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RESEARCH KEY WORDS:

Cancer multi-omics (especially pancreatic cancer), bioinformatics, genome-wide association study (GWAS), transcriptome-wide association study (TWAS), risk prediction models, cancer driver factors.

PROFESSIONAL EXPERIENCE:

Research Fellow.....2022 - present
National Cancer Institute, National Institute of Health, USA

Postdoctoral Fellow.....2017 - 2022
National Cancer Institute, National Institute of Health, USA

Staff Scientist.....2014 - 2017
Beijing Institute of Genomics, University of Chinese Academy of Sciences, China

EDUCATION:

Ph. D Bioinformatics.....2014
Beijing Institute of Genomics, University of Chinese Academy of Sciences, China

B. S Biotechnology.....2009
South-Central University for Nationalities, China

AWARDS AND HONORS:

- DCEG Intramural Research Award, National Cancer Institute 2021
- Fellows Award for Research Excellence (FARE), NIH (Top 25%) 2021
- Reviewers' Choice Abstract Award at American Society of Human Genetics (ASHG) annual meeting (Top 10%) 2020
- Fellows Award for Research Excellence (FARE), NIH (Top 25%) 2020
- Summer Research Mentor Award, NIH 2019
- Cancer Research Training Award (CRTA) from National Cancer Institute, NIH 2017
- Best Paper Award in the Twelfth Asia Pacific Bioinformatics Conference 2014
- Merit Student, University of Chinese Academy of Sciences (Top 15%) 2011
- Merit Student, University of Chinese Academy of Sciences (Top 15%) 2010

PUBLICATIONS FOR JOURNALS:

(# for co-first author, § for co-corresponding author)

1. **Zhong J**^(§), Amundadottir L^(§). Uncovering dark matter in cancer by identifying epigenetic drivers. *Trends in Genetics*. (in press)
2. **Zhong J**^(§), Shi J^(§), Amundadottir LT^(§). Artificial intelligence and improved early detection for pancreatic cancer. *The Innovation*. 2023 Jun 8;4(4):100457.
3. Lindström S, Wang L, Feng H, Majumdar A, Huo S, Macdonald J, Harrison T, Turman C, Chen H, Mancuso N, Bammler T; Breast Cancer Association Consortium (BCAC); Gallinger S, Gruber SB, Gunter MJ, Le Marchand L, Moreno V, Offit K; Colorectal Transdisciplinary Study (CORECT), Colon Cancer Family Registry Study (CCFR), Genetics And Epidemiology Of Colorectal Cancer Consortium (GECCO);

De Vivo I, O'Mara TA, Spurdle AB, Tomlinson I; Endometrial Cancer Association Consortium (ECAC); Fitzgerald R, Gharahkhani P, Gockel I, Jankowski J, Macgregor S, Schumacher J, Barnholtz-Sloan J, Bondy ML, Houlston RS, Jenkins RB, Melin B, Wrensch M, Brennan P, Christiani DC, Johansson M, McKay J, Aldrich MC, Amos CI, Landi MT, Tardon A; International Lung Cancer Consortium (ILCCO); Bishop DT, Demenais F, Goldstein AM, Iles MM, Kanetsky PA, Law MH; Ovarian Cancer Association Consortium (OCAC); Amundadottir LT, Stolzenberg-Solomon R, Wolpin BM; Pancreatic Cancer Cohort Consortium (PanScan, including **Zhong J**); Klein A, Petersen G, Risch H; Pancreatic Cancer Case-Control Consortium (PanC4), The PRACTICAL Consortium; Chanock SJ, Purdue MP, Scelo G, Pharoah P, Kar S, Hung RJ, Pasaniuc B, Kraft P. Genome-wide analyses characterize shared heritability among cancers and identify novel cancer susceptibility regions. *J Natl Cancer Inst.* 2023 Jun 8;115(6):712-732.

4. King SD, Veliginti S, Brouwers MCGJ, Ren Z, Zheng W, Setiawan VW, Wilkens LR, Shu XO, Arslan AA, Beane Freeman LE, Bracci PM, Canzian F, Du M, Gallinger SJ, Giles GG, Goodman PJ, Haiman CA, Kogevinas M, Kooperberg C, LeMarchand L, Neale RE, Visvanathan K, White E, Albanes D, Andreotti G, Babic A, Berndt SI, Brais LK, Brennan P, Buring JE, Rabe KG, Bamlet WR, Chanock SJ, Fuchs CS, Gaziano JM, Giovannucci EL, Hackert T, Hassan MM, Katzke V, Kurtz RC, Lee IM, Malats N, Murphy N, Oberg AL, Orlow I, Porta M, Real FX, Rothman N, Sesso HD, Silverman DT, Thompson IM, Wactawski-Wende J, Wang X, Wentzensen N, Yu H, Zeleniuch-Jacquotte A, Yu K, Wolpin BM, Duell EJ, Li D, Hung RJ, Perdomo S, McCullough ML, Freedman ND, Patel AV, Peters U, Riboli E, Sund M, Tjønneland A, **Zhong J**, Van Den Eeden SK, Kraft P, Risch HA, Amundadottir LT, Klein AP, Stolzenberg-Solomon RZ, Antwi SO. Genetic Susceptibility to Nonalcoholic Fatty Liver Disease and Risk for Pancreatic Cancer: Mendelian Randomization. *Cancer Epidemiol Biomarkers Prev.* 2023 Sep 1;32(9):1265-1269.
5. Hoskins JW, Chung CC, O'Brien A, **Zhong J**, Connelly K, Collins I, Shi J, Amundadottir LT. Inferred expression regulator activities suggest genes mediating cardiometabolic genetic signals. *PLoS Computational Biology*, 2021, 17(11):e1009563.
6. Jermusyk A^(#), **Zhong J**^(#), Connelly KE^(#), Gordon N^(#), Perera S, Abdolalizadeh E, Zhang T, O'Brien A, Hoskins JW, Collins I, Eiser D, Yuan C; PanScan Consortium; PanC4 Consortium, Risch HA, Jacobs EJ, Li D, Du M, Stolzenberg-Solomon RZ, Klein AP, Smith JP, Wolpin BM, Chanock SJ, Shi J, Petersen GM, Westlake CJ, Amundadottir LT. A 584 bp deletion in CTRB2 inhibits chymotrypsin B2 activity and secretion and confers risk of pancreatic cancer. *American Journal of Human Genetics*, 2021, 108(10):1852-1865.
7. Julián-Serrano S, Yuan F, Wheeler W, Benyamin B, Machiela MJ, Arslan AA, Beane-Freeman LE, Bracci PM, Duell EJ, Du M, Gallinger S, Giles GG, Goodman PJ, Kooperberg C, Marchand LL, Neale RE, Shu XO, Van Den Eeden SK, Visvanathan K, Zheng W, Albanes D, Andreotti G, Ardanaz E, Babic A, Berndt SI, Brais LK, Brennan P, Bueno-de-Mesquita B, Buring JE, Chanock SJ, Childs EJ, Chung CC, Fabiánová E, Foretová L, Fuchs CS, Gaziano JM, Gentiluomo M, Giovannucci EL, Goggins MG, Hackert T, Hartge P, Hassan MM, Holcátová I, Holly EA, Hung RI, Janout V, Kurtz RC, Lee IM, Malats N, McKean D, Milne RL, Newton CC, Oberg AL, Perdomo S, Peters U, Porta M, Rothman N, Schulze MB, Sesso HD, Silverman DT, Thompson IM, Wactawski-Wende J, Weiderpass E, Wenstzensen N, White E, Wilkens LR, Yu H, Zeleniuch-Jacquotte A, **Zhong J**, Kraft P, Li D, Campbell PT, Petersen GM, Wolpin BM, Risch HA, Amundadottir LT, Klein AP, Yu K, Stolzenberg-Solomon RZ. Hepcidin-regulating iron metabolism genes and pancreatic ductal adenocarcinoma: a pathway analysis of genome-wide association studies. *American Journal of Clinical Nutrition*, 2021, 114(4), 1408–1417.
8. **Zhong J**, Jermusyk A, Wu L, Hoskins JW, Collins I, Mocci E, Zhang M, Song L, Chung CC, Zhang T, Xiao W, Albanes D, Andreotti G, Arslan AA, Babic A, Bamlet WR, Beane-Freeman L, Berndt S, Borgida

- A, Bracci PM, Brais L, Brennan P, Bueno-de-Mesquita B, Buring J, Canzian F, Childs EJ, Cotterchio M, Du M, Duell EJ, Fuchs C, Gallinger S, Gaziano JM, Giles GG, Giovannucci E, Goggins M, Goodman GE, Goodman PJ, Haiman C, Hartge P, Hasan M, Helzlsouer KJ, Holly EA, Klein EA, Kogevinas M, Kurtz RJ, LeMarchand L, Malats N, Männistö S, Milne R, Neale RE, Ng K, Obazee O, Oberg AL, Orlow I, Patel AV, Peters U, Porta M, Rothman N, Scelo G, Sesso HD, Severi G, Sieri S, Silverman D, Sund M, Tjønneland A, Thornquist MD, Tobias GS, Trichopoulou A, Van Den Eeden SK, Visvanathan K, Wactawski-Wende J, Wentzensen N, White E, Yu H, Yuan C, Zeleniuch-Jacquotte A, Hoover R, Brown K, Kooperberg C, Risch HA, Jacobs EJ, Li D, Yu K, Shu XO, Chanock SJ, Wolpin BM, Stolzenberg-Solomon RZ, Chatterjee N, Klein AP, Smith JP, Kraft P, Shi J, Petersen GM, Zheng W, Amundadottir LT. A Transcriptome-Wide Association Study (TWAS) Identifies Novel Candidate Susceptibility Genes for Pancreatic Cancer. *JNCI: Journal of the National Cancer Institute*, 2020, 112(10):1003-1012.
9. Zhang YD, Hurson AN, Zhang H, Choudhury PP, Easton DF, Milne RL, Simard J, Hall P, Michailidou K, Dennis J, Schmidt MK, Chang-Claude J, Gharahkhani P, Whiteman D, Campbell PT, Hoffmeister M, Jenkins M, Peters U, Hsu L, Gruber SB, Casey G, Schmit SL, O'Mara TA, Spurdle AB, Thompson DJ, Tomlinson I, De Vivo I, Landi MT, Law MH, Iles MM, Demenais F, Kumar R, MacGregor S, Bishop DT, Ward SV, Bondy ML, Houlston R, Wiencke JK, Melin B, Barnholtz-Sloan J, Kinnersley B, Wrensch MR, Amos CI, Hung RJ, Brennan P, McKay J, Caporaso NE, Berndt SI, Birmann BM, Camp NJ, Kraft P, Rothman N, Slager SL, Berchuck A, Pharoah PDP, Sellers TA, Gayther SA, Pearce CL, Goode EL, Schildkraut JM, Moysich KB, Amundadottir LT, Jacobs EJ, Klein AP, Petersen GM, Risch HA, Stolzenberg-Solomon RZ, Wolpin BM, Li D, Eeles RA, Haiman CA, Kote-Jarai Z, Schumacher FR, Al Olama AA, Purdue MP, Scelo G, Dalggaard MD, Greene MH, Grotmol T, Kanetsky PA, McGlynn KA, Nathanson KL, Turnbull C, Wiklund F; Breast Cancer Association Consortium (BCAC); Barrett's and Esophageal Adenocarcinoma Consortium (BEACON); Colon Cancer Family Registry (CCFR); Transdisciplinary Studies of Genetic Variation in Colorectal Cancer (CORECT); Endometrial Cancer Association Consortium (ECAC); Genetics and Epidemiology of Colorectal Cancer Consortium (GECCO); Melanoma Genetics Consortium (GenoMEL); Glioma International Case-Control Study (GICC); International Lung Cancer Consortium (ILCCO); Integrative Analysis of Lung Cancer Etiology and Risk (INTEGRAL) Consortium; International Consortium of Investigators Working on Non-Hodgkin's Lymphoma Epidemiologic Studies (InterLymph); Ovarian Cancer Association Consortium (OCAC); Oral Cancer GWAS; Pancreatic Cancer Case-Control Consortium (PanC4); Pancreatic Cancer Cohort Consortium (PanScan) (including **Zhong J**); Prostate Cancer Association Group to Investigate Cancer Associated Alterations in the Genome (PRACTICAL); Renal Cancer GWAS; Testicular Cancer Consortium (TECAC), Chanock SJ, Chatterjee N, Garcia-Closas M. Assessment of Polygenic Architecture and Risk Prediction based on Common Variants Across Fourteen Cancers. *Nature Communications*, 2020, 11:3353.
 10. Lin Y, Nakatochi M, Hosono Y, Ito H, Kamatani Y, Inoko A, Sakamoto H, Kinoshita F, Kobayashi Y, Ishii H, Ozaka M, Sasaki T, Matsuyama M, Sasahira N, Morimoto M, Kobayashi S, Fukushima T, Ueno M, Ohkawa S, Egawa N, Kuruma S, Mori M, Nakao H, Adachi Y, Okuda M, Osaki T, Kamiya S, Wang C, Hara K, Shimizu Y, Miyamoto T, Hayashi Y, Ebi H, Kohmoto T, Imoto I, Kasugai Y, Murakami Y, Akiyama M, Ishigaki K, Matsuda K, Hirata M, Shimada K, Okusaka T, Kawaguchi T, Takahashi M, Watanabe Y, Kuriki K, Kadota A, Okada R, Mikami H, Takezaki T, Suzuki S, Yamaji T, Iwasaki M, Sawada N, Goto A, Kinoshita K, Fuse N, Katsuoka F, Shimizu A, Nishizuka SS, Tanno K, Suzuki K, Okada Y, Horikoshi M, Yamauchi T, Kadowaki T, Yu H, **Zhong J**, Amundadottir LT, Doki Y, Ishii H, Eguchi H, Bogumil D, Haiman CA, Le Marchand L, Mori M, Risch H, Setiawan VW, Tsugane S, Wakai K, Yoshida T, Matsuda F, Kubo M, Kikuchi S, Matsuo K. Genome-wide association meta-analysis identifies *GP2* gene risk variants for pancreatic cancer. *Nature Communications*, 2020, 11:3175.

11. Huang H^(#), Ding N^(#), Yang T^(#), Li C^(#), Jia X^(#), Wang G^(#), **Zhong J**, Zhang J, Jiang G, Wang S, Zong Z, Jing W, Zhao Y, Xu S, Chen F. Cross-sectional Whole-genome Sequencing and Epidemiological Study of Multidrug-resistant *Mycobacterium tuberculosis* in China. *Clinical Infectious Diseases*, 2019, 69(3):405-413.
12. Klein AP, Wolpin BM, Risch HA, Stolzenberg-Solomon RZ, Mocci E, Zhang M, Canzian F, Childs EJ, Hoskins JW, Jermusyk A, **Zhong J**, Chen F, Albanes D, Andreotti G, Arslan AA, Babic A, Bamlet WR, Beane-Freeman L, Berndt SI, Blackford A, Borges M, Borgida A, Bracci PM, Brais L, Brennan P, Brenner H, Bueno-de-Mesquita B, Buring J, Campa D, Capurso G, Cavestro GM, Chaffee KG, Chung CC, Cleary S, Cotterchio M, Dijk F, Duell EJ, Foretova L, Fuchs C, Funel N, Gallinger S, M Gaziano JM, Gazouli M, Giles GG, Giovannucci E, Goggins M, Goodman GE, Goodman PJ, Hackert T, Haiman C, Hartge P, Hasan M, Hegyi P, Helzlsouer KJ, Herman J, Holcatova I, Holly EA, Hoover R, Hung RJ, Jacobs EJ, Jamroziak K, Janout V, Kaaks R, Khaw KT, Klein EA, Kogevinas M, Kooperberg C, Kulke MH, Kupcinskas J, Kurtz RJ, Laheru D, Landi S, Lawlor RT, Lee IM, LeMarchand L, Lu L, Malats N, Mambrini A, Mannisto S, Milne RL, Mohelníková-Duchoňová B, Neale RE, Neoptolemos JP, Oberg AL, Olson SH, Orlow I, Pasquali C, Patel AV, Peters U, Pezzilli R, Porta M, Real FX, Rothman N, Scelo G, Sesso HD, Severi G, Shu XO, Silverman D, Smith JP, Soucek P, Sund M, Talar-Wojnarowska R, Tavano F, Thornquist MD, Tobias GS, Van Den Eeden SK, Vashist Y, Visvanathan K, Vodicka P, Wactawski-Wende J, Wang Z, Wentzensen N, White E, Yu H, Yu K, Zeleniuch-Jacquotte A, Zheng W, Kraft P, Li D, Chanock S, Obazee O, Petersen GM, Amundadottir LT. Genome-wide meta-analysis identifies five new susceptibility loci for pancreatic cancer. *Nature Communications*, 2018, 9:556.
13. Yang T^(#), **Zhong J**^(#), Zhang J^(#), Li C^(#), Yu X^(#), Xiao J, Jia X, Ding N, Ma G, Wang G, Yue L, Liang Q, Sheng Y, Sun Y, Huang H, Chen F. Pan-genomic study of *Mycobacterium tuberculosis* reflecting the primary/secondary genes, generality/individuality, and the interconversion through copy number variations. *Frontiers in Microbiology*, 2018, 9:1886.
14. Zhang L^(#), **Zhong J**^(#), Liu H, Xin K, Chen C, Li Q, Wei Y, Wang Y, Chen F^(*), Shen X^(*). Complete genome sequence of the drought resistance-promoting endophyte *Klebsiella* sp. LTGP AF-6F. *Journal of Biotechnology*, 2017, 246: 36-39.
15. Zhu L^(#), **Zhong J**^(#), Jia X^(#), Liu G^(#), Kang Y^(#), Dong M, Zhang X, Li Q, Yue L, Li C, Fu J, Xiao J, Yan J, Zhang B, Lei M, Chen S, Lv L, Zhu B, Huang H^(*), Chen F^(*). Precision methylome characterization of *Mycobacterium tuberculosis* complex (MTBC) using PacBio single-molecule real-time (SMRT) technology. *Nucleic Acids Research*, 2016, 44, 730-743.
16. Hao L^(#), Xia L^(#), Huang D^(#), Yang L^(#), Xu X^(#), Yan W^(#), Zhang Y^(#), Zou D^(#), Liu S^(#), Sang J, Deng W, Wang Y, Cheng H, Ma L, Yuan F, **Zhong J**, Li Q, Wu S, He Z, Luo Y, Wang X, Ji Z, Wang X, Xue Y, Chen L, Xiao J, Zhao W, Chen F, Zhang H^(*), He H^(*), Hu S^(*), Zhang Z^(*). Information Commons for Rice (IC4R). *Nucleic Acids Research*, 2016, 44(D1):D1172-D1180.
17. Wang FQ^(#), **Zhong J**^(#), Zhao Y, Xiao J, Liu J, Dai M, Zheng G, Zhang L, Yu J, Wu J^(*), Duan B^(*). Genome sequencing of high-penicillin producing industrial strain of *Penicillium chrysogenum*. *BMC Genomics* 2014, 15 S1:S11.
18. Ling Y^(#), Jin Z^(#), Su M, **Zhong J**, Zhao Y, Yu J^(*), Wu J^(*), Xiao J^(*). VCGDB: a dynamic genome database of the Chinese population. *BMC Genomics* 2014, 15:265.
19. Wu J, Xiao J, Wang L, **Zhong J**, Yin H, Wu S, Zhang Z, Yu J. Systematic analysis of intron size and abundance parameters in diverse lineages. *Sci China Life Sci*, 2013, 56: 1–7.

PUBLICATIONS FOR CONFERENCES:

1. O'Brien A, Hoskins JW, Eiser DR, Connelly KE, **Zhong J**, Andresson T, Collins I, Pancreatic Cancer Cohort Consortium, Pancreatic Cancer Case-Control Consortium, Chanock SJ, Klein AP, Arda HE, Amundadottir LT. Uncovering the functional variants and target genes of the 7q32 pancreatic cancer risk locus. Proceedings of the American Association for Cancer Research Virtual Special Conference on Pancreatic Cancer (AACR). *Cancer Research*, 2022; 82(12_Suppl).
2. Jermusyk A, **Zhong J**, Gordon N, Connelly K, Perera S, Abdolalizadeh E, Zhang T, O'Brien A, Hoskins J, Collins I, Eiser D, Yuan C, Risch G, Jacobs EJ, Li D, Du M, Stolzenberg-Solomon R, Klein AP, Smith J, Wolpin BM, Chanock SJ, Shi J, Petersen GM, Westlake C, Amundadottir LT. An exception to the rule: A coding functional variant at a pancreatic cancer GWAS locus. Proceedings of the American Association for Cancer Research Virtual Special Conference on Pancreatic Cancer (AACR). *Cancer Research*, 2020;80(22 Suppl).
3. **Zhong J**, Jermusyk A, Wu L, Hoskins JW, Collins I, Zhang M, Lei S, Chung CC, Zhang T, Xiao W, Stolzenberg-Solomon R, Klein AP, Wolpin BM, Shu XO, Chanock SJ, Olson S, Chatterjee N, Smith J, Shi J, Kraft P, Petersen GM, Zheng W, Amundadottir LT. Large-scale transcriptome-wide association study identifies novel candidate susceptibility genes for pancreatic cancer. Proceedings of the American Association for Cancer Research Annual Meeting (AACR). *Cancer Research*, 2019; 79(13 Suppl).

MANUSCRIPT IN PREPARATION:

1. **Zhong J**^(#), O'Brien A^(#), Eiser D, Collins I, Connelly K, Shen T, Zhao Y, Wang L, Guo K, TruongVo T, Wells A, Grant S, Arda E, Shi J, Hoskins J^(§), Amundadottir L^(§). Identifying noncoding somatic driver mutations in regulatory elements for pancreatic cancer.

SUBMITTED MANUSCRIPT:

1. Ni Z, Kundu P, McKean D, Wheeler W, Albanes D, Andreotti G, Antwi SO, Arslan AA, Bamlet WR, Beane-Freeman L, Berndt SI, Bracci PM, Brennan P, Buring J, Chanock SJ, Gallinger S, Gaziano JM, Giles GG, Giovannucci E, Goggins M, Goodman PJ, Haiman C, Hassan M, Holly EA, Hung RJ, Katzke V, Kooperberg C, Kraft P, LeMarchand L, Li D, McCullough ML, Milne RL, Moore S, Neale RE, Oberg AL, Patel AV, Peters U, Rabe KG, Risch H, Shu X, Smith-Byrne K, Visvanathan K, Wactawski-Wende J, White E, Wolpin BM, Yu H, Zeleniuch-Jacquotte A, Zheng W, **Zhong J**, Amundadottir LT, Stolzenberg-Solomon RZ, Klein AP. Genome-wide analysis to assess if heavy alcohol consumption modifies the association between SNPs and pancreatic cancer risk. (Submitted to *Clinical Gastroenterology and Hepatology* on Sep. 11th, 2023).

PRESENTATIONS:

Oral:

1. **Identifying noncoding somatic driver mutations in pancreatic cancer.** Presented at NCI DCEG Early Career Scientist seminar, virtually, March 2023.
2. **Pancreatic Cancer Cohort Consortium (PanScan IV) Update.** Presented at Pancreatic Cancer Case-Control Consortium (PanC4) virtual annual meeting, virtually, December 2022.
3. **Identifying non-coding somatic driver mutations in regulatory elements for pancreatic cancer.** Presented (Platform) at American Society of Human Genetics (ASHG) annual meeting, Los Angeles, October 2022.
4. **Pancreatic Cancer Cohort Consortium (PanScan) IV GWAS update.** Presented in the FinnGen Scientific Committee/Analysis group meeting, virtually, January 2022.
5. **PanScan update and preliminary results for PANDORA and Asian GWAS scans.** Presented in the PanScan cohort consortium annual meeting, virtually, October 2021.

6. **Uncovering the dark matter of pancreatic cancer: noncoding somatic driver mutations in regulatory elements.** Presented in the CRL (Consolidated Research Laboratory) seminar, Division of Cancer Epidemiology and Genetics (DCEG, NCI), virtually. September 2020.
7. **Large-scale Transcriptome-Wide Association Study (TWAS) Identifies Novel Candidate Susceptibility Genes for Pancreatic Cancer.** Presented in the 11th Annual Division of Cancer Epidemiology and Genetics (DCEG, NCI) Fellows' Training Symposium, Bethesda, MD. April 2019.
8. **A Transcriptome-Wide Association Study (TWAS) Identifies Novel Candidate Susceptibility Genes for Pancreatic Cancer.** Presented at the LTG (Laboratory of Translational Genomics) seminar, Division of Cancer Epidemiology and Genetics (DCEG, NCI), Gaithersburg, MD. February 2019.
9. **Genome sequencing of high-penicillin producing industrial strain of *Penicillium chrysogenum*.** Invited Speaker at the twelfth Asia Pacific Bioinformatics Conference, Shanghai, China. January 2014. (**Best Paper Award** in the conference)

Poster (select):

1. O'Brien A, Kong H, Patel M, Connelly K, Xu M, Collins I, **Zhong J**, Hoskins J, Ho M, Papenberg B, Patel H, Luong T, International Lung Cancer Consortium (ILCCO), Bladder Cancer Consortium, The Pancreatic Cancer Case-Control Consortium (PanC4), The Pancreatic Cancer Cohort Consortium (PanScan), Melanoma Meta-Analysis Consortium, Iles M, Law M, Landi MT, Stolzenberg-Solomon R, Wolpin B, Orr N, Klein A, Li D, Luo W, Jones K, Lindstroem S, Stern MH, Chanock S, Shi J, Prokunina-Olsson L, Choi J, Brown K, Amundadottir L. *Unravelling Pan-Cancer Susceptibility at 5p15.33: Functional Characterization of a Novel VNTR Variant*. American Society of Human Genetics (ASHG) annual meeting, Washington DC, November 2023.
2. Prasad G, Truongvo T, **Zhong J**, Hoskins J, Amundadottir LT, Arda EH. *Cell type-specific effects of common germline variation on gene expression and pancreatic cancer risk*. American Society of Human Genetics (ASHG) annual meeting, Washington DC, November 2023.
3. Connelly K, Abdolalizadeh E, **Zhong J**, Eiser D, Hoskins J, O'Brien A, Jermusyk A, Collins I, Pancreatic Cancer Cohort Consortium (PanScan), Pancreatic Cancer Case-Control Consortium (PanC4), Stolzenberg-Solomon R, Klein A, Shi J, Wolpin B, Smith J, Petersen G, Amundadottir L. *Functional characterization of the 1p36.33 pancreatic cancer GWAS locus*. American Society of Human Genetics (ASHG) annual meeting, Los Angeles, October 2022.
4. **Zhong J**, Eiser D, Brien A, Connelly K, Hoskins J, Jermusyk A, Collins I, Shen T, Zhao Y, Li Wang3, Guo K, TruongVo T, Wildenthal J, McKinnon K, Wells A, Grant S, Arda E, Shi J, Amundadottir L. *Uncovering the dark matter of pancreatic cancer: identifying driver mutations in non-coding gene regulatory elements*. Presented at American Society of Human Genetics virtual meeting (ASHG), October 2020. [**Reviewers' Choice award, top 10%**]
5. **Zhong J**, Jermusyk A, Wu L, Hoskins J, Collins I, Zhang M, Lei S, Chung C, Zhang T, Xiao W, Stolzenberg-Solomon R, Klein A, Wolpin B, Shu X, Chanock S, Olson S, Chatterjee N, Smith J, Jianxin Shi, Kraft P, Petersen G, Zheng W, Amundadottir L. *Large-scale transcriptome-wide association study (TWAS) identifies novel candidate susceptibility genes for pancreatic cancer*. Presented at American Association for Cancer Research Annual Meeting (AACR), Atlanta, GA. March 2019.
6. Eiser D, Hoskins J, **Zhong J**, Jermusyk A, Collins I, Mobaraki M, Amundadottir L. *Mapping the Epigenomic Landscape of Pancreatic Cell Lines for Post-GWAS Functional Studies*. Presented at NIH Postbac Poster Day, Bethesda, MD. May 2019.
7. **Zhong J**, Wu L, Jermusyk A, Hoskins J, Collins I, Zhang M, Lei S, Chung C, Zhang T, Xiao W, PanScan, PanC4, Stolzenberg-Solomon R, Klein A, Wolpin B, Brown K, Shu X, Chanock S, Olson S, Chatterjee

- N, Petersen G, Smith J, Shi J, Kraft P, Zheng W, Amundadottir L. A *Transcriptome-wide association study for pancreatic cancer*. Presented at American Society of Human Genetics annual meeting (ASHG), San Diego, CA. October 2018.
8. Mavura Y, **Zhong J**, Chung C, Hoskins J, Jermusyk A, Collins I, PanC4, Chanock S, Yu K, S Stolzenberg-Solomon R, Wolpin B, Lin D, Wu C, Low S, Sakamoto H, Risch H, Amundadottir L. *Genome-wide Association Study to identify Risk Loci for Pancreatic Cancer in Asian*. Presented at NIH summer poster day, Bethesda, MD. August 2018.

PROFESSIONAL MEMBERSHIP/ROLE:

- Gold member in American Association for the Advancement of Science (AAAS) 2023 - present
- Member in American Society of Human Genetics 2022 - present
- Review Committee Member in DCEG Fellows Award for Research Excellence competition (DFARE) 2019
- Associate Member in American Association for Cancer Research 2018 - 2020
- Member in Tumor Microenvironment Group of the AACR 2018 - 2019
- Planning Committee Member in 10th Annual NCI DCEG Fellows' Training Symposium 2017 - 2018
- Member in American Society of Human Genetics 2017 - 2018

PROFESSIONAL JOURNAL SERVICE:

Editorial Service:

- Youth Editor in *The Innovation* 2022 - present
- Associate Editor in *Frontiers in Oncology*. 2021 - present

Reviewer Service (select):

Nature Communications, Genome Biology, BMC Medicine, eLife, The Innovation, Molecular Oncology, Molecular Cancer, Cancer Letters.

Full peer-review and editor records have been publicly verified by [Web of Science](#). 43 times reviewing and 12 times editing by Nov. 30th, 2023.

MENTORSHIP:

- A Ph. D candidate, Morehouse School of Medicine, summer intern
Project: *Uncovering the dark matter of pancreatic cancer by assessing non-coding regulatory variations.*
2019
- A M.S candidate, Georgia Institute of Technology, summer intern
Project: *Genome-wide association study to identify risk loci for pancreatic cancer in Asian.*
2018
- 2 Ph. D candidates, Beijing Institute of Genomics, University of Chinese Academy of Sciences
Projects: *The methylome and pan-genome analysis of Mycobacterium tuberculosis complex*
2014-2016