**Zechen Chong**

**RANK/TITLE**

Tenure-track Assistant Professor

Department of Genetics

UAB Informatics Institute THT #134

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<https://sites.google.com/view/chonglab>

**EDUCATION**

2007 B.E. in Computer Science Harbin Institute of Technology (HIT), Harbin, China

2010 M.S. in Bioinformatics Beijing Institute of Genomics (BIG), Chinese Academy of Sciences (CAS), Beijing, China, Advisor: Dr. Chung-I Wu

2013 Ph.D. in Genomics Beijing Institute of Genomics (BIG),

Chinese Academy of Sciences (CAS),

Beijing, China, Advisor: Dr. Chung-I Wu

**POSTODOCTORAL TRAINING**

2013-2017 Postdoctoral Fellow and CPRIT’s CCBTP fellow, University of Texas MD Anderson Cancer Center; Dr. Ken Chen, Advisor

**ACADEMIC APPOINTMENTS**

2017-present Assistant Professor, Department of Genetics, Division of Research

Core faculty member, UAB Informatics Institute

2019-present Associate Scientist, UAB Minority Health and Health Disparities Research Center (MHRC)

2020-present Associate Scientist, UAB Center for Clinical and Translational Science Center (CCTS)

**HONORS AND AWARDS**

2016 Fellow of Computational Cancer Biology Training Program (CCBTP) of CPRIT, Texas

2015 Best Performer of ICGC-TCGA Somatic Mutation Calling DREAM SV Sub-Challenges

2014 Best Performer of ICGC-TCGA Somatic Mutation Calling DREAM SV Sub-Challenges

2013 First-Class National Scholarship, CAS

2013 Hao Bolin Scholarship, CAS

2011-2012 CAS Merit Student

2010 CAS Second-Class PhD candidate Scholarship

2004-2005 Twice Third-Class Scholarship, Harbin Institute of Technology

2004 Excellent student cadres, Harbin Institute of Technology

**PROFESSIONAL AFFILIATIONS**

International Society for Computational Biology (ISCB)

American Society of Human Genetics (ASHG)

American Heart Association (AHA)

American Association for Cancer Research (AACR)

**CONSORTIUM MEMBER**

Human Genome Structural Variation Consortium (HGSVC)

ICGC-TCGA Pan-cancer Analysis of Whole Genome (PCAWG) Consortium

Trans-Omics for Precision Medicine (TOPMed)

Alabama Genomic Health Initiative (AGHI)

**COUNCILS AND COMMITTEES**

2020 AHA COVID-19 Data Challenge, Peer Reviewer

2020 The International Conference on Intelligent Biology and Medicine (ICIBM 2020), Program Committee member

2020 BIOKDD Program Committee, committee member and Reviewer

2019 BIOKDD Program Committee, committee member and Reviewer

2019 IEEE BHI Manuscript Review Committee, Reviewer

2017 16th International Workshop on Data Mining in Bioinformatics (BIOKDD'17), Committee member

**UNIVERSITY ACTIVITIES**

2020 UAB Comprehensive Neuroscience Center Pilot Award, Peer Reviewer

2020- Faculty Council for Medical Humanitarianism Interest Group (MHIG)

2019- UAB Department of Genetics Chair Candidate interviews

2018- UAB Department of Genetics Protocol Review Committee, Committee member

2018- UAB Annual Translational and Transformative Informatics Symposium (ATTIS),

Steering Committee member

2018- UAB Informatics Institute Bioinformatics PowerTalk Colloquia, Organizer

2018- UAB Informatics Institute Scientist Recruitment Committee

2018- UAB Graduate Biomedical Sciences, Admission Committee, Committee

member

2018- UAB Informatics Institute Infrastructure, Steering Committee member

2018 UAB Informatics Institute, UBRITE system, Committee member

2017- Bioinformatics Education Subcommittee

2017 Graduate Student Research Symposium, Poster Judge

2017- Faculty candidate interviews

2017- UAB Informatics Gateway bioinformatics expert panel

**EDITORIAL BOARD MEMBERSHIPS**

*Editorial Board*

PloS One

*Reviewer*

Nucleic Acids Research Bioinformatics

Genome Biology PLoS Computational Biology

Cancer Letters Molecular Ecology Resources

Genomics Proteomics and Bioinformatics Scientific Reports

Journal of Genetics and Genome Research BioMed Research International

PLoS One Current Bioinformatics

BioKDD PeerJ

Computational and Structural Biotechnology Journal

BMC Supplements

**MAJOR RESEARCH INTERESTS**

Current primary research interests include:

1. Novel methods/tools development on sequencing data from new sequencing platforms, including 10X Genomics, PacBio, Nanopore, etc.
2. Hypothesis driven secondary analysis of large-scale consortium data such as human population data (1000 Genomes), cancer genomics data (ICGC/TCGA), and heart disease related data (TOPMed).
3. The genetic basis for obese cancer patients.
4. Mechanisms of CNVs/SVs and gene fusions and their functional impact to diseases

**TEACHING EXPERIENCE**

***Courses***

2018-present INFO 601/701, “Introduction to Bioinformatics” (3hr)

Designed new course

Course Director and Instructor (40 contact hours/16 weeks)

Department of Genetics and Informatics Institute, UAB

***Lectures***

2020 INFO604/704, Next Generation Sequencing, invited two guest lectures

2017 7th NHGRI Short Course on Next Generation Sequence, “Structural variant analysis”, invited guest lecture (1.25 contact hours)

Department of Biostatistics, UAB

2017 UAB Genetics colloquium, Undergraduate Course, “Making sense of biology using Bioinformatics”, invited guest lecture (1 contact hour)

Department of Genetics, UAB

***Research Training***

1. *Doctoral Students*

2020-Present Yiqing Wang, GBS/GGB, UAB, predoctoral candidate

2019-Present Fengyuan Huang, GBS/GGB, UAB, predoctoral candidate.

2018-Present Yu Chen, GBS/GGB, UAB, predoctoral candidate.

1. *Postdoctoral Fellows*

2017-2019 Peng Xu, Ph.D., postdoctoral research: meiotic recombination discovery using 10X Genomics whole genome sequencing and SV detection methods development

1. *Research Assistant*

2019-2020 Yiqing Wang, Computer Science Department, UAB

1. *Undergraduates*

09/2020-Present Katrina Whitten, UAB

09/2020-Present Ethan Vallely, UAB

2019-2020 Yixin Zhang, Computer Science Department, UAB

2019-2019 Trinity Lauren Lebkuecher, Pre-Med student in Bioinformatics Major, UAB

1. *Visiting Scientists/Scholars*

2017-2018 Ming Ye, Ph.D., Associate Professor, Southwest University, China

1. *Rotation Students*

2020 Weisheng Chen, GBS/GGB, UAB, predoctoral candidate

2019 Ari Ginsparg, GBS/GGB, UAB, predoctoral candidate

2018 Mary Bunton, GBS/GGB, UAB, predoctoral candidate

1. *Thesis Committees*

2020-Present Mary Grabowski Smithson Master Advisor: Karin Hardiman

2019-Present Yu Chen GBS/GGB, UAB Advisor: Zechen Chong

2019-Present Bre` Minniefield GBS/GGB, UAB Advisor: Ryan Irvin

2018-Present Zongliang Yue GBS/GGB, UAB Advisor: Jake Chen

**GRANT SUPPORT (PAST AND CURRENT)**

1. ***Active***

University of Alabama at Birmingham 12 mos

UAB Informatics Institute recruitment startup fund

PI: Zechen Chong

Goal: startup fund for PI’s salary and fringe, hiring, equipment, and research.

5116790 subaward of 1 OT3 HL147154-01 (PI: Stanley Ahalt), NIH/NHLBI

PI: Zechen CHONG 03/20/20-03/19/21 5.28 mos

$69,733/yr Annual Direct Costs to Dr. Zechen Chong lab

*Title*: Study the Contribution of Structural Variations to Cardiovascular Diseases on the BioData Catalyst Platform

Goal: The goal of this project is to study structural variations in TOPMed GOLDN and HyperGEN subjects on the Cloud computing platform BioData Catalyst Platform

NIH: National Institute of General Medical Sciences (NIGMS)

1R35GM138212 (PI: ZECHEN CHONG) 07/01/2020-06/30/2025 6.12 mos

$250,000/yr Annual Direct Costs to Dr. Zechen Chong Lab

Request Total: $1,799,946.35

*Title: Structural variation analysis with and without a reference genome*

Goal: Accurate SV characterization and understanding their formation mechanisms using new sequencing data

1. ***Pending***

American Heart Association (AHA)

Title: Study the contribution of structural variants to cardiovascular disease on the Precision

Medicine Platform

Goal: Systematically and comprehensively characterize SVs and their contribution to the

phenotypes in TOPMed GOLDN and HyperGEN projects, which involve in more than 3,000

CVD patients and have multiple data types.

Request Total: $1,000,000

PI: Zechen Chong

12/01/2019-11/30/2023

National Science Foundation (NSF CAREER)

Title: CAREER: study the mechanisms of structural variations using new sequencing data

Goal: Develop novel SV detection algorithms using new sequencing data and study the SV

formation mechanisms

Requested Total: $695,049

PI: Zechen Chong

02/01/2020-01/31/2025

NIH: National Human Genome Research Institute (NHGRI) (R01)

Title: Efficient Detection of Structural Variations using New Sequencing Data

Goal: Develop efficient and novel methods for SV detection using new sequencing data

PI: Zechen Chong

Requested Total: $1,771,794

09/01/2019-08/31/2024

NIH: National Institute of Allergy and Infectious Diseases (NIAID) (U01)

Title: Natural Killer Cells and HLA Region KIR Genomics in Common Variable Immune Deficiency

Goal: Establish the association between HLA/KIR and CVID

PI: Harry Schroeder, Co-I: Zechen Chong

Requested Total: $3,770,898

06/01/2020-05/31/2025

Department of Defense Breast Cancer Research Program Breakthrough Award (DOD)

Title: FOXP3-mediated Tumor-immune Interaction and Metastasis

Goal: Study the FOXP3-mediated microenvironment and its relationship with tumor immune interaction and metastasis

PI: Lizhong Wang, Co-I: Zechen Chong

Requested Total: $742,500

08/01/2019-08/31/2023

NIH: National Institute of Allergy and Infectious Diseases (NIAID) (R21)

Title: Exploring the Mechanisms of Ureaplasma Pathogenesis by Multi-omics Approach

Goal: Study the mechanisms of Ureaplasma using multi-omics approaches

PI: Li Xiao, Co-I: Zechen Chong

Requested Total: $422,299

09/01/2019-08/31/2021

NIH: National Cancer Institute (NCI) (R01)

Title: Development of an Integrated Multi-Omic Database for Subgroup and Molecular Subtype Specific Analyses of Cancers to Identify New Biomarkers and Therapeutic Targets

Goal: Develop an integrative cancer related database to identify new biomarkers and therapeutic targets

PI: Sooryanarayana Varambally, Co-I: Zechen Chong

Requested Total: $1,885,615

09/01/2019-08/31/2024

1. ***Previous***

UAB Obesity Health Disparities Research Center (OHDRC)

Title: The mutational landscape of obesity cancer genomes

Goal: Pan-cancer analysis of TCGA data to characterize the mutational landscape of cancer patients with obesity

Amount: $50,000/year

PI: Zechen Chong

01/09/2019-01/08/2020

American Heart Association (17IF33890015)

Title: Institutional Data Fellowship

Goal: Train a next-generation cloud computing researcher for 2 years

Amount: $75,000/year + $50,000/year of Amazon Web Services Credit

PI: James Cimino, Co-PI: Zechen Chong

10/01/2017-09/30/2019

Computational Cancer Biology Training Program (CCBTP) of Cancer Prevention and Research Institute of Texas (CPRIT)

Title: Comprehensive Characterization of Structural Alterations in Cancer Genomes and Transcriptomes

Goal: The project focused on the optimization and extension of novoBreak and its applications.

Amount: $46,344/year

PI: Zechen Chong

2016-2017

NIH: National Human Genome Research Institute (NHGRI), subawarded by HudsonAlpha Institute for Biotechnology

Title: South-seq: DNA Sequencing for Newborn Nurseries in the South

Goal: Use whole genome sequencing (WGS) to diagnose ill neonates of diverse backgrounds in the Deep South

Amount: $45,148

PI: Gregory Cooper, Co-I: Zechen Chong

06/01/2018-05/31/2019

**INVITED SEMINARS AND LECTURES**

**2020**

* Invited seminar talk, UAB Informatics Institute PowerTalk Seminars, “Genomic Tools for Third-Generation Sequencing Data Analysis”, Virtual, 10/09/2020.
* Invited talk, U54 Obesity Health Disparities Research Center (OHDRC) and Minority Health and Health Disparities Research Center (MHRC) 2020 External Advisory Board Meeting, “The Genomic Landscape of Obese Cancer Patients in Minority Groups”, Virtual Meeting, 09/09/2020.
* Talk, NHLBI Biodata Catalyst Quarterly Meeting, “Contribution of Structural Variations to Cardiovascular Diseases on the BioData Catalyst Ecosystem”, Virtual Meeting, 09/01/2020.
* Talk, Human Genome Structural Variation Consortium Meeting, “DeBreak Callset, Compound SVs, and structural errors evaluation of the de novo assembly results”, Virtual Meeting, 08/24/2020.
* Invited Talk, TOPMed Structural Variation Working Group Meeting, “Integrating SVs from NGS callers based on long-read results​”, Virtual Meeting, 08/10/2020.
* Invited talk, 2020 Annual Translational And Transformative Informatics Symposium, “A suite of solutions to biological questions using the third generation”, UAB, Birmingham, AL, 03/13/2020.

**2019**

* Platform Talk, ASHG 2019, “DeBreak: Deciphering the exact breakpoints of structural variants using long sequencing reads”, Houston, TX, 10/16/2019.
* Speaker, Human Genome Structural Variation Consortium meeting, “DeBreak analysis on the HGSVC CLR and CCS samples”, Houston, TX, 10/15/2019.
* Invited panelist, 2019 AHA Research Leaders Academy, “The Ticket to Your Next Grant: Learn Cloud Computing”, Baltimore, MD, 09/19/2019.
* Speaker, Human Genome Structural Variation Consortium meeting, “DeBreak update”, Cold Spring Harbor Laboratory, NY, 05/11/2019.
* Speaker, 2019 UAB Health Disparities Research Symposium, “The Mutational Landscape of Cancer Patients With Overweight and Obesity”, UAB, Birmingham, AL, 04/18/2019

**2018**

* Invited talk, American Heart Association Scientific Sessions 2018, “Bioinformatics is best fit for the cloud”, Chicago, IL, 11/10/2018.
* Platform Talk, ASHG 2018, “Identification of meiotic recombination events through gamete genome reconstruction by linked-read sequencing technology”, San Diego, CA, 10/22/2018.
* Speaker, Human Genome Structural Variation Consortium meeting, “DeBreak: Deciphering the exact Breakpoints of structural variants using long sequencing reads”, San Diego, CA, 10/15/2018.

**2017**

* Invited lecture, 7th NHGRI Short Course on Next Generation Sequence, “Structural variant analysis”, UAB, Birmingham, AL, 12/20/2017.
* Invited lecture, UAB Genetics colloquium, Undergraduate Course, “Making sense of biology using Bioinformatics”, UAB, Birmingham, AL, 11/08/2017.
* Invited talk, UAB 1st Annual Translational Bioinformatics mini-Symposium, “Structural variation analysis from short and long reads”, UAB, Birmingham, AL, 05/03/2017.

**Before joining UAB (postdoc training)**

* Invited talk, RECOMB/ISCB Conference on Regulatory & Systems Genomics with DREAM Challenges & Cytoscape Workshop, “novoBreak: a k-mer targeted assembly algorithm for breakpoint detection in cancer genomes”, Philadelphia, PA, 11/17/2015.
* Invited talk, RECOMB/ISCB Conference on Regulatory & Systems Genomics with DREAM Challenges & Cytoscape Workshop, “novoBreak: robust characterization of structural breakpoints in cancer genomes”, San Diego, CA, 11/11/2014.

**PUBLICATION METRICS**

**Google Scholar: All Since 2015**

Citations 9,926 9,749

h-index 21 21

i10-index 29 29

**PUBLICATIONS**

**(first or corresponding senior-author publications – designated with \*)**

1. ***Research Articles***
2. Bailey MH, Meyerson WU, Dursi LJ, Wang LB, Dong G, Liang WW, Weerasinghe A, Li S, Kelso S; MC3 Working Group; PCAWG novel somatic mutation calling methods working group (including **Zechen Chong**), Saksena G, Ellrott K, Wendl MC, Wheeler DA, Getz G, Simpson JT, Gerstein MB, Ding L; PCAWG Consortium (including **Zechen Chong**). Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. Nat Commun. 2020 Sep 21;11(1):4748. doi: 10.1038/s41467-020-18151-y. PMID: 32958763; PMCID: PMC7505971.
3. Li CH, Prokopec SD, Sun RX, Yousif F, Schmitz N; PCAWG Tumour Subtypes and Clinical Translation, Boutros PC; PCAWG Consortium (including **Zechen Chong**). Sex differences in oncogenic mutational processes. Nat Commun. 2020 Aug 28;11(1):4330. doi: 10.1038/s41467-020-17359-2. PMID: 32859912; PMCID: PMC7455744.
4. Liu RM, **Chong Z**, Chen JC. Ozone and Particulate Matter Exposure and Alzheimer's Disease: A Review of Human and Animal Studies. J Alzheimers Dis. 2020;76(3):807-824. doi: 10.3233/JAD-200435. PMID: 32568209.
5. ICGC/TCGA Pan-Cancer Analysis of Whole Genomes Consortium (including **Zechen Chong**). Pan-cancer analysis of whole genomes. Nature. 2020 Feb;578(7793):82-93. doi:10.1038/s41586-020-1969-6. Epub 2020 Feb 5. PubMed PMID: 32025007; PubMed Central PMCID: PMC7025898.
6. Rodriguez-Martin B, Alvarez EG, Baez-Ortega A, Zamora J, Supek F, Demeulemeester J, Santamarina M, Ju YS, Temes J, Garcia-Souto D, Detering H, Li Y, Rodriguez-Castro J, Dueso-Barroso A, Bruzos AL, Dentro SC, Blanco MG, Contino G, Ardeljan D, Tojo M, Roberts ND, Zumalave S, Edwards PAW, Weischenfeldt J, Puiggròs M, **Chong Z**, Chen K, Lee EA, Wala JA, Raine K, Butler A, Waszak SM, Navarro FCP, Schumacher SE, Monlong J, Maura F, Bolli N, Bourque G, Gerstein M, Park PJ, Wedge DC, Beroukhim R, Torrents D, Korbel JO, Martincorena I, Fitzgerald RC, Van Loo P, Kazazian HH, Burns KH; PCAWG Structural Variation Working Group, Campbell PJ, Tubio JMC; PCAWG Consortium. Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. Nat Genet. 2020 Mar;52(3):306 319. doi: 10.1038/s41588-019-0562-0. Epub 2020 Feb 5. PubMed PMID: 32024998; PubMed Central PMCID: PMC7058536.
7. Shanta O, Noor A; Human Genome Structural Variation Consortium (HGSVC) (including **Zechen Chong**), Sebat J. The effects of common structural variants on 3D chromatin structure. BMC Genomics. 2020 Jan 30;21(1):95. doi: 10.1186/s12864-020-6516-1. PubMed PMID: 32000688; PubMed Central PMCID: PMC6990566.
8. Kessler MD, Loesch DP, Perry JA, Heard-Costa NL, Taliun D, Cade BE, Wang H, Daya M, Ziniti J, Datta S, Celedón JC, Soto-Quiros ME, Avila L, Weiss ST, Barnes K, Redline SS, Vasan RS, Johnson AD, Mathias RA, Hernandez R, Wilson JG, Nickerson DA, Abecasis G, Browning SR, Zöllner S, O'Connell JR, Mitchell BD; National Heart, Lung, and Blood Institute Trans-Omics for Precision Medicine (TOPMed) Consortium (including **Zechen Chong**); TOPMed Population Genetics Working Group, O'Connor TD. De novo mutations across 1,465 diverse genomes reveal mutational insights and reductions in the Amish founder population. Proc Natl Acad Sci U S A. 2020 Feb 4;117(5):2560-2569. doi: 10.1073/pnas.1902766117. Epub 2020 Jan 21. PubMed PMID: 31964835; PubMed Central PMCID: PMC7007577.
9. Sulovari A, Li R, Audano PA, Porubsky D, Vollger MR, Logsdon GA; Human Genome Structural Variation Consortium (including **Zechen Chong**), Warren WC, Pollen AA, Chaisson MJP, Eichler EE. Human-specific tandem repeat expansion and differential gene expression during primate evolution. Proc Natl Acad Sci U S A. 2019 Nov 12;116(46):23243-23253. Doi: 10.1073/pnas.1912175116. Epub 2019 Oct 28. PubMed PMID: 31659027; PubMed Central PMCID: PMC6859368.
10. Xu P, Kennell T, Gao M; Human Genome Structural Variation Consortium, Kimberly RP, **Chong Z**. MRLR: unraveling high-resolution meiotic recombination by linked reads. Bioinformatics. 2020 Jan 1;36(1):10-16. doi: 10.1093/bioinformatics/btz503. PubMed PMID: 31214684; PubMed Central PMCID: PMC6956785.
11. Guo G, Chen H, Yan D, Cheng J, Chen J, **Chong Z**. Scalable De Novo Genome Assembly Using a Pregel-Like Graph-Parallel System. *IEEE/ACM Trans Comput Biol Bioinform*. 2019 Jun 5. doi: 10.1109/TCBB.2019.2920912. [Epub ahead of print] PubMed PMID: 31180898.
12. Chaisson MJ, Sanders AD, Zhao X, Malhotra A, Porubsky D, Rausch T, Gardner EJ, Rodr RL, Fan X, et al. (including **Zechen Chong**) Multi-platform discovery of haplotype-resolved human genomes. *Nature Commu.* 2019 Apr 16.
13. Beck CR, Carvalho CMB, Akdemir ZC, Sedlazeck FJ, Song X, Meng Q, Hu J, Doddapaneni H, **Chong Z**, Chen ES, Thornton PC, Liu P, Yuan B, Withers M, Jhangiani SN, Kalra D, Walker K, English AC, Han Y, Chen K, Muzny DM, Ira G, Shaw CA, Gibbs RA, Hastings PJ, Lupski JR. Megabase Length Hypermutation Accompanies Human Structural Variation at 17p11.2. *Cell*. 2019 Mar 7;176(6):1310-1324.e10. doi: 10.1016/j.cell.2019.01.045. Epub 2019 Feb 28. PubMed PMID: 30827684; PubMed Central PMCID: PMC6438178.
14. Lee AY, Ewing AD, Ellrott K, Hu Y, Houlahan KE, Bare JC, Espiritu SMG, Huang V, Dang K, **Chong Z**, Caloian C, Yamaguchi TN; ICGC-TCGA DREAM Somatic Mutation Calling Challenge Participants, Kellen MR, Chen K, Norman TC, Friend SH, Guinney J, Stolovitzky G, Haussler D, Margolin AA, Stuart JM, Boutros PC. Combining accurate tumor genome simulation with crowdsourcing to benchmark somatic structural variant detection. *Genome Biol.* 2018 Nov 6;19(1):188. doi: 10.1186/s13059-018-1539-5. PubMed PMID: 30400818; PubMed Central PMCID: PMC6219177.
15. Zhu W, Zhang E, Zhao M, **Chong Z**, Fan C, Tang Y, Hunter JD, Borovjagin AV, Walcott GP, Chen JY, Qin G, Zhang J. Regenerative Potential of Neonatal Porcine Hearts. *Circulation*. 2018 Dec 11;138(24):2809-2816. doi: 10.1161/CIRCULATIONAHA.118.034886. PubMed PMID: 30030418; PubMed Central PMCID: PMC6301098.
16. Grzeskowiak CL, Kundu ST, Mo X, Ivanov AA, Zagorodna O, Lu H, Chapple RH, Tsang YH, Moreno D, Mosqueda M, Eterovic K, Fradette JJ, Ahmad S, Chen F, **Chong Z**, Chen K, Creighton CJ, Fu H, Mills GB, Gibbons DL, Scott KL. In vivo screening identifies GATAD2B as a metastasis driver in KRAS-driven lung cancer. *Nat Commun*. 2018 Jul 16;9(1):2732. doi: 10.1038/s41467-018-04572-3. PubMed PMID: 30013058; PubMed Central PMCID: PMC6048166.
17. Grochowski CM, Gu S, Yuan B, Tcw J, Brennand KJ, Sebat J, Malhotra D, McCarthy S, Rudolph U, Lindstrand A, **Chong Z**, Levy DL, Lupski JR, Carvalho CMB. Marker chromosome genomic structure and temporal origin implicate a chromoanasynthesis event in a family with pleiotropic psychiatric phenotypes. *Hum Mutat*. 2018 Jul;39(7):939-946. doi: 10.1002/humu.23537. Epub 2018 May 11. PubMed PMID: 29696747; PubMed Central PMCID: PMC5995661.
18. Gönen M, Weir BA, Cowley GS, Vazquez F, Guan Y, Jaiswal A, Karasuyama M, Uzunangelov V, Wang T, Tsherniak A, Howell S, Marbach D, et al. (including **Zechen Chong**). A Community Challenge for Inferring Genetic Predictors of Gene Essentialities through Analysis of a Functional Screen of Cancer Cell Lines. *Cell Syst*. 2017 Nov 22;5(5):485-497.e3. doi: 10.1016/j.cels.2017.09.004. Epub 2017 Oct 4. PubMed PMID: 28988802; PubMed Central PMCID: PMC5814247
19. Federico L, **Chong Z**, Zhang D, McGrail DJ, Zhao W, Jeong KJ, Vellano CP, Ju Z, Gagea M, Liu S, Mitra S, Dennison JB, Lorenzi PL, Cardnell R, Diao L, Wang J, Lu Y, Byers LA, Perou CM, Lin SY, Mills GB. A murine preclinical syngeneic transplantation model for breast cancer precision medicine. *Sci Adv*. 2017 Apr 19;3(4):e1600957. doi: 10.1126/sciadv.1600957. eCollection 2017 Apr. PubMed PMID: 28439535; PubMed Central PMCID: PMC5397135.

**Before joining UAB:**

1. Liu P, Yuan B, Carvalho CM, Wuster A, Walter K, Zhang L, Gambin T, **Chong Z**, Campbell IM, Coban Akdemir Z, Gelowani V, Writzl K, Bacino CA, Lindsay SJ, Withers M, Gonzaga-Jauregui C, Wiszniewska J, Scull J, Stankiewicz P, Jhangiani SN, Muzny DM, Zhang F, Chen K, Gibbs RA, Rautenstrauss B, Cheung SW, Smith J, Breman A, Shaw CA, Patel A, Hurles ME, Lupski JR. An Organismal CNV Mutator Phenotype Restricted to Early Human Development. *Cell*. 2017 Feb 23;168(5):830-842.e7. doi: 10.1016/j.cell.2017.01.037. PubMed PMID: 28235197.
2. Cancer Genome Atlas Research Network (including **Chong Z**). Integrated genomic and molecular characterization of cervical cancer. *Nature*. 2017 Jan 23. doi: 10.1038/nature21386. [Epub ahead of print] PubMed PMID: 28112728.
3. **\*Chong Z**, Ruan J, Gao M, Zhou W, Chen T, Fan X, Ding L, Lee AY, Boutros P, Chen J, Chen K. novoBreak: local assembly for breakpoint detection in cancer genomes. *Nat Methods*. 2017 Jan;14(1):65-67. doi: 10.1038/nmeth.4084. PubMed PMID: 27892959; PubMed Central PMCID: PMC5199621.
4. Zhang K, Gao M, **Chong Z**, Li Y, Han X, Chen R, Qin L. Single-cell isolation by a modular single-cell pipette for RNA-sequencing. *Lab Chip*. 2016 Nov 29;16(24):4742-4748. PubMed PMID: 27841430.
5. Chen T, Wang Z, Zhou W, **Chong Z**, Meric-Bernstam F, Mills GB, Chen K. Hotspot mutations delineating diverse mutational signatures and biological utilities across cancer types. *BMC Genomics*. 2016 Jun 23;17 Suppl 2:394. doi: 10.1186/s12864-016-2727-x. PubMed PMID: 27356755; PubMed Central PMCID: PMC4928158.
6. Tsang YH, Dogruluk T, Tedeschi PM, Wardwell-Ozgo J, Lu H, Espitia M, Nair N, Minelli R, **Chong Z**, Chen F, Chang QE, Dennison JB, Dogruluk A, Li M, Ying H, Bertino JR, Gingras MC, Ittmann M, Kerrigan J, Chen K, Creighton CJ, Eterovic K, Mills GB, Scott KL. Functional annotation of rare gene aberration drivers of pancreatic cancer. *Nat Commun*. 2016 Jan 25;7:10500. doi: 10.1038/ncomms10500. PubMed PMID: 26806015; PubMed Central PMCID: PMC4737758.
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23. ***Reviews and Book Chapters***
24. Liu RM, **Chong Z**, Chen JC. Ozone and Particulate Matter Exposure and Alzheimer's Disease: A Review of Human and Animal Studies. J Alzheimers Dis. 2020;76(3):807-824. doi: 10.3233/JAD-200435. PMID: 32568209.
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26. ***Meeting Abstracts/Posters***
27. **\***Yu Chen, **Zechen Chong.** ASHG 2020. “Inspector: A tool for inspecting long-read genome assemblies”. Virtual Meeting. 10/26/2020
28. **\***Fengyuan Huang, Li Xiao, Kevin Dybvig, Thomas Atkinson, and **Zechen Chong.** ASHG 2020. “B-assembler – a circular bacterial genome assembler”. Virtual Meeting. 10/26/2020
29. **\***Peng Xu and **Zechen Chong**. ASHG 2019. “ClipSV: Structural variation detection by read extension, spliced alignment, and local de novo assembly”. Houston, TX. 10/16/2019. (Reviewers' Choice Abstracts).
30. **\***Fengyuan Huang, Li Xiao, Thomas P. Atkinson, Ken B. Waites, Kevin Dybvig, and **Zechen Chong**. 2019 UAB GBS Symposium. “*De novo* assembly of mycoplasmas”. UAB, Birmingham, AL. 08/16/2019.
31. **\***Yu Chen and **Zechen Chong**. Annual Translational and Transformative Informatics Symposium (ATTIS 19). “DeBreak: Detect Structural Variants using long-read DNA sequencing reads”. UAB, Birmingham, AL. 03/28/2019.
32. **\***Peng Xu and **Zechen Chong**. 16th Annual Conference of the Midsouth Computational Biology & Bioinformatics Society (MCBIOS). “Meiotic recombination in human genomes: a landscape of crossovers and non-crossover gene conversions”. Birmingham, AL. 3/28/2019.
33. **\***Yu Chen, Peng Xu, and **Zechen Chong.** UAB GBS Recruitment Poster Session. “Accurate detection of structural variations using new sequencing platforms”. UAB, Birmingham, AL. 02/22/2019.
34. **\***Peng Xu and **Zechen Chong**. 2019 UAB Postdoc Research Day. “A comprehensive landscape of meiotic recombination in human genome”. Birmingham, AL. 2/18/2019. (Won the 3rd place award).
35. **\***Yu Chen and **Zechen Chong**. 2018 UAB GBS Symposium. “DeBreak: Deciphering the exact Breakpoints of structural variants using long sequencing reads”. UAB, Birmingham, AL. 08/10/2018.
36. **\***Peng Xu and **Zechen Chong**. The annual international conference on Intelligent Systems for Molecular Biology (ISMB 2018). “Identification of meiotic recombination events through gamete haplotype reconstructionby linked-read sequencing method”. Chicago, IL. 7/6/2018.
37. **\***Peng Xu and **Zechen Chong**. 2nd Annual Translational and Transformative Informatics Symposium(ATTIS 18). “Identification of meiotic recombination events through gamete haplotype reconstruction by linked-read sequencing method”. Birmingham, AL. 4/25/2018. (Won the 2nd place award).

**MISCELLANEOUS**

1. ***SOFTWARE***

All the software can be found in <https://github.com/ChongLab>.

DeBreak, A SV caller for long single-molecular sequencing reads. <https://github.com/ChongLab/DeBreak>.

*ClipSV*, detecting structural variations by spliced alignment and local assembly. <https://github.com/ChongLab/ClipSV>.

*Rainbow,* a tool for short reads clustering and local assembly. <https://sourceforge.net/projects/bio-rainbow/>.

*novoBreak,* robust detection of somatic structural breakpoints in cancer genomes. <https://sourceforge.net/projects/novobreak/>.

*MRLR*, a tool for meiotic recombination discovery using 10X genomics data. <https://github.com/ChongLab/MRLR>.