

## Hong ZHENG, Ph.D.

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Stanford Center for Biomedical Informatics Research  
School of Medicine  
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### EDUCATION

- Ph.D. 2012-2016     **Cancer Genomics**  
The University of Hong Kong, Hong Kong, China  
Supervisor: Prof. Maria Li Lung  
Thesis title: Identification of Genetic Susceptibility Genes and Characterization of Somatic Mutations in Nasopharyngeal Carcinoma
- B.E. 2006-2010     **Biomedical Engineering**, Xi'an Jiaotong University, China  
Graduated with Distinguished Graduate Student Award

### PROFESSIONAL APPOINTMENTS

- 2017-present     Postdoctoral researcher, Gevaert Lab, Biomedical Informatics, Stanford University, CA

### PUBLICATIONS

#### Original Articles

1. **Zheng H**, Brennan K, Hernaez M, Gevaert O, Benchmark of lncRNA Quantification for RNA-Seq of Cancer Samples, bioRxiv preprint, doi.org/10.1101/241869, 2018 Jan, under review in *Nucleic Acid Research*
2. Qiu Y, **Zheng H**, Gevaert O, A deep learning framework for imputing missing values in genomic data, bioRxiv preprint, doi: https://doi.org/10.1101/406066
3. Lin W, Yip YL, Jia L, Deng W, **Zheng H**, Dai W, et al, Establishment and characterization of new tumor xenografts and cancer cell lines from EBV-positive nasopharyngeal carcinoma, *Nat Commun.* 2018 Nov 7
4. Bakr S, Gevaert O, Echegaray S, Ayers K, Zhou M, Shafiq M, **Zheng H**, Benson J, Zhang W, Leung A, Kadoch M, Shrager J, Quon A, Rubin D, Plevritis S, Napel S, A Radiogenomic Dataset of Non-Small Cell Lung Cancer, *Sci Data.* 2018 Oct 16;5:180202
5. Dai W, Ko JMY, Choi SSA, Yu Z, Ning L, **Zheng H**, et al. Whole-exome sequencing reveals critical genes underlying metastasis in esophageal squamous cell carcinoma. *J Pathol.* 2017 Aug;242(4):500-510
6. **Zheng H\***, Dai W\*, Cheung AKL\*, Ko JMY, et.al. Whole-exome sequencing identifies multiple loss-of-function mutations of NF- $\kappa$ B pathway regulators in nasopharyngeal carcinoma, *Proc Natl Acad Sci U S A.* 2016, 113(40):11283–11288  
\*contributed equally
7. Dai W\*, **Zheng H\***, Cheung AKL, Tang CS, Ko JMY, Wong BWY, et al. Whole-exome sequencing identifies MST1R as a genetic susceptibility gene in

- nasopharyngeal carcinoma. *Proc Natl Acad Sci U S A*. 2016, 113(12):3317-3322.  
\*contributed equally
8. Dai W, Cheung AKL, Ko JM, Cheng Y, **Zheng H**, Ngan RK, Ng WT, Lee AW, Yau CC, Lee VH et al: Comparative methylome analysis in solid tumors reveals aberrant methylation at chromosome 6p in nasopharyngeal carcinoma. *Cancer Med*. 2015, 4(7):1079-1090.
  9. Wu J, Yang Z, Wang Y, Zheng L, Ye R, Ji Y, Zhao S, Ji S, Liu R, Xu L, **Zheng H** et al: Viral-inducible Argonaute18 confers broad-spectrum virus resistance in rice by sequestering a host microRNA. *eLife*. 2015, 4.
  10. Jiang L, Qian D, **Zheng H**, Meng LY, Chen J, Le WJ, Zhou T, Zhou YJ, Wei CH, Li Y: RNA-dependent RNA polymerase 6 of rice (*Oryza sativa*) plays role in host defense against negative-strand RNA virus, Rice stripe virus. *Virus Res*. 2012, 163(2):512-519.
  11. Du P, Wu J, Zhang J, Zhao S, **Zheng H**, Gao G, Wei L, Li Y: Viral infection induces expression of novel phased microRNAs from conserved cellular microRNA precursors. *PLoS Pathog*. 2011, 7(8):e1002176.

## Reviews

1. Dai W, **Zheng H**, Cheung AKL, Lung ML. Genetic and epigenetic landscape of nasopharyngeal carcinoma. *Chin Clin Oncol*. 2016, 5(2):16.

## AWARDS AND HONORS

2017	Summer Institutes Scholarship, Department of Biostatistics, University of Washington
2016	Y S and Christabel Lung Postgraduate Scholarship, The University of Hong Kong
2012-2016	Postgraduate Scholarship, The University of Hong Kong
2011	Excellent Academic Performance Scholarship, Peking University
2011	Dupont Scholarship, Peking University
2007-2010	Cyrus Tang Scholarship
2010	Distinguished Graduate Student Award, Xi'an Jiaotong University
2007-2009	Distinguished Student Xi'an Jiaotong University
2008-2010	Siyuan Scholarship, Xi'an Jiaotong University

## INVITED TALKS

2016 Nasopharyngeal Carcinoma Gordon Research Conference, Hong Kong, June 26 - July 1, Identification of genetic susceptibility genes in nasopharyngeal carcinoma by next-generation sequencing

## PRESENTATIONS AND CONFERENCES

### International

- 2018 Poster presentation at AACR Annual Meeting, Chicago, April 14-18, Benchmark of lncRNA Quantification for RNA-Seq of Cancer Samples
- 2016 Poster presentation at AACR Annual Meeting, New Orleans, April 16-20, Whole-exome sequencing identifies NF- $\kappa$ B pathway regulators frequently mutated in nasopharyngeal carcinoma

2015 Poster presentation at AACR Annual Meeting, Philadelphia, April 18-22, Unraveling the genetic basis of nasopharyngeal carcinoma using next-generation sequencing approaches

### **Local**

2018 Presentation at Stanford NCI CTD<sup>2</sup> Site Visit, May 10, Differential methylation analysis of bisulfite sequencing data

2016 Presentation at NPC AoE General Meeting, The University of Hong Kong, August 27, Whole-exome sequencing of NPC xenografts and human tumors

2016 Presentation at departmental postgraduate seminar, August 20, Genetic and genomic characterization of nasopharyngeal carcinoma, received best presentation award

2015 Presentation at Joint NPC AoE and TBRS Thematic meeting, The University of Hong Kong, September 5, Whole-Exome sequencing analysis identifies the landscape of somatic mutations in NPC

2014 Poster presentation at 19th Research Postgraduate Symposium, Li Ka Shing Faculty of Medicine, The University of Hong Kong, December 10-11, Whole-exome sequencing of nasopharyngeal carcinoma

2014 Presentation at NPC AoE Genetics and Genomics Thematic Meeting, The University of Hong Kong, September 29, Whole-exome sequencing of NPC

2013 Presentation at NPC AoE General Meeting, The University of Hong Kong, August 31, Whole-exome sequencing of nasopharyngeal cancer

### **PROFESSIONAL MEMBERSHIPS**

2014-present Associate member of American Association for Cancer Research (AACR)

### **RESEARCH EXPERIENCE**

#### **2017-present Stanford University**

Postdoctoral researcher at Gevaert Lab, Stanford Center for Biomedical Informatics Research, School of Medicine, Stanford University. My research focuses on integration of multi-omics datasets in biomedical research.

- DNA methylation profiling in cancers. I'm working on developing a framework to model DNA methylation from bisulfite sequencing of cancer samples, aiming to identify genes or non-coding regions that are epigenetically-regulated in cancers and reveal epigenetically distinct cancer subtypes.
- Long noncoding RNAs in cancer. I'm exploring the expression pattern of long noncoding RNAs in cancer samples and integrating with other omics data such as DNA methylation to identify regulatory lncRNAs in cancer.
- Module network analysis of single-cell RNA sequencing datasets. I'm developing a module network analysis framework based on AMARETTO that aims to capture major biological pathways driving cell type evolution and tumor subtype classification from single-cell RNA sequencing datasets in cancer.

#### **2012-2016 The University of Hong Kong**

Ph.D. candidate in the lab of Prof. Maria Li Lung, Department of Clinical Oncology, Faculty of Medicine, studying the genetic and genomic basis of nasopharyngeal carcinoma (NPC). Established the pipeline for analysis of multiple next-generation sequencing datasets, including whole-exome sequencing (WES), targeted sequencing and RNASeq. Worked collaboratively on several projects.

- Genetic susceptibility study of NPC. WES and targeted sequencing were used to examine blood samples of cancer cases and controls to identify genes or pathways associated with disease risk.
- Characterization of somatic mutations of NPC tumors. Paired tumor and blood samples were sequenced to characterize the mutation landscape and signatures in NPC tumors and to identify significantly mutated genes and pathways.
- Expression profiling of NPC tumors. Paired tumor and non-tumor samples were examined with RNASeq to characterize the expression profiles, alternative splicing, and fusion events in tumors.
- DNA methylome profiling of NPC tumors. Helped in the analysis of DNA methylome data using HumanMethylation450 BeadArray to study the methylation patterns in NPC tumors.

### **2010-2012      Peking University**

Worked at the State Key Laboratory of Protein and Plant Gene Research, studying plant pathogens and host defense responses, particularly the role of small RNAs and host microRNAs in the defense response of *Oryza sativa* against two rice viruses. Conducted both bench-top experiments and data analysis.

- Constructed small RNA libraries from rice infected by viruses for Solexa/Illumina high throughput sequencing
- Analyzed the small RNASeq data to investigate the profile of small RNAs and host microRNAs

### **TEACHING EXPERIENCE**

- 2018    Mentor, Stanford Canary CREST Program
- 2018    Instructor, Principles of Cancer Systems Biology (CBIO 243), DNA methylation analysis, Stanford University
- 2011    Teaching assistant, New Thinkings of Life Science, School of Life Sciences, Peking University
- 2011    Teaching assistant, Molecular Virology, School of Life Sciences, Peking University

### **NON-ACADEMIC WORK**

- 2017-present    Board member, Chinese Life-science Postdocs and Students (CLIPSS), Stanford University
- 2016-2017      Bioinformatic Consultant, Prenetics Limited, Hong Kong.  
Developed next-generation sequencing (NGS) product and set up the analysis pipeline for sequencing data
- 2010-present    Science writer of Scientific Guokr
- 2014            Organized One Youth Talk at HK, The University of Hong Kong, October 5
- 2014            Invited talk, One Youth Talk at HK, City University of Hong Kong, April 13, DNA sequencing, genetic testing and risk prediction

### **SKILLS**

- Hands-on experiences in bioinformatics toolkits and programs. Intensive analysis and interpretation skills of multiple next-generation sequencing datasets
  - DNA sequencing
    - Whole-exome sequencing
    - Whole-genome sequencing
  - RNA sequencing

- RNA-Seq
  - Small RNA-seq
  - Single-cell RNA-Seq
  - Epi-genomics
    - HumanMethylation450 array
    - Bisulfite sequencing
    - ChIP-Seq
- Familiar with statistical methods, high-dimensional data analysis, and machine learning algorithms
- **Programming languages**

R	Professional working proficiency
Linux/Bash	Professional working proficiency
Perl	Professional working proficiency
Python	Professional working proficiency
MATLAB	Limited working proficiency
- **Experimental skills**
  - DNA/RNA extraction
  - PCR and quantitative PCR
- **Languages**

Chinese	Native
English	Full professional proficiency
Cantonese	Full professional proficiency
German	Elementary proficiency