UNIVERSITY OF CALIFORNIA, SAN FRANCISCO

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University of California, San Francisco **Prepared: 8/1/2021**

CURRICULUM VITAE

Name: **Carolyn Sangokoya, MD, PhD**
Position: Adjunct Instructor
Department of Pathology
School of Medicine

Address: UCSF Medical Center
Department of Pathology
505 Parnassus Ave
Room M580, Box 0102
San Francisco, CA 94143-0102
Email: carolyn[dot]sangokoya[AT]ucsf.edu

EDUCATION

				ADVISOR
1999-2003	Stanford University	A.B.	Human Biology (conc: Molecular Genetics)	Virginia Walbot, PhD
2004-12	Duke University School of Medicine	M.D.	Medicine, Medical Scientist Training Program (MSTP)	Nancy Andrews, MD, PhD
2006-11	Duke University Graduate School	Ph.D.	Genetics and Genomics	Jen-Tsan Ashley Chi, MD, PhD
2012-	University of California, San Francisco		Physician-Scientist Pathway	Abul Abbas, MBBS
2012-14	University of California, San Francisco	Resident	Anatomic Pathology	Patrick Treseler, MD, PhD
2014-15	University of California, San Francisco	Fellow	Liver/GI Pathology	Linda Ferrell, MD
2014-15	University of California, San Francisco	Fellow	Surgical Pathology	Linda Ferrell, MD
2015-21	University of California, San Francisco	Postdoc	Stem Cell Biology	Robert Blelloch MD, PhD

LICENSES AND CERTIFICATION

2014- Medical licensure, California
2015 Board Certification, Anatomic Pathology, American Board of Pathology

HONORS AND AWARDS

1999	National Merit Scholarship	Baton Rouge Magnet High School
2000	Dean's Award for Academic Excellence	Stanford University
2001	Dean's Award for Academic Excellence	Stanford University
2002	Dean's Award for Academic Excellence	Stanford University
2007	Fellow, Aspen Health Forum	The Aspen Institute
2009	Graduate Student Conference Travel Fellowship	Duke University Graduate School
2010	Keystone Symposia Student Travel Fellowship	Keystone Symposia
2010	Fuqua/Coach K Leadership Conference	Duke University
2012	Dean's Recognition Award (for outstanding performance as medical student)	Duke University School of Medicine
2014	USCAP Annual Meeting Stowell Orbison competition (outstanding trainee abstract)	US & Canadian Academy of Pathology
2015	USCAP Annual Meeting Stowell Orbison competition (outstanding trainee abstract)	US & Canadian Academy of Pathology
2015	Eli & Edythe Broad Regeneration Medicine and Stem Cell Fellowship	University of California, San Francisco
2016	F32 Ruth L. Kirschstein Postdoctoral Individual National Research Service Award	NIH/NICHD

2017	UCSF Program for Breakthrough Biomedical Science Independent Postdoctoral Research Award	University of California, San Francisco
2018	Outstanding trainee award, UCSF Center/Reprod Sci	University of California, San Francisco
2020	Gordon Research Conference Travel Award "Post-Transcriptional Gene Regulation"	Gordon Research Conferences (postponed to 2022)
2021	K08 Mentored Clinical Scientist Research Career Development Award	NIH/NICHD
2021	John A. Watson Faculty Scholar	School of Medicine, University of California, San Francisco

KEYWORDS/AREAS OF INTEREST

hepatology, liver pathology, liver transplantation, cellular reprogramming, translational molecular pathology, post-transcriptional regulatory networks, iron, small RNA, microRNA, RNA biology, functional genomics, genomic engineering, CRISPR, genome-editing, stem cell biology, stem cell-based embryo models, regenerative medicine

CLINICAL ACTIVITIES SUMMARY

I trained as a consultant in the clinical diagnosis of adult and pediatric gastrointestinal, liver, pancreas, and biliary tract disease and liver transplant service. Additional clinical responsibilities have included serving as an on-call night/weekend Attending Surgical Pathologist and including transplant pathology service.

Following post-graduate research training, I have concentrated my clinical activities specifically in medical, surgical, and transplant liver pathology.

PROFESSIONAL ACTIVITIES

MEMBERSHIPS

2012- United States and Canadian Academy of Pathology (USCAP)
2015- Rodger C. Haggitt Gastrointestinal Pathology Society
2015- Hans Popper Hepatopathology Society
2020- International Society for Stem Cell Research
2020- Society for Developmental Biology

SERVICE TO PROFESSIONAL PUBLICATIONS

2010-2012 Ad-hoc reviewer (with Jen-Tsan Ashley Chi): *Public Library of Science*
2015- Ad-hoc reviewer (with Robert Blelloch): *Cell*, *Science*, *Nature Cell Biology*, *PNAS*, *Genome Research*, *Cell Reports*, *Nature Methods*, *EMBO*

INVITED PRESENTATIONS - INTERNATIONAL

2011 Keystone Symposium: MicroRNAs and Human Disease (Banff, AB, Canada)
2013 Keystone Symposium: Noncoding RNAs in Development and Cancer (Vancouver, BC, Canada)
2021 International Society for Stem Cell Research (ISSCR), Platform Presentation (Virtual2021)
"Illuminating Post-Transcriptional Regulation of Pluripotent Cell State Transition and Fate at Single Cell Resolution" 6/24/21

INVITED PRESENTATIONS - NATIONAL

2008 National MD-PhD Student Annual Research Conference (Keystone, CO)
2014 United States and Canadian Academy of Pathology, Annual Meeting (San Diego, CA)
2015 United States and Canadian Academy of Pathology, Annual Meeting (Boston, MA)
2019 NICHD Career Planning and Networking Workshop for Developmental Biologists (Bethesda, MD)
2020 Gordon Research Conference- Post-Transcriptional Gene Regulation (postponed to 2022)

INVITED PRESENTATIONS – REGIONAL AND OTHER INVITED PRESENTATIONS

2013 UCSF Mechanisms of Disease Conference, Department of Pathology
2014 UCSF Mechanisms of Disease Conference, Department of Pathology
2018 UCSF Center for Reproductive Sciences Symposium
2019 UCSF Center for Reproductive Sciences Symposium
2020 UCSF Pathology Research Day 2020

CONTINUING EDUCATION AND PROFESSIONAL DEVELOPMENT ACTIVITIES

2012 Mechanisms of Disease, Department of Pathology, University of California, San Francisco
2013 Mechanisms of Disease, Department of Pathology, University of California, San Francisco
2013 California Society of Pathologists Annual Meeting
2014 Mechanisms of Disease, Department of Pathology, University of California, San Francisco
2014 United States and Canadian Academy of Pathology, Annual Meeting (San Diego, CA)
2015 Mechanisms of Disease, Department of Pathology, University of California, San Francisco
2015 United States and Canadian Academy of Pathology, Annual Meeting (Boston, MA)
2015 Rodger C. Haggitt Gastrointestinal Pathology Society Companion Meeting (Boston, MA)
2015 Hans Popper Hepatopathology Society Companion Meeting (Boston, MA)
2016 Mechanisms of Disease, Department of Pathology, University of California, San Francisco
2016 United States and Canadian Academy of Pathology, Annual Meeting (Seattle, WA)
2016 Rodger C. Haggitt Gastrointestinal Pathology Society Companion Meeting (Seattle, WA)
2016 Hans Popper Hepatopathology Society Companion Meeting (Seattle, WA)
2017 Mechanisms of Disease, Department of Pathology, University of California, San Francisco
2017 United States and Canadian Academy of Pathology, Annual Meeting (San Antonio, TX)
2017 Rodger C. Haggitt Gastrointestinal Pathology Society Companion Meeting (San Antonio, TX)
2017 Hans Popper Hepatopathology Society Companion Meeting (San Antonio, TX)
2017 California Tumor Tissue Registry Membership
2018 United States and Canadian Academy of Pathology, Annual Meeting (Vancouver, Canada)
2018 Rodger C. Haggitt Gastrointestinal Pathology Society Companion Meeting (Vancouver, Canada)
2018 Hans Popper Hepatopathology Society Companion Meeting (Vancouver, Canada)
2018 Mechanisms of Disease, Department of Pathology, University of California, San Francisco
2018 California Tumor Tissue Registry Membership
2019 Mechanisms of Disease, Department of Pathology, University of California, San Francisco
2020 Mechanisms of Disease, Department of Pathology, University of California, San Francisco
2020 United States and Canadian Academy of Pathology, Annual Meeting (Los Angeles, CA)
2020 Rodger C. Haggitt Gastrointestinal Pathology Society Companion Meeting (Los Angeles, CA)
2020 Hans Popper Hepatopathology Society Companion Meeting (Los Angeles, CA)
2021 Diversity and Inclusion Champion Training, UCSF School of Medicine

UNIVERSITY AND PUBLIC SERVICE

UCSF CAMPUSWIDE

2020-	UCSF Women Physician-Scientists Supergroup	Founder, Executive Director
	UCSF Women Physician-Scientists Supergroup	Executive Council
2020-21	UCSF conceptualization NIH FIRST Cohort 2021 grant application	Member

DEPARTMENTAL SERVICE

2012-	Department of Pathology Faculty QA/QI Committee	Member
2016-	Department of Pathology Women Pathologist-Scientist Career Interest Group	Leader
2018	Department Chair candidate interviews	

SERVICE AT OTHER UNIVERSITIES

2007-8	Medical Scientist Training Program Executive Admissions Committee, Duke University School of Medicine	Member
2007-8	Liaison Committee on Medical Education (LCME) Accreditation Review Committee, Duke University School of Medicine	Student Director

COMMUNITY AND PUBLIC SERVICE

2020-	Public outreach, UCSF Women Physician-Scientist Supergroup: @MDPhDEquity	Manager/Contributor

TEACHING AND MENTORING

FORMAL TEACHING

UCSF SCHOOL OF MEDICINE

Acad. Year	Course No & Title	Teaching Contribution	Class Size
2012-13	Organs 102B: Respiratory-Pathology and Radiology of the Respiratory System	Lab instructor	40
2012-13	Organs 102B: Respiratory-Restrictive and Obstructive Lung Disease	Lab instructor	40
2012-13	Organs 102B: Renal Morphology	Lab instructor	40
2012-13	Organs 102B: Renal-Pathology of Glomerular Diseases	Lab instructor	40
2012-13	Organs 102B: Renal-Pathology of Non-Glomerular Diseases	Lab instructor	40
2013-14	Prologue (Interdisciplinary Studies 101): Inflammation and Neoplasia	Lab instructor	40
2013-14	M3 (Methods, Mechanisms, & Malignancies) Interdisc Studies 106: Pathologic Characteristics of Benign and malignant neoplasms	Lab instructor	40
2013-14	Organs 102B: Respiratory-Pathology and Radiology of the Respiratory System	Lab instructor	40
2013-14	Organs 102B: Respiratory-Restrictive and Obstructive Lung Disease	Lab instructor	40
2013-14	Organs 102B: Renal Morphology	Lab instructor	40
2013-14	Organs 102B: Renal-Pathology of Glomerular Diseases	Lab instructor	40
2013-14	Organs 102B: Renal-Pathology of Non-Glomerular Diseases	Lab instructor	40
2015-16	Organs 102B: Respiratory-Pathology and Radiology of the Respiratory System	Lab instructor	40
2015-16	Organs 102B: Respiratory-Restrictive and Obstructive Lung Disease	Lab instructor	40
2015-16	Organs 102B: Renal Morphology	Lab instructor	40
2015-16	Organs 102B: Renal-Pathology of Glomerular Diseases	Lab instructor	40
2015-16	Organs 102B: Renal-Pathology of Non-Glomerular Diseases	Lab instructor	40
2016-17	Bridges Curriculum: Foundations 1 Course IDS 121A: Ground School small group	small group leader	15
2016-17	Bridges Curriculum: Foundations 1 Course IDS 121B: ABC small group	small group leader	15
2016-17	Bridges Curriculum: Foundations 1 Course IDS 121C: Regulation small group	small group leader	15
2016-17	Bridges Curriculum: Foundations 1 Course IDS 121D: PHD small group	small group leader	15
2016-17	Bridges Curriculum: Foundations 1 Course IDS 122A: Life Stages small group	small group leader	15
2017-18	Bridges Curriculum: Foundations 1 Course IDS 121A: Ground School small group	small group leader	15
2017-18	Bridges Curriculum: Foundations 1 Course IDS 121B: ABC2 small group	small group leader	15

INFORMAL TEACHING

UCSF MEDICAL CENTER

2014-15	Resident teaching while on-call Attending one-on-one resident teaching in preparation and submission of surgical or transplant specimens, frozen-section evaluation, diagnosis) 3.5 weeks per academic year
2014-15	Gross Room Supervisor one-on-one resident teaching in preparation and submission of surgical specimens) 5 weeks per year
2014-15	Pediatric GI/Liver Conference Leader (teaching gastroenterology, hepatology, general/transplant surgery residents, fellows, and attendings) bi-weekly
2014-15	(Liver) Transplant Pathology Conference Leader (3-4 meetings per year)
2014-15	Liver Pathology Conference Leader (quarterly meeting)
2014-15	Joint Rounds (GI/Liver Pathology and Surgery) Conference (3-4 meetings per year)
2015-16	Pediatric GI/Liver Conference Leader (biweekly)
2016-17	Department of Pathology Research Interest Group (RIG) Leader (organized monthly research presentations by Department of Pathology and Lab Medicine Physician-Scientist Pathway trainees)

RESEARCH AND CREATIVE ACTIVITIES

RESEARCH AND CREATIVE ACTIVITIES SUMMARY

My most significant contributions to science thus far are in the **basic study of microRNA functions** in cellular stress response, cellular iron homeostasis, and **translational methods in the RNA isolation from clinical materials**. My post-doctoral studies have centered on post-transcriptional regulation in pluripotent stem cell biology. Seeking greater independence as a physician-scientist, I have also built a focus on **posttranscriptional regulation in human liver development and disease** during residency and fellowship training as well as during my postdoctoral studies. Due to space restrictions, an abbreviated list is below:

Post-transcriptional regulation and microRNA function in pluripotent stem cell biology

We demonstrate that the miR-290/302 target Profilin-2 regulates many aspects of pluripotent stem cell (PSC) biology, defining an axis of post-transcriptional control, endocytosis, and signal transduction that is essential for stem cell growth, cell cycle control, and early differentiation (1). We continue to explore the role of post-transcriptional control mechanisms in cell fate decisions (2).

1. **Sangokoya C**, and R Blelloch. MicroRNA-dependent inhibition of PFN2 orchestrates ERK activation and pluripotent state transitions by regulating endocytosis. Proc Natl Acad Sci. 2020 Aug25;117(34):20625-20635. PMID:32788350
2. **Sangokoya C**, and R Blelloch. Coordinate control of PFN2 by RNA-binding proteins regulate cell fate. (manuscript in preparation)

MicroRNA function in cellular iron homeostasis

Ferroportin (FPN) is the only known cellular iron exporter in mammalian cells and plays a critical role in the maintenance of both cellular and systemic iron balance. During iron deprivation, the translation of FPN is repressed by iron regulatory proteins (IRPs), which bind to the 5' untranslated region (UTR), to reduce iron export and preserve cellular iron. This study used functional genomic methods to identify differential expression and characterize the role of microRNAs in cellular iron homeostasis in human primary cells and cell lines. Here, we reported a novel iron-responsive mechanism for the post-transcriptional regulation of FPN, mediated by miR-485-3p, which is induced in human cell lines and primary cells during iron deficiency and represses FPN expression by directly targeting the FPN 3'UTR (1). These findings support a model that includes both IRPs and microRNAs as iron-responsive post-transcriptional regulators of FPN. The involvement of microRNA in the iron-responsive regulation of FPN offers additional stability and fine-tuning of iron homeostasis within different cellular contexts.

1. **Sangokoya C**, Doss JF, Chi JT. Iron-responsive miR-485-3p regulates cellular iron homeostasis by targeting ferroportin. PLoS Genet. 2013 Apr;9(4):e1003408. doi: 10.1371/journal.pgen.1003408. Epub 2013 Apr 4. PMID: 23593016; PMCID: PMC3616902.

Post-transcriptional regulation in human liver development and disease

In a series of studies, I have learned and applied methods for the unbiased efficient capture of small RNAs from formalin-fixed paraffin-embedded (FFPE) liver tissue samples, allowing for the performance and coordination of unbiased high-throughput RNA sequencing from clinical liver tissue samples with immunohistochemistry and RNA in-situ hybridization. Using resources in UCSF Pathology, I designed eight tissue microarrays (TMAs) from FFPE patient liver tissues ranging from fetal liver to different etiologies of cirrhosis, tested the ability of these TMAs to demonstrate robust expression of control and specific microRNAs by quantitative PCR, microRNA in situ hybridization, and immunohistochemistry, and identified differential spatial localization of microRNAs within liver parenchyma (1-2).

1. **Sangokoya C** et al. Expression of the Iron-Regulating MicroRNA miR-485-3p in Hepatic cirrhosis. Laboratory investigation; a journal of technical methods and pathology. 2014 February; 94:427.
2. **Sangokoya C** et al. MicroRNA In Situ Hybridization Analysis of MIR-485-3p and MiR-122 Expression in Human Liver Development and Disease. Laboratory investigation; a journal of technical methods and pathology. 2015 February; 95:423A.

MicroRNA function in cellular stress response

MicroRNAs are essential for fine-tuning physiological functions and responding to changing environments and stress conditions. We demonstrate a role for microRNA in the regulation of oxidative stress response in erythroid cells and the functional consequences of dysregulated microRNA expression in Sickle Cell Disease (SCD) pathobiology (1). Homozygous Sickle Cell (HbSS) erythrocytes are known to have reduced tolerance for
oxidative stress, yet the basis for this phenotype has remained unknown. Here we use erythrocyte microRNA expression profiles to identify a subset of HbSS patients with higher miR-144 expression and more severe anemia. In our study we revealed that in K562 erythroid cells and primary erythroid progenitor cells, miR-144 directly regulates NRF2, a transcription factor and central regulator of cellular response to oxidative stress, and modulates the oxidative stress response. We further demonstrate that increased miR-144 is associated with the reduced NRF2 levels, decreased glutathione regeneration, and attenuated antioxidant capacity found in HbSS erythroid progenitor cells, thereby providing a mechanism for the reduced oxidative stress tolerance and increased anemia severity seen in HbSS patients.

1. **Sangokoya C**, Telen MJ, Chi JT. MicroRNA miR-144 modulates oxidative stress tolerance and associates with anemia severity in sickle cell disease. Blood. 2010 Nov 18;116(20):4338-48. doi: 10.1182/blood-2009-04-214817. PMID: 20709907; PMCID: PMC2993631.
2. Lamonte G, Tang X, Chen JL, Wu J, Ding CK, Keenan MM, **Sangokoya C**, Kung HN, Ilkayeva O, Boros LG, Newgard CB, Chi JT. Acidosis induces reprogramming of cellular metabolism to mitigate oxidative stress. Cancer Metab. 2013 Dec 23;1(1):23. doi: 10.1186/2049-3002-1-23. PMID: 24359630; PMCID: PMC4178214.

Translational methods from clinic to bench: erythrocyte microRNA profiling in anemia disorders

Approaches to study of the molecular basis for phenotypic heterogeneity in SCD in the past have used candidate genes, quantitative trait loci, and genome-wide association studies to identify DNA-based genetic variants associating with particular phenotypes. These approaches required large sample sizes in order to detect significant associations. We developed a novel approach employing the use of erythrocyte microRNA expression profiles (1) from easily accessible peripheral blood shown to demonstrate abundant, diverse, and disease-specific microRNA expression profiles in a pilot study where samples from normal erythrocytes or from anemia disorders grouped into their respective types simply based on microRNA expression (1). Since erythrocytes do not contain DNA or larger RNAs, the RNA extracted from these cells is enriched for microRNAs, thus only a small amount is needed for robust analysis. Erythrocytic microRNA expression can give insight into the total molecular picture of the life of the red blood cell and further illustrate temporal, developmental, stress-responsive, and otherwise functionally meaningful relationships. The use of erythrocytic microRNA expression profiles is thus a tool which can be used to further identify novel disease modifiers and potential therapeutic targets. We published a key protocol paper (1) and applied these methods in large and small scale form in the study of anemia disorders

including paroxysmal nocturnal hemoglobinuria (2) and Sickle Cell Disease (3). These methods were used in profiling microRNA expression over HbSS erythroid progenitor cell development in (3).

1. **Sangokoya C**, LaMonte G, Chi JT. Isolation and characterization of microRNAs of human mature erythrocytes. Methods Mol Biol. 2010;667:193-203. doi: 10.1007/978-1-60761-811-9_13. PMID: 20827535; PMCID: PMC4347925.
2. Chi JT, **Sangokoya C**, de Castro CM. MicroRNA Expression in Red Blood Cells from Patients with PNH. Blood. 2007 November; 110(11):3675
3. **Sangokoya C**, Telen MJ, Chi JT. MicroRNA miR-144 modulates oxidative stress tolerance and associates with anemia severity in sickle cell disease. Blood. 2010 Nov 18;116(20):4338-48. doi: 10.1182/blood-2009-04-214817. PMID: 20709907; PMCID: PMC2993631.

NCBI/MyBibliography List of Publications:
https://www.ncbi.nlm.nih.gov/myncbi/carolyn.sangokoya.1/bibliography/public/

RESEARCH AWARDS - CURRENT

K08HD105017 Sangokoya (PI)

NIH-NICHD 04/01/2021 03/31/2026

Post-transcriptional regulation of cell fate in early mammalian development

The award supports a period of supervised research and research career development to prepare the candidate to successfully obtain an NIH R01 or equivalent major research award by the end of the K award period.

RESEARCH AWARDS - PAST

T32GM007171 Predoctoral Trainee Pizzo (PI)

Ruth L. Kirschstein National Research Service Award (NRSA) 07/2004 07/2008

Medical Scientist Training Program

3R01CA125618-03S1 Fellow Chi (PI)

NIH/NCI 07/2008 05/2011

Gene expression programs of lactic acidosis in human cancers

Acidosis induces reprogramming of cellular metabolism to mitigate oxidative stress. The goal of this project was to understand the metabolic adaptations that cancer cells make under acidosis.

R21DK080994 Fellow Chi (PI)

NIH/NIDDK 07/2008 05/2011

The Genomic Analysis of Erythrocyte microRNA in Sickle Cell Diseases

Human mature erythrocytes possess abundant and diverse microRNAs (miRNAs), a class of 21-23 nucleotide non-coding RNA with important regulatory functions. This project explored the potential regulatory roles of miRNAs in the biological phenotypes of erythrocytes.

UCSF Department of Pathology — Sangokoya (PI)

UCSF — 12/2012 — 06/2017

Expression and In situ Hybridization Analysis of Liver MicroRNAs: From Early Development to Cirrhosis

Pilot studies with paraffin-embedded formalin-fixed liver tissue samples have shown increased expression of miR-485-3p of specific etiologies of cirrhotic liver. The goals of this pilot study were to perform and characterize endogenous expression of microRNAs in formalin-fixed human liver and develop methodology to determine spatial localization of microRNA expression in formalin-fixed human liver tissue samples.

UCSF Eli and Edythe Broad Regeneration Medicine and Stem Cell Fellowship — Sangokoya (PI)

09/01/2015 — 09/01/2016

Mapping Post-transcriptional RNA Binding Regulatory Networks Within Embryonic Stem Cell Fate Transition

UCSF Program for Breakthrough Biomedical Research — Sangokoya (PI)

Independent Postdoctoral Research Award

07/01/2017 — 06/30/2018

To encourage creative/independent research driven by postdoctoral scholars

F32HD088051 — Sangokoya (PI)

NIH-NICHD — 09/01/2016 — 09/01/2019

Mapping Post-transcriptional RNA Binding Regulatory Networks Within Embryonic Stem Cell Fate Transition

PEER REVIEWED PUBLICATIONS

1. **Sangokoya C**, Blelloch R. MicroRNA-dependent inhibition of PFN2 orchestrates ERK activation and pluripotent state transitions by regulating endocytosis. Proc Natl Acad Sci U S A. 2020 Aug 11. PMID: 32788350
2. **Sangokoya,** C, Doss JF, and JT Chi. Iron-Responsive miR-485-3p Regulates Cellular Iron Homeostasis by Targeting Ferroportin. PLoS Genetics 9.4 (2013): e1003408.
3. **Sangokoya C,** Telen MJ, and JT Chi. MicroRNA miR-144 modulates oxidative stress tolerance and associates with anemia severity in sickle cell disease. Blood. 2010 Nov 18;116(20):4338-48. PMID: 20709907
4. LaMonte G, Tang X, Chen JL, Wu J, Ding CK, Keenan MM, **Sangokoya** C, Kung HN, Ilkayeva O, Boros LG, Newgard CB, and Chi, JT. Acidosis induces reprogramming of cellular metabolism to mitigate oxidative stress. *Cancer Metab* 1(2013): 23.

5. Hao K, Niu T, **Sangokoya C,** Li J, and X Xu. SNPkit: an efficient approach to systematic evaluation of candidate single nucleotide polymorphisms in public databases. Biotechniques. 2002 Oct 33(4):822, 824-6, 828 passim. PMID: 12398191

BOOKS AND CHAPTERS

1. **Sangokoya C**, LaMonte G, and JT Chi. Isolation and characterization of microRNAs of Human Mature Erythrocytes MicroRNAs and the Immune System: Methods in Molecular Biology. 2010, 667:193-203. PMID: 20827535
2. [in preparation] **Sangokoya C.** Measuring endocytosis and endosomal uptake at single cell resolution. Methods in Molecular Biology. 2021

OTHER PUBLICATIONS

1. **Sangokoya C.** MicroRNA Function in Cellular Stress Response. PhD Dissertation, Duke University, University Program in Genetics and Genomics (2011)
2. Chi JT, **Sangokoya C**, de Castro CM. MicroRNA Expression in Red Blood Cells from Patients with PNH. Blood. 2007 November; 110(11):3675
3. **Sangokoya C** et al. MicroRNA In Situ Hybridization Analysis of MIR-485-3p and MiR-122 Expression in Human Liver Development and Disease. Laboratory investigation; a journal of technical methods and pathology. 2015 February; 95:423A.
4. **Sangokoya C** et al. Expression of the Iron-Regulating MicroRNA miR-485-3p in Hepatic cirrhosis. Laboratory investigation; a journal of technical methods and pathology. 2014 February; 94:427.

SIGNIFICANT PUBLICATIONS

1. **Sangokoya C**, Blelloch R. MicroRNA-dependent inhibition of PFN2 orchestrates ERK activation and pluripotent state transitions by regulating endocytosis. Proc Natl Acad Sci U S A. 2020 Aug 11. PMID: 32788350

   Co-conceived, developed, and performed experiments, co-wrote paper. These findings define a previously unknown axis of post-transcriptional control, endocytosis, and signal transduction important for stem cell biology
2. **Sangokoya C,** Telen MJ, and JT Chi. MicroRNA miR-144 modulates oxidative stress tolerance and associates with anemia severity in sickle cell disease. Blood. 2010 Nov 18;116(20):4338-48. PMID: 20709907

   Developed methods for isolation and characterization of microRNA expression in human erythrocytes (red blood cells) for novel study of cellular stress response (oxidative stress) and hematologic diseases (anemias).
3. **Sangokoya,** C, Doss JF, and JT Chi. "Iron-Responsive miR-485-3p Regulates Cellular Iron Homeostasis by Targeting Ferroportin." PLoS Genetics 9.4 (2013): e1003408.

   Conceived and developed novel study using functional genomic methods to characterize the role of microRNAs in cellular iron homeostasis in human primary cells and cell lines.