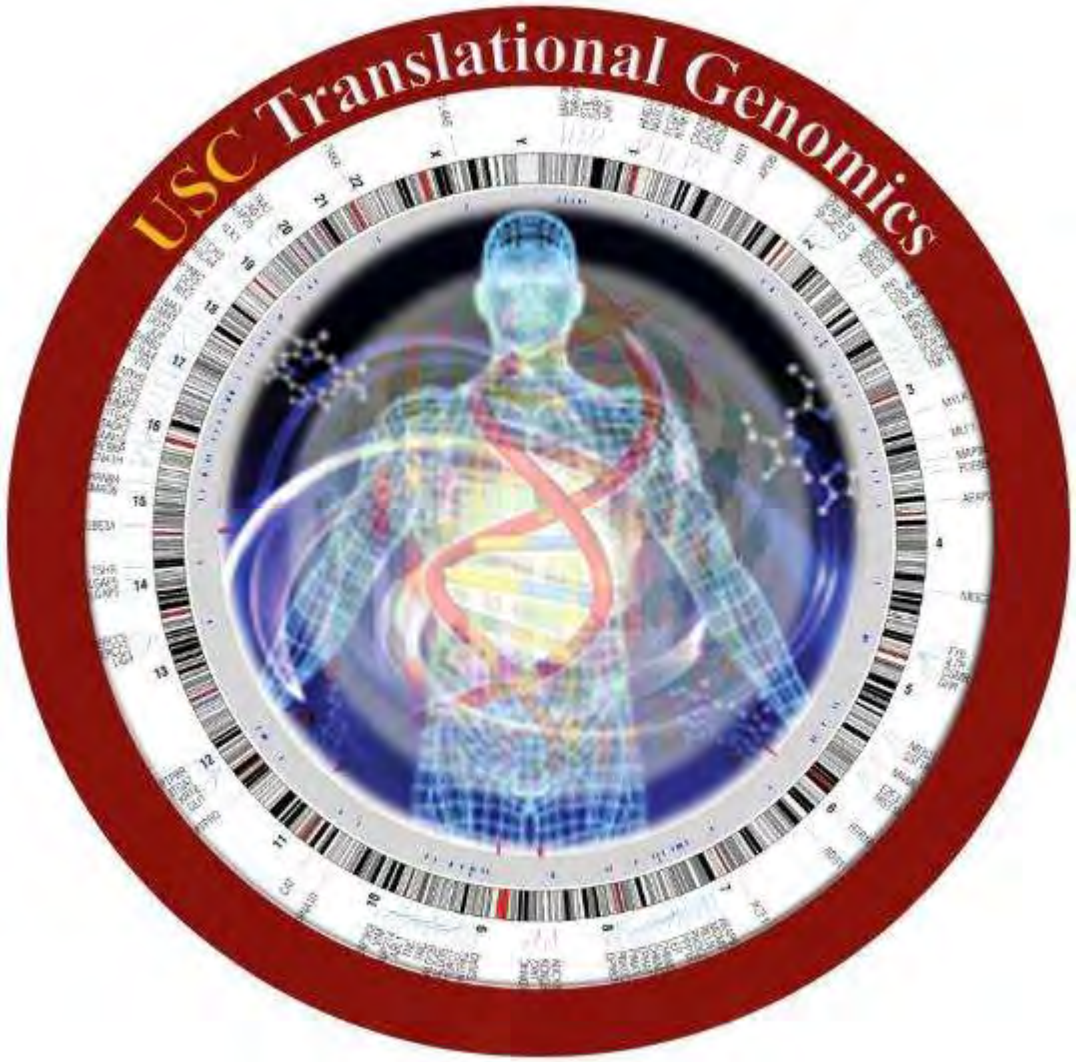
Accelerating improvements in healthcare at USC KSOM through intentional integration between basic discovery research and clinical science!

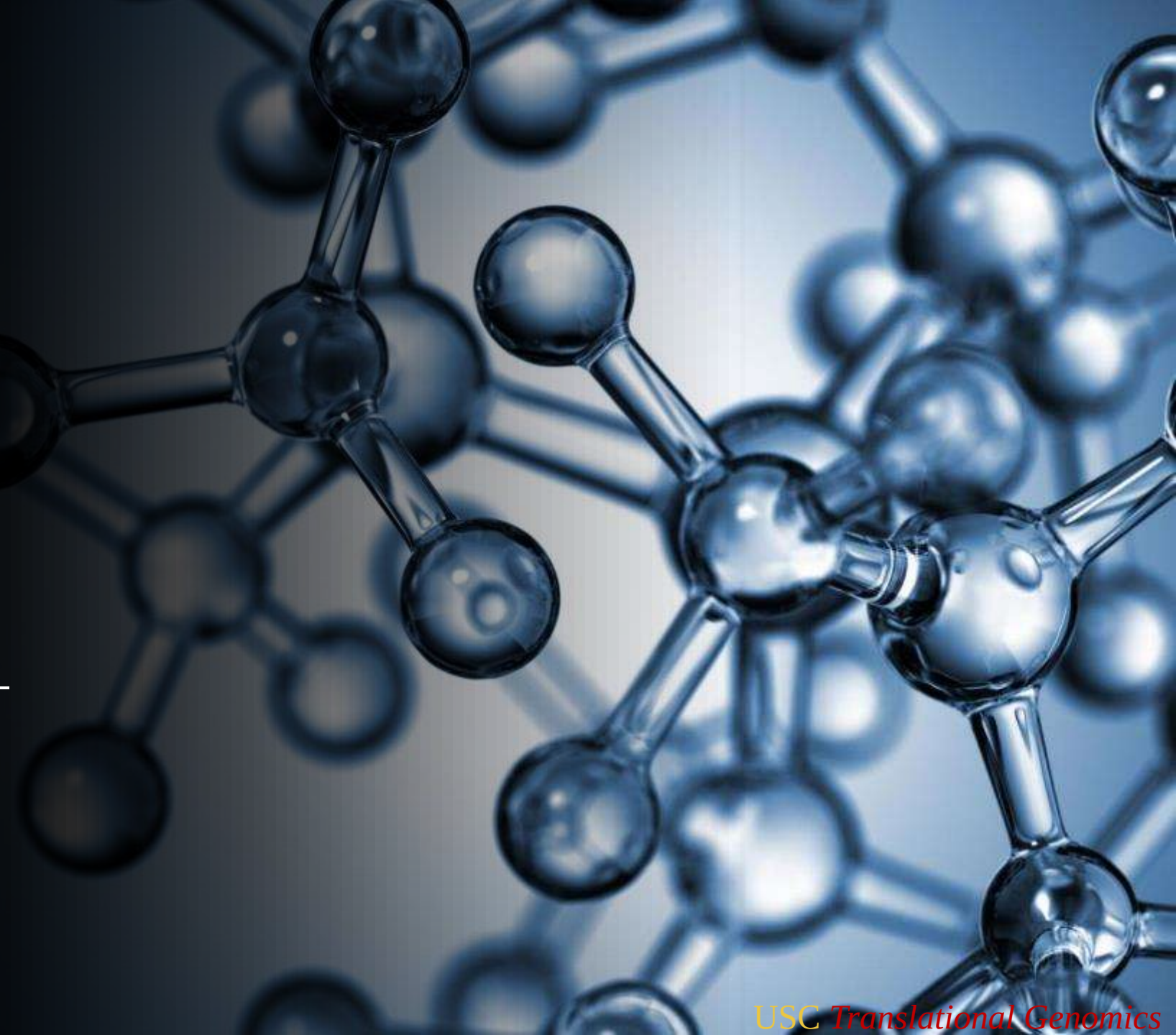


USC Translational Genomics Leadership

John D. Carpten, PhD
Chair

David W. Craig, PhD
Vice Chair

“Translational Research purposefully helps to improve patient outcomes and clinical management, with the additional academic sequelae of scholarship, teaching/training/education, and service.”

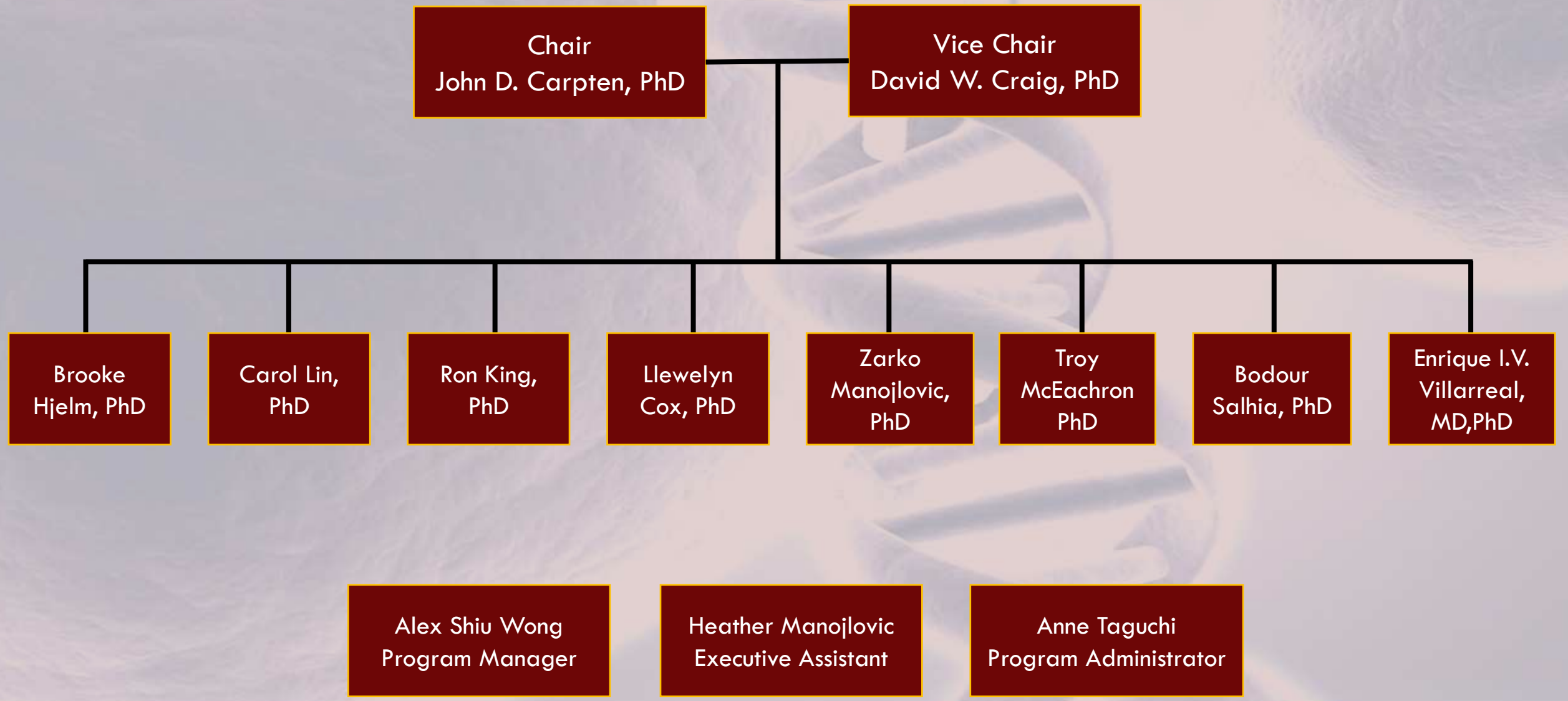


Mission Statement

Drive genome science towards a deeper understanding of human disease processes to improve patient management and outcomes.

- Basic discovery and clinical translational research.
- Training and education.
- Grow status of the KSOM and NCCC in the area of genome sciences.
- Strong commitment to diversity

Organizational Chart



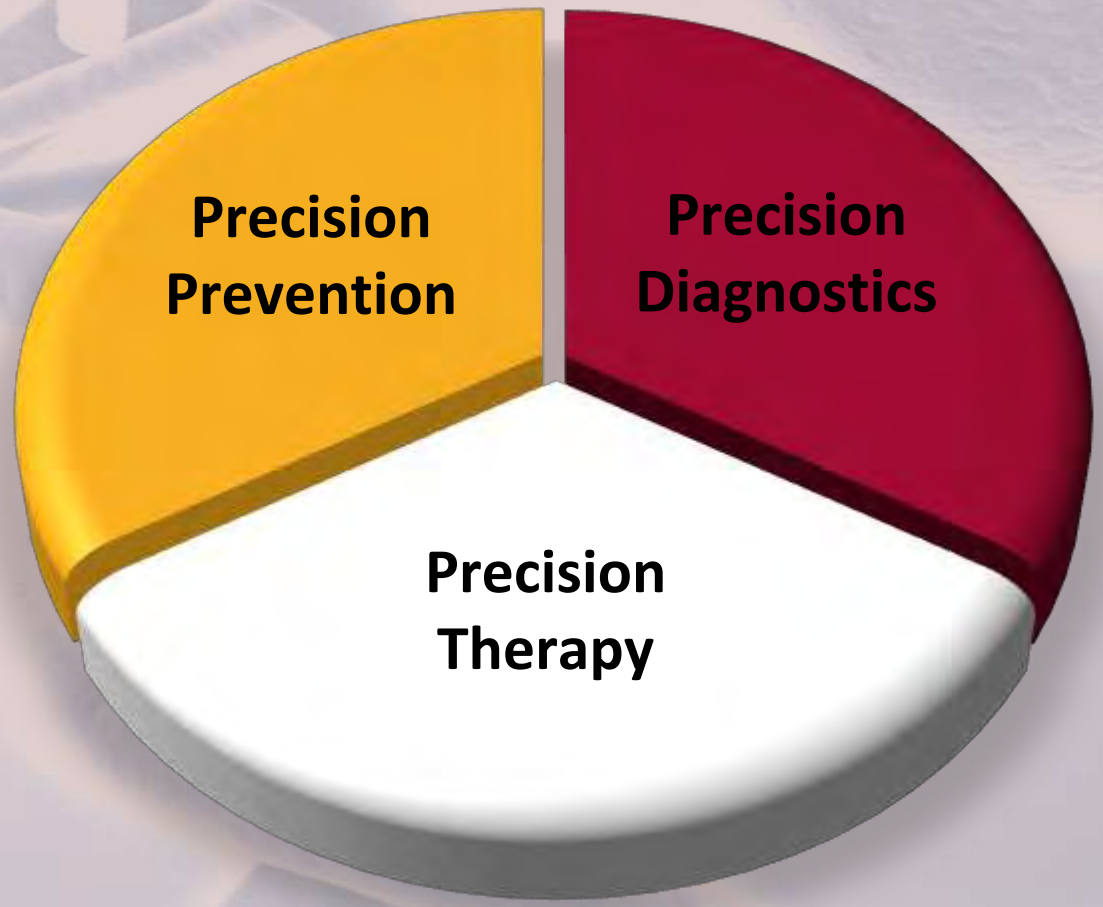
Research Platform

- **Genome science**
  - Germline genetics and risk (Cancer and Rare Genetic Disorders)
  - Somatic cancer interrogation (discovery and clinical relevance)

- **Bioinformatics**
  - Molecular Genomic Data Processing and Analysis
  - Integration with Oncology Pharmacopeias
  - Integration with Clinical Data Parameters

- **Cell biology and Functional genomics**
  - Target validation
  - Functional and cell-based screens
  - PDX model development

- **Applied Epigenetics**
  - Developmental regulation
  - Prediction of metastasis



Educational and Training Platform

- Translational Biotechnology Masters Degree Program
- Translational Biomedical Informatics Masters Degree Program
- Undergraduate Student Research Training
- Medical Student Education
- PIBBS PhD student Training
- Fellowship Training
  - Postdoctoral Fellows
  - Clinical Fellows
  - Fulbright Fellows

Advanced Genomics Technologies


Scholarship

Nucleic Acids Research, 2019 1
doi: 10.1093/nar/gkz164

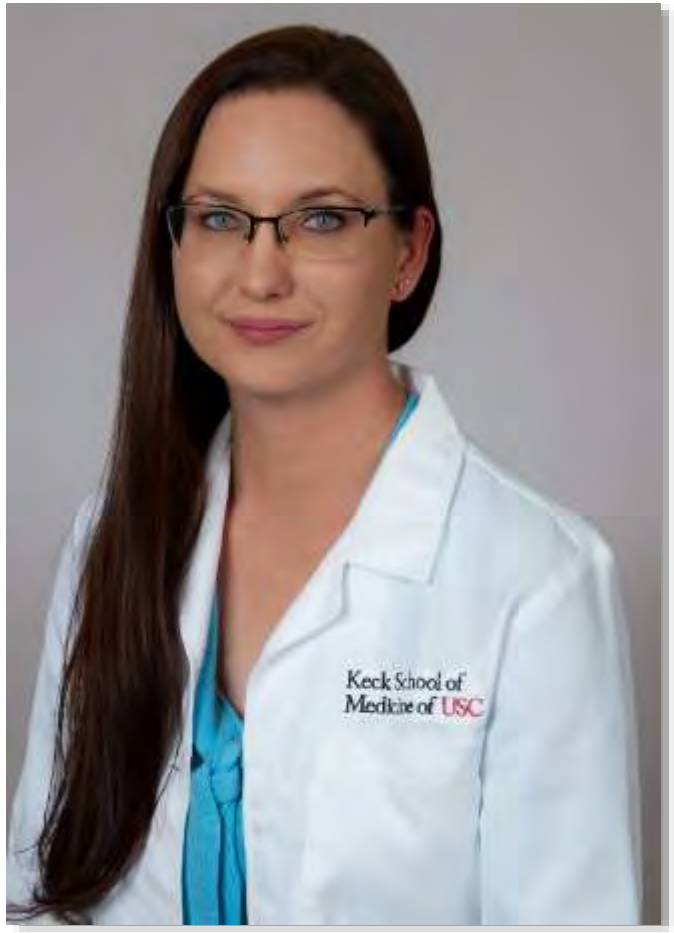
Splice-Break: exploiting an RNA-seq splice junction algorithm to discover mitochondrial DNA deletion breakpoints and analyses of psychiatric disorders

Brooke E. Hjelm[1,2,*], Brandi Rollins[1], Ling Morgan[1], Adolfo Sequeira[1], Firoza Mamdani[1], Filipe Pereira[3], Joana Damas[4], Michelle G. Webb[2], Matthieu D. Weber[1], Alan F. Schatzberg[5], Jack D. Barchas[6], Francis S. Lee[6], Huda Akil[7], Stanley J. Watson[7], Richard M. Myers[8], Elizabeth C. Chao[9], Virginia Kimonis[9], Peter M. Thompson[10], William E. Bunney[1] and Marquis P. Vawter[1,*]

[1]Department of Psychiatry and Human Behavior, University of California-Irvine (UCI), Irvine, CA 92697, USA, [2]Department of Translational Genomics, Keck School of Medicine of USC, University of Southern California (USC), Los Angeles, CA 90033, USA, [3]Interdisciplinary Centre of Marine and Environmental Research (CIIMAR), University of Porto, Matosinhos 4050-123, Portugal, [4]The Genome Center, University of California-Davis, Davis, CA 95616, USA, [5]Department of Psychiatry and Behavioral Sciences, Stanford University, Stanford, CA 94305, USA, [6]Department of Psychiatry, Weill Cornell Medical College at Cornell University, New York, NY 10065, USA, [7]The Molecular and Behavioral Neuroscience Institute, University of Michigan, Ann Arbor, MI 48109, USA, [8]HudsonAlpha Institute for Biotechnology, Huntsville, AL 35806, USA, [9]Division of Genetics and Genomic Medicine, Department of Pediatrics, UCI, Irvine, CA, USA and [10]Southwest Brain Bank, Department of Psychiatry, Texas Tech University Health Sciences Center (TTUHSC), El Paso, TX 79905, USA

Received January 29, 2019; Editorial Decision February 25, 2019; Accepted February 28, 2019

My research focuses on gene expression and DNA variation in complex neurological disorders. Our lab works on both neurodegenerative disorders like Alzheimer's Disease and Parkinson's Disease, as well as psychiatric disorders like Schizophrenia and Major Depressive Disorder. We have a strong focus in mitochondrial genetics and how mitochondrial DNA (mtDNA) structural variation contributes to both aging and disease. In addition, we utilize spatial transcriptomics and single-cell sequencing methods to evaluate postmortem human brain tissue from subjects with these debilitating diseases to assess gene expression and DNA variation in specific neuron/glia cell types and/or cortical layers of the brain.



Brooke E. Hjelm, PhD
Assistant Professor

USC *Translational Genomics*

Troy McEachron, PhD
Assistant Professor of Research

ONCOIMMUNOLOGY
2018, VOL. 7, NO. 12, e1475873 (12 pages)
https://doi.org/10.1080/2162402X.2018.1475873

OncoImmunology

Taylor & Francis
Taylor & Francis Group

ORIGINAL RESEARCH

Profiling targetable immune checkpoints in osteosarcoma

Troy A McEachron[a,b,c], Timothy J Triche[b,d], Laurie Sorenson[a], David M Parham[d], and John D Carpten[a,b]

[a]Department of Translational Genomics; [b]Norris Comprehensive Cancer Center; [c]Department of Pediatrics, Keck School of Medicine of the University of Southern California, Los Angeles, CA, USA; [d]Department of Pathology, Children's Hospital Los Angeles, Los Angeles, CA, USA

BRIEF COMMUNICATIONS

nature genetics

Somatic histone H3 alterations in pediatric diffuse intrinsic pontine gliomas and non-brainstem glioblastomas

St. Jude Children's Research Hospital–Washington University Pediatric Cancer Genome Project

My research focuses on two separate yet complimentary areas: (1) the utilization of next generation genomic, transcriptomic, and proteomic technologies to profile recurrent and/or refractory cancer patients for clinical decision making; (2) the use of functional genomics to identify and interrogate the developmental and therapeutic aspects of cancers, with a focus on sarcomas, which predominantly arise in the pediatric and AYA populations. Moreover, our laboratory is interested in uncovering and understanding the immune microenvironment of cancers using novel molecular technologies in hopes of exploiting these data to identify smarter approaches for the therapeutic management of cancer.

Zarko Manojlovic, PhD
Assistant Professor of Research
Director Keck Genomics Platform

PLOS | GENETICS

RESEARCH ARTICLE

Comprehensive molecular profiling of 718 Multiple Myelomas reveals significant differences in mutation frequencies between African and European descent cases

Zarko Manojlovic[1,2*], Austin Christofferson[2], Winnie S. Liang[2], Jessica Aldrich[2], Megan Washington[2], Shukmei Wong[2], Daniel Rohrer[3], Scott Jewell[3], Rick A. Kittles[4], Mary Derome[5], Daniel Auclair[5], David Wesley Craig[1], Jonathan Keats[2], John D. Carpten[1,2]

IJC International Journal of Cancer | UICC

Innovative Tools and Methods | Full Access

Cancer transcriptomic profiling from rapidly enriched circulating tumor cells

Gareth J Morrison, Alexander T Cunha, Nita Jojo, Yucheng Xu, Yili Xu, Eric Kwok, Peggy Robinson, Tanya Dorff, David Quinn, John Carpten, Zarko Manojlovic, Amir Goldkorn

USC Keck Genomics Platform

"The present moment is filled with joy and happiness. If you are attentive you will see it."
-Thich Nhat Hanh

As Director of Keck Genomics Platform (high-throughput sequencing center), my goal is to provide cutting-edge genomic service to Keck School of Medicine, greater USC, and its affiliates with complete high throughput next-generation sequencing workflows. In this role, my focus is to build a collaborative environment and provide team-driven research support within the scope of the next-generation technologies. In my role as an Assistant Professor of Research, my primary interest is in delineating the molecular interplay of tumor heterogeneity and microenvironments in metastatic disease to help guide clinical decision-making. Furthermore, building on my fellow training, I am interested in interrogating the ancestry effects on cancer progression and outcomes in multi-ethnic prostate tumors.

Bodour Salhia, PhD
Associate Professor

Legendre et al. Clinical Epigenetics (2015) 7:100
DOI 10.1186/s13148-015-0135-8

CLINICAL EPIGENETICS

RESEARCH Open Access

Whole-genome bisulfite sequencing of cell-free DNA identifies signature associated with metastatic breast cancer

Christophe Legendre†, Gerald C. Gooden†, Kyle Johnson, Rae Anne Martinez, Winnie S. Liang and Bodour Salhia*

70

Neuro-Oncology

22(1), 70–83, 2020 | doi:10.1093/neuonc/noz137 | Advance Access date 21 August 2019

Patient-derived xenografts of central nervous system metastasis reveal expansion of aggressive minor clones

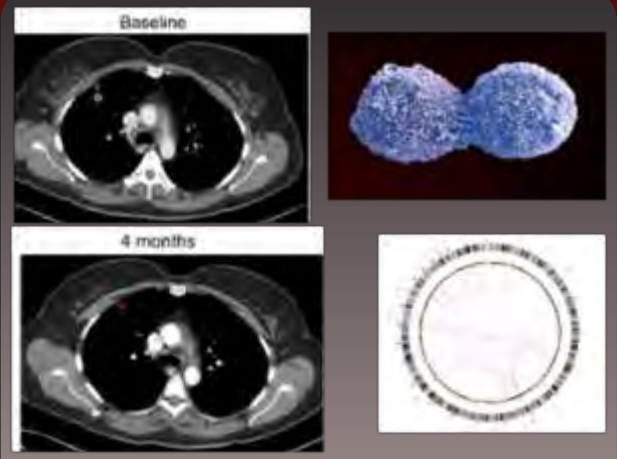
Ben Yi Tew, Christophe Legendre, Mark A. Schroeder, Tim Triche Jr, Gerald C. Gooden, Yizhou Huang, Loren Butry, Daniel J. Ma, Kyle Johnson, Rae Anne Martinez, Mariaelena Pierobon, Emanuel F. Petricoin, Joyce O'Shaughnessy, Cindy Osborne, Coya Tapia, David N. Buckley, Jennifer Glen, Mark Bernstein, Jann N. Sarkaria, Steven A. Toms, and Bodour Salhia

My research centers around the development and application of cutting-edge epigenomic technologies. I have been working on developing liquid biopsies using cell-free DNA methylation for the indications of minimal residual disease in breast cancer, bladder cancer and for the early detection of ovarian cancer. My lab has also been studying the underlying genomic underpinnings of brain metastasis and developed preclinical models to study novel treatment interventions.

RESEARCH

David W. Craig, PhD
Professor and Vice Chair

NEUROGENOMICS



ONCOLOGY GENOMICS

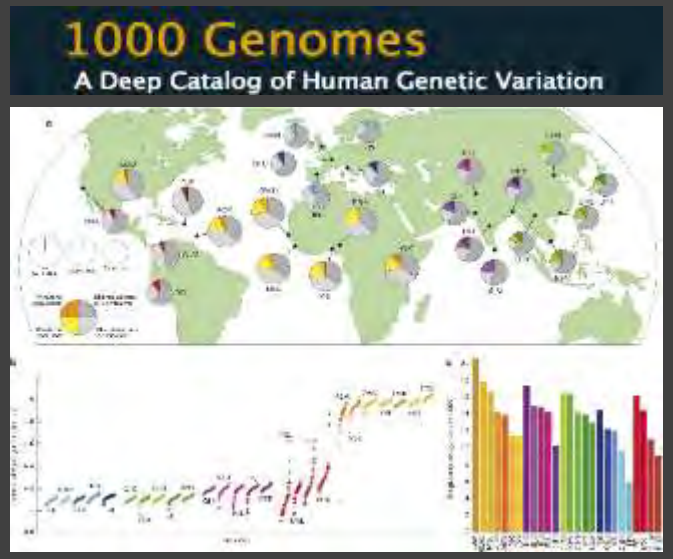
APPLIED BIOINFORMATICS

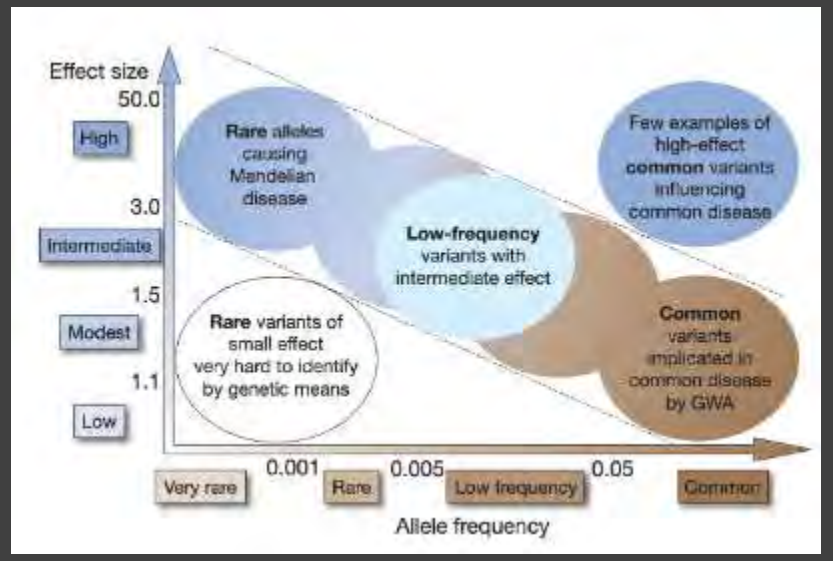
GENOMIC TECHNOLOGY

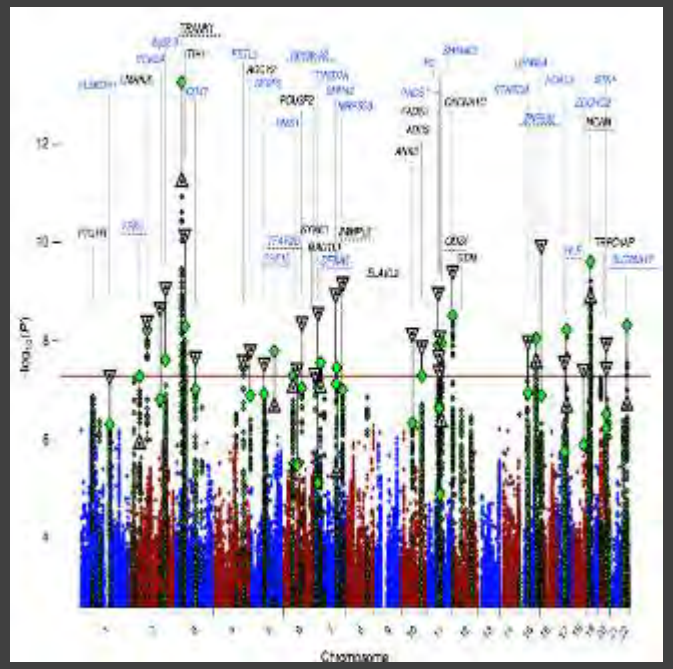
USC University of Southern California

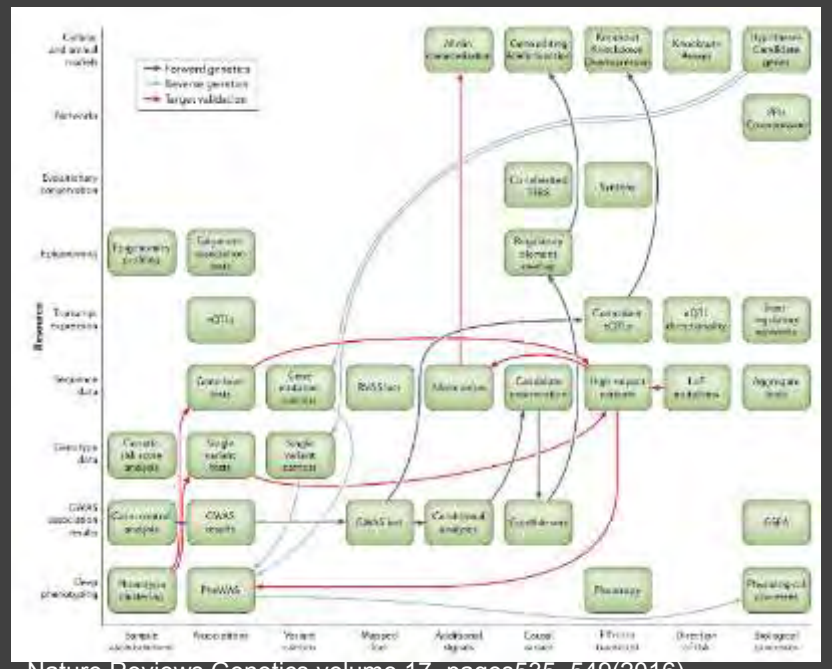
USC Institute Of Translational Genomics
Keck Medicine of USC

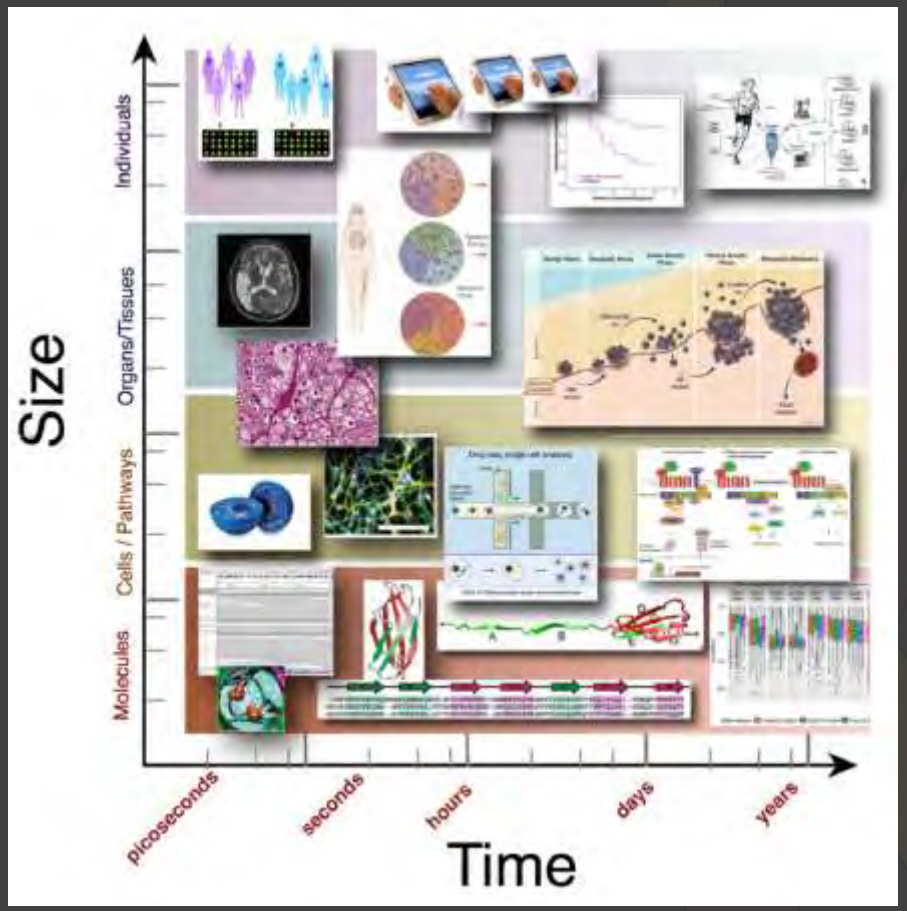
Translation Genetic Basis Of Disease; Translating DNA -> RNA











Role of Integrative Multi-Scale Analysis Of RNA

https://doi.org/10.1038/s41588-019-0397-8
Nature Reviews Genetics volume 17, pages535–549(2016)

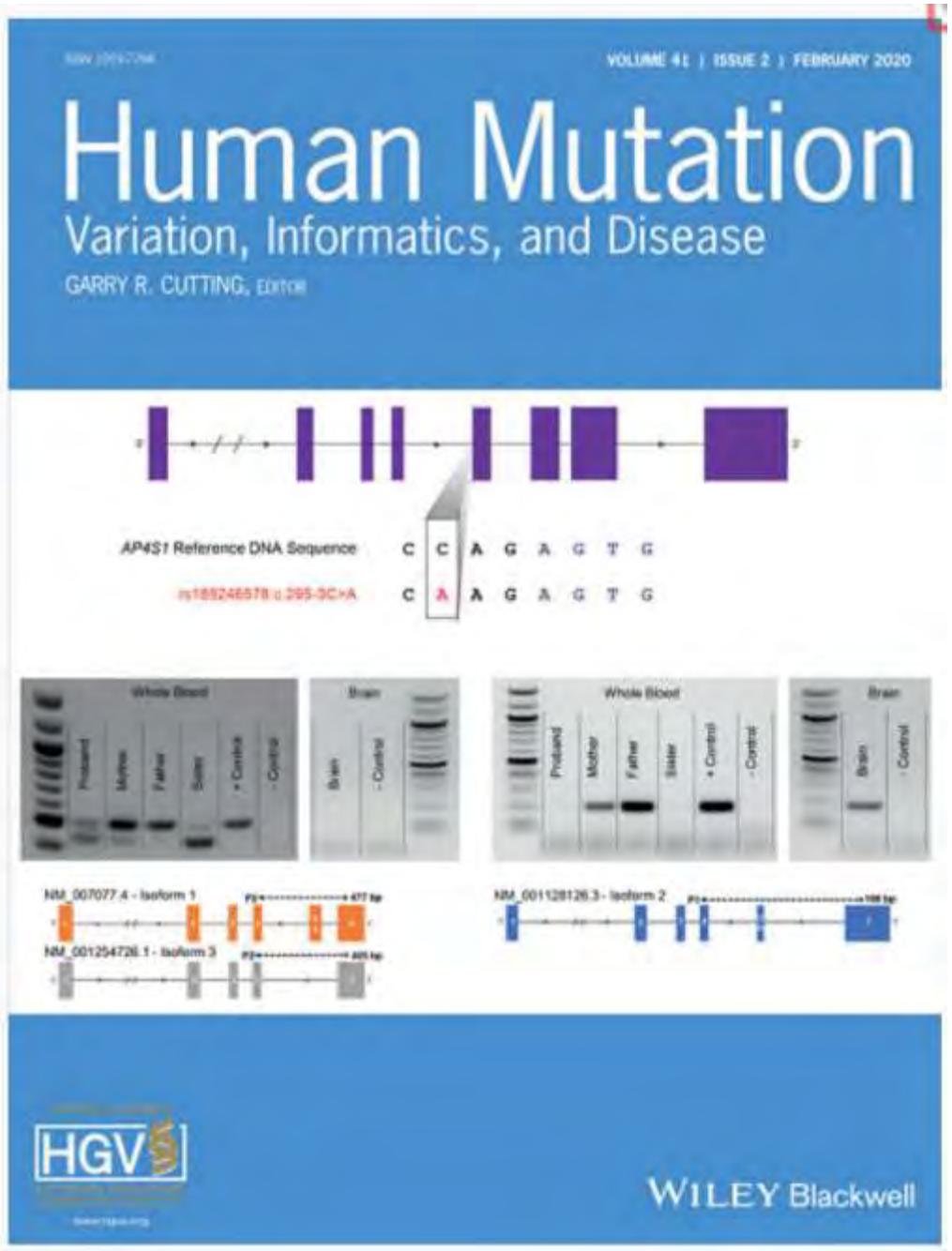
David W. Craig, PhD
Professor and Vice Chair

Carmel McCullough, B.S.

Utilizing RNA and Outlier Analysis to Identify an Intronic Splice-Altering Variant in AP4S1 in a Sibling Pair with Progressive Spastic Paraplegia

McCullough et al., Human Mutation. 2020 Feb;41(2):412-419.

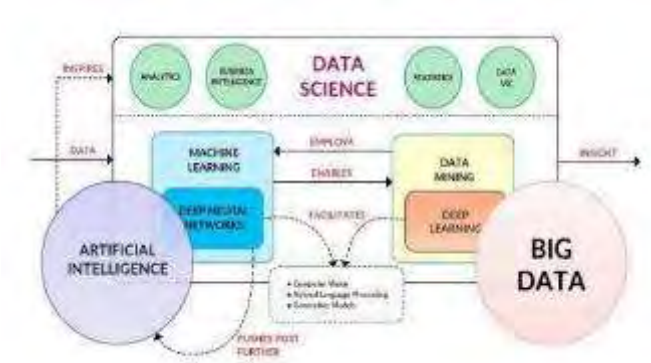
Whole exome sequencing with the inclusion of mRNA-seq allowed for the identification of a previously missed splice-altering variant, and thereby expands the mutational spectrum of AP-4 Deficiency Syndrome to include impacts to some tissue-dependent isoforms.

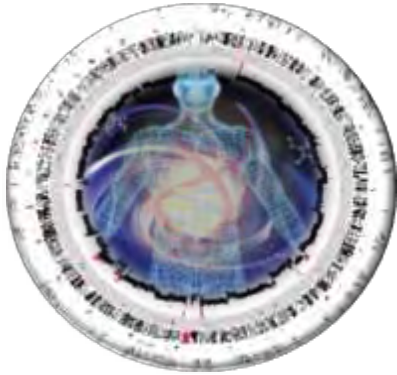


COMMUNICATIONS BIOLOGY

a natureresearch journal

Single-cell sequencing of genomic DNA resolves sub-clonal heterogeneity in a melanoma cell line

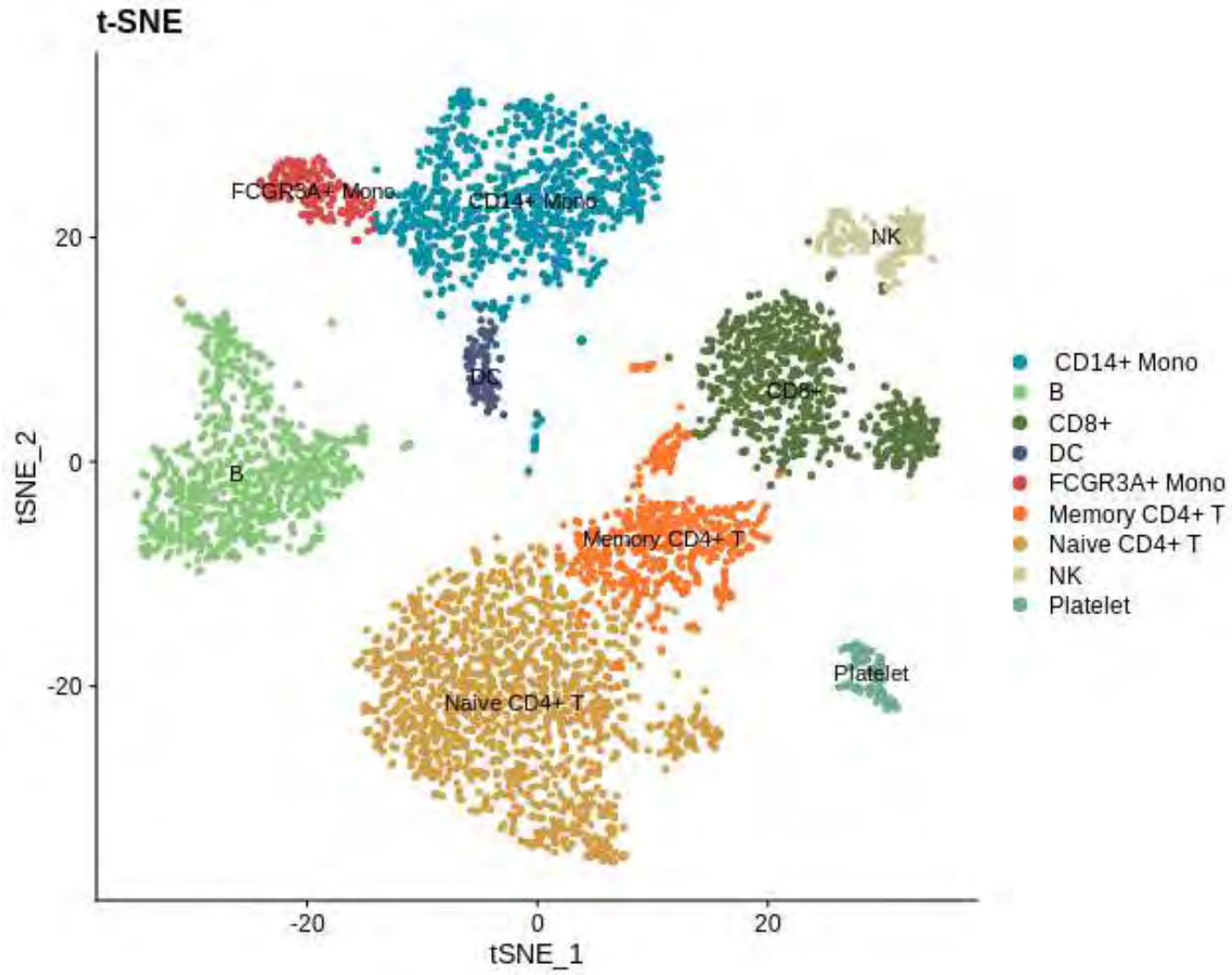


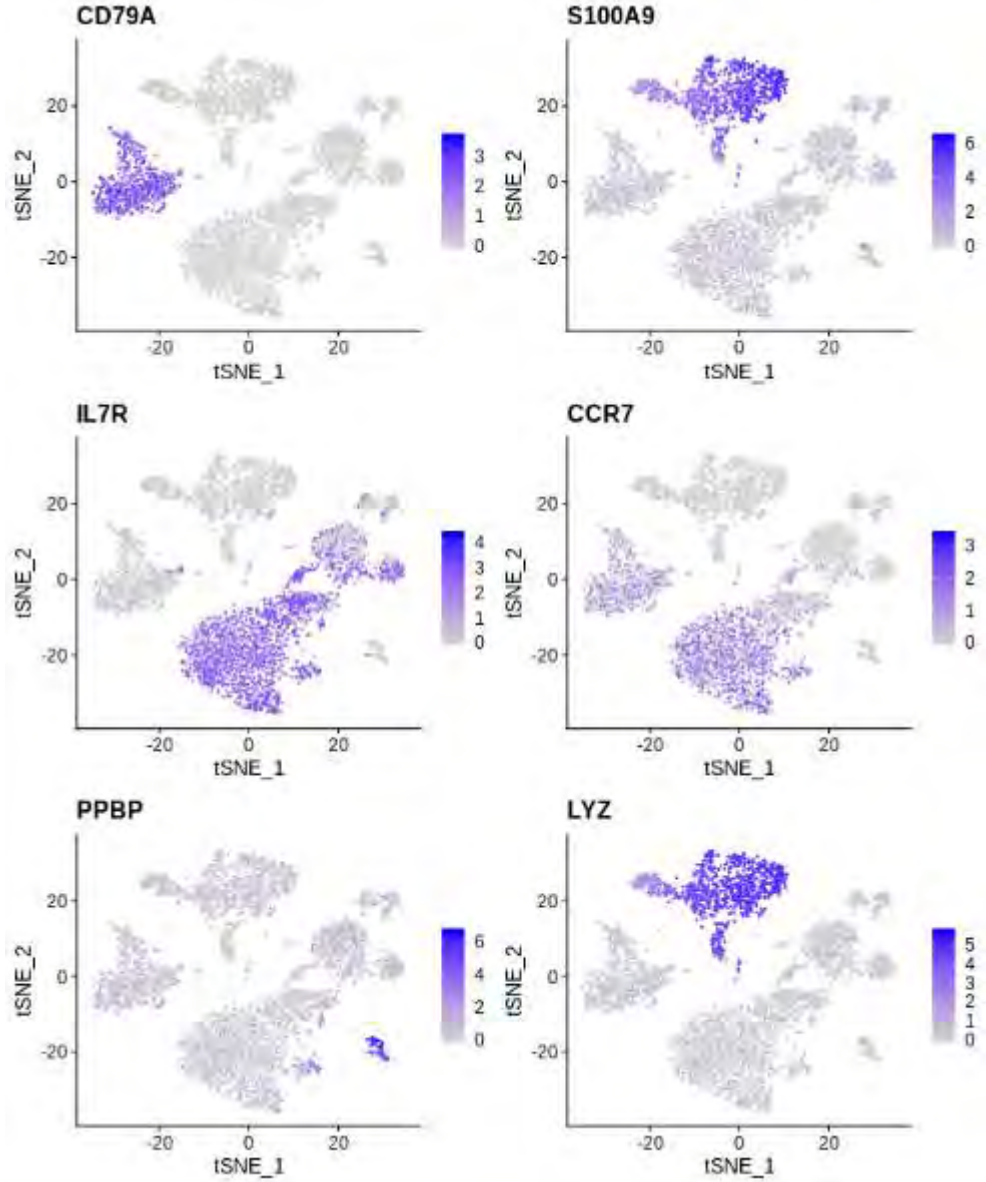


Enrique I. Velazquez Villarreal, MD, PhD, MPH, MS
Assistant Professor

My research involves two main components. First, it performs statistical and computational genomics analyses, also by developing novel bioinformatics methods, using cutting-edge genomic technologies with emphasis in single cell to identify molecular/genomic alterations in cancer health disparities, with strong emphasis on gynecological cancers from Latinos and African American populations. Second, it integrates clinical and genomic data by using Big Data science management systems and Artificial Intelligence/Machine Learning to uncover clues for treating cancer, immunological and neurological diseases.

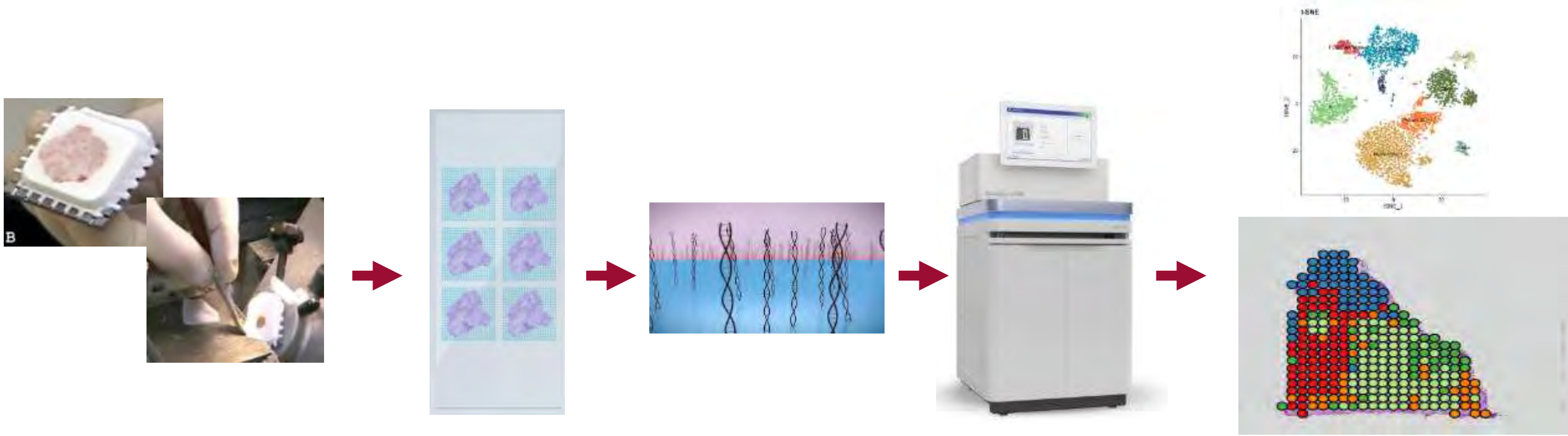
Single Cell Technologies





Gene expression level shown on t-SNE plot

Spatial Transcriptomics



Keck School of Medicine of USC


Lynda Roman


John Carpten


David Craig


Lee Gibbs


Diana Da Silva


Troy McEachron


Laila Muderspach

Saloni Walia

Moli Chen

Alex Trana

David Sands

USC GTFR


Heather Miller


Solomon Rotimi


Rania Bassiouni

10x GENOMICS


Yifeng Yin


Neil Weisenfeld


Nigel Delaney


Stephen Williams


Erik Borgstrom


Amy Tam


Edwin Hauw

Spatial Transcriptomics

Studies underway:

- Ovarian Cancer
- Brain Tissue/Neurological
- Triple Negative Brain Cancer (African American)
- Brain Tumors