

# CURRICULUM VITAE

Personal Information			
Name	Jing Gong	Gender	Female
Position Title	Professor		
Working Department	Department of bioinformatics, College of informatics		
Email	Gong.jing@mail.hzau.edu.cn		
Address	No.1,Shizishan Street, Hongshan District, Wuhan P.R.China		
Tel	8618971176892	Fax	
Research Interest			
<p><b>Our research interests mainly focus on:</b> Functional prediction of genetic variant, database construction, tumor-associated molecular epidemiology, and large-scale data integration, analysis and mining.</p>			
Professional Memberships			
Other Roles			
Education & Working Experience			
10/2018-present	<b>Professor in Bioinformatics</b> , College of Informatics, Huazhong Agricultural University, Wuhan, China		
05/2018-09/2018	<b>Associate professor</b> , School of public health, Huazhong University of Science & Technology, Wuhan, China		
04/2016-04/2018	<b>Post-doctoral Research Fellow</b> , University of Texas Health Science Center at Houston Medical School, USA		
07/2013-03/2016	<b>Post-doctoral Research Fellow/ Lecturer</b> , School of public health, Huazhong University of Science & Technology, Wuhan, China		
09/2008-06/2013	<b>Ph.D.</b> in Bioinformatics, Huazhong University of Science & Technology, Wuhan, China		
09/2003-06/2008	<b>Bachelor</b> of medicine in Public Health, Huazhong University of Science & Technology, Wuhan, China		



## Publications

1. Yingjie Gao, Guanghui Jiang, Wenqian Yang, Weiwei Jin, **Jing Gong\***, Xuewen Xu\*, Xiaohui Niu\*. (2023) Animal-SNPAtlas: a comprehensive SNP database for multiple animals, *Nucleic Acids Research*, 51(D1), D816–D826.
2. Yanbo Yang, Dongyang Wang, Ya-Ru Miao, Xiaohong Wu, Haohui Luo, Wen Cao, Wenqian Yang, Jianye Yang, An-Yuan Guo\*, **Jing Gong\***. (2023) lncRNASNP v3: an updated database for functional variants in long non-coding RNAs, *Nucleic Acids Research*, 51(D1), D192-D198.
3. Dongyang Wang, Wen Cao, Wenqian Yang, Weiwei Jin, Haohui Luo, Xiaohui Niu\*, **Jing Gong\***. (2022) Pancan-MNVQTLdb: systematic identification of multi-nucleotide variant quantitative trait loci in 33 cancer types, *NAR Cancer*, 4(4), zcac043.
4. Yanbo Yang, Xiaohong Wu, Wenqian Yang, Weiwei Jin, Dongyang Wang, Jianye Yang, Guanghui Jiang, Wen Zhang, Xiaohui Niu, **Jing Gong\***. (2022) Dynamic alternative polyadenylation during iPSC differentiation into cardiomyocytes, *Comput Struct Biotechnol J*, 20, 5859-5869.
5. Dongyang Wang, Xiaohong Wu, Guanghui Jiang, Jianye Yang, Zhanhui Yu, Yanbo Yang, Wenqian Yang, Xiaohui Niu\*, Ke Tang\*, **Jing Gong\***. (2022) Systematic analysis of the effects of genetic variants on chromatin accessibility to decipher functional variants in non-coding regions, *Front Oncol*, 12, 1035855.
6. Weiwei Jin, Guanghui Jiang, Yanbo Yang, Jianye Yang, Dongyang Wang, Xiaohui Niu, Rong Zhong\*, Zhao Zhang\*, **Jing Gong\***. (2022) Animal-eRNADB: a comprehensive animal enhancer RNA database. *Nucleic Acids Research*. 50(D1), D46-D53.
7. Jiang Li, Yawen Xue, Muhammad Talal Amin, Yanbo Yang, Jiajun Yang, Wen Zhang, Wenqian Yang, Xiaohui Niu, Hong-Yu Zhang, and **Jing Gong\***. ncRNA-eQTL: a database to systematically evaluate the effects of SNPs on non-coding RNA expression across cancer types. *Nucleic acids research*. (2020) 48, D956-D963.
8. Yanbo Yang, Qiong Zhang, Ya-Ru Miao, Jiajun Yang, Wenqian Yang, Fangda Yu, Dongyang Wang, An-Yuan Guo\*, and **Jing Gong\***. SNP2APA: a database for evaluating effects of genetic variants on alternative polyadenylation in human cancers. *Nucleic acids research*. (2020) 48, D226-D232.
9. **Gong, J.#**, Tian, J.#, Li, J., Gong, Y., Yang, Y., Zhu, Y., Zhang, Y., Zhong, R., Chang, J., Miao, X. A polymorphic MYC response element in KBTBD11 influences colorectal cancer risk, especially in interaction with a MYC regulated SNP rs6983267. *Annals of oncology*. (2018) 29(3), 632-639.
10. **Gong, J.#**, Li, Y.#, Liu, C.J.#, Xiang, Y., Li, C., Ye, Y., Zhang, Z., Hawke, D.H., Park, P.K., Diao, L., Putkey, J.A., Yang, L., Guo, A.Y., Lin, C. and Han, L. A Pan-cancer Analysis of the Expression and Clinical Relevance of Small Nucleolar RNAs in Human Cancer. *Cell reports*, (2017) 21, 1968-1981.
11. **Gong, J.**, Mei, S., Liu, C., Xiang, Y., Ye, Y., Zhang, Z., Feng, J., Liu, R., Diao, L., Guo, A.Y., Miao, X., and Han, L. PancanQTL: systematic identification of cis-eQTLs and trans-eQTLs in

- 33 cancer types, **Nucleic Acids Research**. (2018) 46, D971-D976.
12. Yang J, Wang D, Yang Y, Jin W, Niu X\*, **Gong J\***. A systematic comparison of normalization methods for eQTL analysis. **Briefings in Bioinformatics**. 2021 May.
  13. Jin W., Zhu Q., Yang Y., Yang W., Wang D., Yang J., Niu X., Yu D.\*, and **Gong J\***. Animal-APAdb: a comprehensive animal alternative polyadenylation database. **Nucleic acids research**. (2021) 49, D47-D54.
  14. Gao Y., Yang Z., Yang W., Yang Y., **Gong J.\***, Yang Q. Y.\*, and Niu X\*. Plant-ImputeDB: an integrated multiple plant reference panel database for genotype imputation. **Nucleic acids research**. (2021) 49, D1480-D1488.
  15. Wenqian Yang, Yanbo Yang, Cecheng Zhao, Kun Yang, Dongyang Wang, Jiajun Yang, Xiaohui Niu\*, and **Jing Gong\***. Animal-ImputeDB: a comprehensive database with multiple animal reference panels for genotype imputation. *Nucleic acids research*. (2020) 48, D659-D667.
  16. Jianbo Tian#, Jiang Chang#, **Jing Gong#**, Jiao Lou, Mingpeng Fu, Jiaoyuan Li, Juntao Ke, Ying Zhu, Yajie Gong, Yang Yang, Danyi Zou, Xiating Peng, Nan Yang, Shufang Mei, Xiaoyang Wang, Rong Zhong, Kailin Cai, and Xiaoping Miao\*. Systematic functional interrogation of genes in GWAS loci identified ATF1 as a key driver in colorectal cancer modulated by a promoter-enhancer interaction. **The American Journal of Human Genetics**. (2019) 105, 29-47.
  17. **Gong, J.**, Liu, C., Liu, W., Xiang, Y., Diao, L., Guo, A.Y. and Han, L. (2017) LNCediting: a database for functional effects of RNA editing in lncRNAs. **Nucleic acids research**, 45, D79-D84.
  18. **Gong, J.**, Liu, W., Zhang, J., Miao, X. and Guo, A.Y. (2015) lncRNASNP: a database of SNPs in lncRNAs and their potential functions in human and mouse. **Nucleic acids research**, 43, D181-186.
  19. **Gong, J.**, Tong, Y., Zhang, H.M., Wang, K., Hu, T., Shan, G., Sun, J. and Guo, A.Y. (2012) Genome-wide identification of SNPs in microRNA genes and the SNP effects on microRNA target binding and biogenesis. **Human mutation**, 33, 254-263.