biologically relevant pathways in frailty. *Journal of Gerontology A Biological Sciences and Medical Sciences* **66**, 975-979.
7. Shen A., Baker J., Scott G., Davis Y., **Ho Y.-Y.**, Siliciano R. (2013). Endothelial cell stimulation overcomes restriction and promotes productive and latent HIV-1 infection of resting CD4+ T cells. *Journal of Virology* **87**, 9768-79. doi: 10.1128/JVI.01478-13.

8. Terrell A.N., Huynh M., Grill A., Kovi R.C., O'Sullivan M.G., Guttenplan J.B., **Ho Y.-Y.**, Peterson L.A. (2014). Mutagenicity of furan in female Big Blue B6C3F1 mice. *Mutation Research/Genetic Toxicology and Environmental Mutagenesis* **770**, 46-54.
- 9.* **Ho Y.-Y.**, Cope, L.M., Parmigiani, G. (2014). Modular network construction using eQTL data: an analysis of computational costs and benefits. *Frontiers in Genetics* **5**, 40. doi: 10.3389/fgene.2014.00040
- 10.* **Ho Y.-Y.**, Baechler E.C., Ortmann W., Behrens T.W., Graham R.R., Bhangale T.R., Pan W. (2014). Using gene expression to improve the power of genome-wide association analysis. *Human Heredity* **78**, 94-103. doi: 10.1159/000362837
11. Abbott, K., Nyre, E., Abrahante, J., **Ho Y.-Y.**, Isaksson, R.V., Starr, T. (2014) The candidate cancer gene database: a database of cancer driver genes from forward genetic screens in mice. *Nucleic Acids Research* **43**, D844-8. doi: 10.1093/nar/gku770.
- 12.* Gunderson T., **Ho Y.-Y.*** (2014) An efficient algorithm to explore liquid association on a genome-wide scale. *BMC Bioinformatics* **15**, 371. *Ho was the corresponding author and the first author's thesis advisor.
13. Gupta M., McCauley J., Farkas A., Gudeloglu A., Neuberger M.M., **Ho Y.-Y.**, Yeung L., Vieweg J, Dahm P. (2014) Clinical practice guidelines on prostate cancer: a critical appraisal. *The Journal of Urology* pii: S0022-5347(14)04811-3. doi: 10.1016/j.juro.2014.10.105.
14. Nho R., Im J., **Ho Y.-Y.**, Hergert P. (2014) MicroRNA-96 inhibits FoxO3a function in IPF fibroblasts on type I collagen matrix. *American Journal of Physiology-Lung Cellular and Molecular Physiology* **307**, 632-42. doi: 10.1152/ajplung.00127.2014.
15. Gavin K., Linde J.A., Pacanowski C.R., French S.A., Jeffery R.W., **Ho Y.-Y.** (2015) Weighing frequency among working adults: cross-sectional analysis of two community samples. *Preventive Medicine Reports* **2**, 44-46. doi: 10.1016/j.pmedr.2014.12.005.
- 16.* **Ho Y.-Y.**, O'Connell M., Guan W., Basu S. (2015) Powerful association test combining rare variant and gene expression using family data from Genetic Analysis Workshop 19. *BMC Proceedings* **10 Suppl 7**, 251-255.
- 17.* **Ho Y.-Y.**, LaRue R.S., Timothy T. Starr, Largaespada D.A. (2016) Case-oriented pathways analysis in pancreatic adenocarcinoma using data from a sleeping beauty transposon mutagenesis screen. *BMC Medical Genomics* **9**, 16.
- 18.* **Ho Y.-Y.***, Vo T.N.* , Chu H., Luo X., Le C.T. (2016) A Bayesian hierarchical model for demand curve analysis. *These authors contribute equally to this

- paper. *Statistical Methods in Medical Research* **27**, 2038-2049. DOI: 10.1177/0962280216673675
19. Arsoniadis E.G., **Ho Y.-Y.**, Melton G.B., Madoff R.D., Le C., Kwaan M.R. (2017) African Americans and short-term outcomes After Surgery for Crohn's Disease: An ACS-NSQIP Analysis. *Journal of Crohn's and Colitis*. **11**, 468-473.
 20. Abbott K, **Ho Y.-Y.**, Erickson J. (2017) Automatic health record review to identify gravely ill social security disability applicants. *Journal of the American Medical Informatics Association* **24**, 709-716.
 21. Warlick C., Berge J.M., **Ho Y.-Y.**, Yeazel M. (2017) Impact of a prostate specific antigen screening decision aid on clinic function. *Urology Practice* **4**, 448-453.
 - 22.* Wang L., Liu S., Ding Y., **Ho Y.-Y.**, Yuan S.-S., Tseng G.C. (2017) Meta-analytic framework for liquid association. *Bioinformatics* **15**, 2140-2147.
 23. Fagan D.H, Fettig L.M, Avdulov S, Beckwith H., Peterson M.S, **Ho Y.-Y.** , Wang F., Polunovsky V.A, and Yee D. (2017) Acquired tamoxifen resistance in MCF-7 breast cancer cells requires hyperactivation of eIF4F-mediated translation. *Hormones and Cancer* **8**, 219-229.
 24. Pulvers K., Cupertino A. P., Scheuermann T. S., Cox L.S., **Ho Y.-Y.**, Nollen N.L., Cuellar R., Ahluwalia J.S. (2018) Daily and nondaily smoking varies by acculturation among English-speaking, U.S. Latino men and women. *Ethnicity and Disease* **28**, 105-114.
 25. Nallandhighal S., Park G.S., **Ho Y.-Y.**, Opoka R. O., John C. C., Tran T. M. (2018) Whole-blood transcriptional signatures composed of erythropoietic and NRF2-regulated genes differ between cerebral malaria and severe malarial anemia. *The Journal of Infectious Disease* **219**, 154-164.
 - 26.* Kinzy T., Starr T., Tseng G, **Ho Y.-Y.*** (2018) Meta-analytic framework for modeling gene coexpression dynamics. *Statistical Applications in Genetics and Molecular Biology* **18**, 1- 12. *Ho is the corresponding author and the first author's thesis advisor.
 27. Peterson L., Ignatovich I., Grill A., Beauchamp A., **Ho Y.-Y.**, DiLernia A., Zhang L. (2019) Individual differences in the response of human β -lymphoblastoid cells to the cytotoxic, mutagenic and DNA-damaging effects of a DNA methylating agent, N-methylnitrosourea. *Chemical Research in Toxicology* **32**, 2214-2226.
 - 28.* Baek S., **Ho Y.-Y.**, Ma Y. (2020) Using sufficient direction factor model to analyze latent activities associated with breast cancer survival. *Biometrics*, **76**, 1340-1350.

29. Krizek B.A., Blakley I.C, **Ho Y.-Y.**, Freese N., Loraine A.E. (2020) The Arabidopsis transcription factor AINTEGUMENTA orchestrates patterning genes and auxin signaling in the establishment of floral growth and form. *The Plant Journal*, **103**, 752-768.
- 30.* Ma Z., Hanson T, **Ho Y.-Y.*** (2020) Flexible bivariate correlated count data regressions. *Statistics in Medicine*, **39**, 3476–3490. *Ho is the first author’s thesis co-advisor.
31. Peterson L.A., Oram M.K., Flavin M., Seabloom D., Smith W.E., O’Sullivan M.G., Vevang K.R, Upadhyaya, P., Stornetta A., Floeder A.C., **Ho Y.-Y.**, Zhang L, Hecht S.S, Balbo S., Wiedmann T.S. (2021+) Co-exposure to inhaled aldehydes or carbon dioxide enhances the carcinogenic properties of the tobacco specific nitrosamine 4-methylanitrosamino-1-(3-pyridyl)-1-butanone (NNK) in the A/J mouse lung. *Chemical Research in Toxicology* (To appear).

Submitted

1. Yang Z., **Ho Y.-Y.*** Modeling dynamic correlation in zero-inflated bivariate count data with applications to single-cell RNA sequencing data. [Under Revision *Biometrics*] *Ho is the first author’s thesis advisor.
2. **Ho, Y.-Y.**, Zhang W., Huang H.-H., Habiger J.D., and Nho R. A powerful integrative genomics approach to incorporate both prior knowledge and multiple data types through p -value weight adjustment. [Under Revision]
3. Hill L.N., Yang Z., Zgodic A., Josey M., Hussey J., **Ho Y.-Y.**, Adams S.A., Caldwell R., Thibault A., Berger F.G., Eberth J.M. (2021+) Predictors of polyp count among uninsured patients receiving colorectal cancer screening. [Under Revision *Cancer Epidemiology*].

In Preparation

1. Zhang W., **Ho, Y.-Y.** (2021+) A fast search algorithm for identifying dynamic coexpression via Bayesian variable selection.
2. Ma Z., **Ho Y.-Y.** (2021+) Bayesian models for integrating correlated single-cell sequencing multi-omics data.
3. Yang Z., **Ho Y.-Y.** (2021+) Use sufficient direction factor model to classify cell types using single-cell RNA sequencing data.

Presentations

Oral Presentation

1. Ho Y.-Y., Cope L., Dettling M., and Parmigiani G. (2007) Statistical methods for identifying differentially expressed gene combinations. *International Biometric Society Eastern North American Region (ENAR)*.

2. Ho Y.-Y., Cope L., and Parmigiani G. (2008) Exploring liquid association in non-gaussian multivariate distributions. *Joint Statistical Meetings*.
3. Ho Y.-Y., Cope L., and Parmigiani G. (2011) nPARS: A comprehensive search algorithm for constructing Bayesian networks using large-scale genomic data. *Joint Statistical Meetings, Miami*.
4. Ho Y.-Y. (2014) Using gene expression to improve the power of genome-wide association analysis (2014). *International Biometric Society Eastern North American Region (ENAR)*.
5. **Ho, Y.-Y.**, O'Connell M., Guan W., Basu S. (2015) Powerful association test combining rare variant and gene expression using family data from genetic analysis workshop 19. *Genetic Analysis Workshop 19, Vienna, Austria* [Presented by O'Connell M]
6. **Ho Y.-Y.**, LaRue R.S., Timothy T. Starr, Largaespada D.A. (2016) Individual-oriented gene set analysis using insertional mutation data. *Joint Statistical Meetings, Chicago*.
7. **Ho Y.-Y.** (2017) Statistical methods for integrating large-scale genomic data and constructing gene association networks. *Department of Mathematical Sciences, Clemson University*.
8. **Ho Y.-Y.** (2017) Case-oriented pathway analysis using data from a sleep beauty transposon mutagenesis screen. Lighting Talk, *Research Computing Symposium, University of South Carolina*.
9. **Ho Y.-Y.** (2018) Statistical methods for integrating large-scale genomic data and constructing gene association networks. *Center for Colon Cancer Research Annual Retreat, Saluda Shoals Park*.
10. **Ho Y.-Y.** (2018) Statistical methods for integrating large-scale genomic data and identifying higher-order interactions. *Department of Biostatistics, Arnold School of Public Health, University of South Carolina*.
11. **Ho Y.-Y.** (2019) Invited Talk: p -value adjustment procedure using empirical weights. *Lifetime Data Science, Pittsburgh, Pennsylvania*.
12. **Ho Y.-Y.** (2019) Invited Talk: p -value adjustment procedure using empirical weights. *Applied Statistics Symposium, International Chinese Statistical Association, Raleigh, North Carolina*.
13. **Ho Y.-Y.** (2020) Modeling Dynamic Dependence Structure in Zero-inflated Bivariate Count Data with Application to Single-Cell RNA sequencing Data. *Joint Statistical Meetings Philadelphia, Pennsylvania (Virtual Conference Due to COVID-19)*.

Grants Submitted

1. Regulation of SIRT6 tumor suppressor in breast cancer by tyrosyl-tRNA synthetase
PI: Dr. Sajish Mattew (College of Pharmacy)
Role: Statistician
Mechanism: Susan G Komen Foundation (submitted Nov 2016)
2. Integrating Somatic Mutation and Gene Expression Data to Identify Active Driver Pathways Associated with Cancer Survival
Role: Principal Investigator
Mechanism: ASPIRE I, University of South Carolina (submitted Jan 2017)
Status: **Funded**
3. Genomics of autism-related traits in Peromyscus (deer mice)
PI: Dr. Michael Felder (Department of Biological Sciences)
Role: Co-Investigator
Mechanism: NIH R01 (submitted Feb, 2017, re-submitted Oct, 2017)
4. Identifying Genetic Loci Associated with Neurocristopathies using the Deer Mouse Peromyscus maniculatus
PI: Dr. Shannon Davis (Department of Biological Sciences)
Role: Co-Investigator
Mechanism: NIH R03 (submitted June 2017, re-submitted Jan 2018, re-submitted Aug 2018, re-submitted Nov 2018, re-submitted Feb 2019)
Status: **Funded**
5. Chromatin regulatory mechanisms in autism spectrum disorders
PI: Dr. Sofia Lizarraga (Department of Biological Sciences)
Role: Co-Investigator
Mechanism: NIH R01 (submitted June 2017, re-submitted June 2018)
6. Secondary Analysis and Integration Existing Data to Elucidate the Genetic Architecture of Cancer Risk and Related Outcomes
Role: Principal Investigator
Mechanism: CAS Faculty Research Initiative, 07/2017 – 09/2018
Status: **Funded**
7. A Chemopreventive Strategy Based on Edible MicroRNAs Produced in Plants
PI: Dr. Vicki Vance (Department of Biological Sciences)
Role: Statistician
Mechanism: NIH R21 (submitted Feb 2018)
Status: **Funded**
8. Mechanism of Replication Rescue by the Human CST Complex
PI: Dr. Jason Stewart (Department of Biological Sciences)
Role: Statistical Consultant
Mechanism: NIH R01 (submitted Feb 2018)

Grants Submitted

9. A novel technology for isolating and imaging cell type specific exosomes in inter-organ communication
PI: Dr. Guiren Wang (Department of Mechanical Engineering)
Role: Co-Investigator
Mechanism: ASPIRE II (submitted Feb 2018, re-submitted Feb 2019)
10. Dysregulation of miR489 expression impacts breast cancer tumorigenesis and heterogeneity
PI: Dr. Hexin Chen (Department of Biological Sciences)
Role: Co-Investigator
Mechanism: Department of Defense (submitted May 2018)
11. Early Onset Colorectal Cancer (EOCRC): A PPG to support our ongoing mission at the Center for Cancer Research at the University of South Carolina
PI: Lorne Hofseth and Frank Berger
Mechanism: UofSC Excellent Initiative (submitted June, 2018)
Role: Co-investigator
12. Mechanism of MHC heterozygote advantage during anti-commensal germinal center B cell selection
PI: Dr. Jason Kubinak (School of Medicine)
Role: Co-Investigator
Mechanism: NIH R21 (submitted November, 2018)
Status: **Funded**
13. Playing with Data is Exhilaratingly Fun!
PI: Yen-Yi Ho
Role: **Principal Investigator**
Mechanism: UofSC Center of Teaching Excellence
2018-2019 Innovative Pedagogy Grants (submitted December 2018)
14. The role of CST in DNA replication origin licensing and activation
PI: Dr. Jason Stewart (Department of Biological Sciences)
Role: Co-Investigator Mechanism: NIH R01 (submitted March 2019)
15. Stress granule protein functions in PNS and CNS axon regeneration
PI: Dr. Jeff Twiss (Department of Biological Sciences)
Role: Co-Investigator
Mechanism: NIH R01 (submitted March 2019)
16. Functional evolution of microRNA-489 and microRNA-425
PI: Dr. Hexin Chen (Department of Biological Sciences)
Role: Co-Investigator
Mechanism: NIH R01 (submitted June 2019)

Grants Submitted

17. Pathological alteration of lung fibroblasts by e-cig vapor increases the risk of developing lung fibrosis
PI: Dr. Richard Nho (Department of Medicine, University of Minnesota)
Role: Statistical Consultant
Mechanism: NIH R21 (submitted June 2019)
18. Targeted nanoparticle delivery of microRNA-489 rejuvenates anthracycline-based chemotherapy for TNBC
PI: Dr. Hexin Chen (Department of Biological Sciences)
Role: Co-Investigator
Mechanism: DOD (submitted September 2019)
19. miR-96 as a therapeutic target for Idiopathic Pulmonary Fibrosis
PI: Dr. Richard Nho (Department of Department of Medicine, University of Minnesota)
Role: Statistical Consultant
Mechanism: NIH R01 (submitted September 2019)
20. Nanoparticle-delivered miR-489 rejuvenates anthracycline-based chemotherapy
PI: Dr. Hexin Chen (Department of Biological Sciences)
Role: Co-Investigator
Mechanism: NIH R21 (submitted October 2019)
Status: **Funded**
21. MHCII Polymorphism Regulates Antibody-Mediated Selection on Microbiota Composition
PI: Dr. Jason Kubinak (School of Medicine)
Role: Co-Investigator
Mechanism: NIH R01 (submitted February, 2020; resubmitted November, 2020)
22. Targeting Interleukin 1 α -mediated immune suppression in HER2-positive breast cancer
PI: Dr. Hexin Chen (Department of Biological Sciences)
Role: Co-Investigator
Mechanism: DOD (submitted March 2020)
23. **scDECO: A novel statistical framework to systematically identify differential co-expression gene combinations using single-cell RNA sequencing data**
PI: Yen-Yi Ho (Department of Statistics)
Mechanism: NIH R21 (submitted November 2020)
Role: **Principal Investigator**
24. Counteracting epigenetic mechanisms in autism spectrum disorders
PI: Dr. Sofia Lizarraga (Department of Biological Sciences)
Role: Co-Investigator
Mechanism: Eagle Grants Program (Submitted January, 2021)

Current Grants

1. Mechanism of MHC heterozygote advantage during anti-commensal germinal center B cell selection

PI: Dr. Jason Kubinak (School of Medicine)

Role: Co-Investigator

Mechanism: NIH R21, 07/2019 – 06/2021

Status: **Funded**

2. Identifying Genetic Loci Associated with Neurocristopathies using the Deer Mouse *Peromyscus maniculatus*

PI: Dr. Shannon Davis (Department of Biological Sciences)

Role: Co-Investigator

Mechanism: NIH R03, 07/2019 – 06/2021

Status: **Funded**

3. Nanoparticle-delivered miR-489 rejuvenates anthracycline-based chemotherapy

PI: Dr. Hexin Chen (Department of Biological Sciences)

Role: Co-Investigator

Mechanism: NIH R21, 06/01/2020 – 05/31/2022

Status: **Funded**

Past Funded Grants

1. Models for Tobacco Products Evaluation
Principal investigator: Dorothy Hatsukami, PhD (UMN)
Mechanism: U19 (NIH/FDA)
2. Transdisciplinary Collaborative Center for Research African American Men's Health
Principal investigator: Selwyn Vickers, PhD (UMN/UAB)
Mechanism: U54
3. Constituent Yields and Biomarkers of Exposure for Tobacco Product Regulation
Principal Investigator: Irina Stepanov, PhD (UMN)
Mechanism: R01
4. Inducing NK cells to remember and fight cancer
Principal Investigator: Jeff Miller, MD (UMN)
Mechanism: R01
5. Minnesota Obesity Center
Principal Investigator: Allen Levine, PhD (UMN)
Mechanism: P30
6. Interactions between tobacco smoke constituents in rodent tumor models
Principal Investigator: Lisa Peterson, PhD (UMN)
Mechanism: R01
7. Molecular mechanisms of leukemia stem cell persistence in AML relapse
Principal Investigator: Zohar Sachs, PhD (UMN)
Mechanism: CTSI/KL2
8. Secondary Analysis and Integration Existing Data to Elucidate the Genetic Architecture of Cancer Risk and Related Outcomes
Role: Principal Investigator
Mechanism: UofSC CAS Faculty Research Initiative, 07/2017 – 12/2018
9. Integrating Somatic Mutation and Gene Expression Data to Identify Active Driver Pathways Associated with Cancer Survival
Role: Principal Investigator
Mechanism: UofSC ASPIRE I, University of South Carolina 07/2017 – 09/2019
10. A Chemopreventive Strategy Based on Edible MicroRNAs Produced in Plants
PI: Dr. Vicki Vance (Department of Biological Sciences)
Role: Co-Investigator
Mechanism: NIH R21, 07/2018 – 06/2020