## Kuanwei Sheng

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#### **EDUCATION**

# Baylor College of Medicine, Graduate School of Biomedical Sciences Houston, TX Ph.D., Dept. of Molecular and Human Genetics 2013- May. 2019 Wuhan University, College of Life Science Wuhan, China

B.S., Biology 2009- 2013

### RESEARCH EXPERIENCE

#### Wyss Institute at Harvard University, Peng Yin Lab

Boston, MA

Postdoctoral Fellow Jul. 2019- Present

Research Interests: Proximity recording, Protein multiplexing profiling, Single-cell Omics

#### **Baylor College of Medicine, Chenghang Zong Lab**

Houston, TX

**Ph.D. Student**Apr. 2014- May. 2019

Developed a new sensitive total RNA single-cell RNA-seq chemistry, MATQ-seq

Developed a robotic platform for high throughput single-cell RNA-seq

Developed a microfluidic droplet-base high sensitivity single-cell RNA-seq

Utilized MATQ-seq and Laser Capture Microdissection to study pancreatic cancer tumorigenesis in mice

Utilized the robotic MATQ-seq to identify heterogeneity of lung cancer associated fibroblasts in mice

Analyzed Single-cell RNA-seq data using Bash, Python, MATLAB and R

Tutored two graduate students and multiple rotation students in the lab

Collaborated with multiple labs to study single cells in various biological processes

#### Wuhan University, Yan Zhou Lab

Wuhan, China

#### **Undergraduate Research Assistant**

Sep. 2011- Jun. 2013

Study the role of long noncoding RNA in neurogenesis

Screened for more than 40 long noncoding RNA using in-situ hybridization in embryonic mouse brain

Used In utero electroporation to study the effect of long noncoding RNA in vivo

#### International Genetically Engineered Machine (iGEM) Competition

Wuhan, China

**Team Leader** *Nov. 2011- Nov. 2012* 

Designed two synthetic promoter that respond to glucose and fatty acid concentration respectively

Tested, verified and characterized related promoters and metabolic genes in E.Coli

Presented at Asia and World Jamboree

#### **PUBLICATIONS**

**Kuanwei Sheng**, Wenjian Cao, Yichi Niu, Qing Deng, Chenghang Zong. Effective Detection of Variations in Single Cell Transcriptomes by MATQ-seq. **Nature Methods** 2017. doi:10.1038/nmeth.4145

Min Luo\*, Mira Jeong\*, Deqiang Sun\*, Hyun-Jung Park\*, Benjamin A.T. Rodriguez\*, Zheng Xia, Liubin Yang, Xiaotian Zhang, **Kuanwei Sheng**, Gretchen J. Darlington, Wei Li, and Margaret A. Goodell. Long non-coding RNAs control hematopoietic stem cell function. **Cell Stem Cell**. 2015;16(4):426-38.

Lin Tian, Amit Goldstein, Hai Wang, Ik Sun Kim, Hin Ching Lo, Thomas Welte, **Kuanwei Sheng**, Lacey Dobrolecki, Xiaomei Zhang, Nagireddy Putluri, Thuy Phung, Sendura Mani, Fabio Stossi, Arun Sreekumar, Michael A. Mancini, Chenghang Zong, William K. Decker, Michael T. Lewis, and Xiang H.-F. Zhang. Mutual Regulation of Tumour Vessel Normalization and Immunostimulatory Reprogramming. **Nature** 2017. doi:10.1038/nature21724.

Hai Wang, Lin Tian, Amit Goldstein, Hin-Ching Lo, Jun Liu, **Kuanwei Sheng**, Fabio Stossi, Chenghang Zong, Michael A. Mancini, and Xiang H.-F. Zhang. Bone-in-culture array (BICA) as a platform to model early-stage bone metastases and discover metastasis-specific therapies. **Nature Communications** 2017. doi:10.1038/ncomms15045.

Marissa A. Scavuzzo\*, Matthew Hill\*, Jolanta Chmielowiec, Diane Yang, **Kuanwei Sheng**, Jessica Teaw, Chenghang Zong, James F. Martin, and Malgorzata Borowiak. Endocrine lineage biases arise in temporally distinct endocrine progenitors during pancreatic morphogenesis. **Nature Communications**. 2018; 9:3356

Hsin-I Jen, Matthew C. Hill, Litao Tao, **Kuanwei Sheng**, Wenjian Cao, Hongyuan Zhang, Chenghang Zong, James F. Martin, Neil Segil, and Andrew K. Groves. Hair cell regeneration in the mammalian vestibular system and its potentiation by Atoh1: A transcriptomic and epigenetic analysis. **Elife.** 2019; 8:e44328

**Kuanwei Sheng** and Chenghang Zong. Single-cell RNA-seq by Multiple Annealing and Tailing Based Quantitative Single-cell RNA-seq (MATQ-seq). **Single Cell Methods**. 2019. pp 57-71 (*Book Chapter*)

Chenghang Zong, Michael Gundry, **Kuanwei Sheng**. Methods of linearly amplifying whole genome of a single cell. **US Patent App**. 15/308,592

#### **AWARDS**

Silver Medal in International Genetically Engineered Machine Competition 2012

Outstanding Graduation Thesis of Hubei Province 2013

Cold Spring Harbor Asia Fellowship Award 2016

The Claude W. Smith Fellowship Award 2017