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**Education**

2009-2015 Ph.D. School of Life Sciences, Fudan University, Shanghai, China  
2005-2009 B.S. School of Life Sciences, Northeast Agricultural University, Harbin, China

**Present Position**

2019-2021 NIH supported training program in Computation and Informatics in Biology and Medicine, NIH/NLM  
2017-Pres Postdoctoral Research Fellow, Center for Precision Medicine Research, Marshfield Clinic Research Institute, Marshfield, WI

**Experience**

2015-2017 Postdoctoral Fellow, Department of Bioengineering, University of California, San Diego, CA  
2013-2014 Research Assistant, University of Texas Health Science Center at Houston, Houston, TX  
2012-2013 Visiting Scholar, University of Texas Health Science Center at Houston, Houston, TX  
2012-2013 Internship, CAS-MPG Partner Institute for Computational Biology, Shanghai, China  
2011-2014 Internship, Institute of Rheumatology, Immunology and Allergy, Shanghai, China

**Patents**

*Methods and kits for diagnosing of bladder cancer with urine exfoliated cell, China*  
*Methods and kits for prognosing of bladder cancer after surgery with urine exfoliated cell, China*  
*Methods for quantitative deconvolution and detection of heterogeneous nucleic acid sample, US (under review)*

**Awards and Honors**

2018 Computation and Informatics in Biology and Medicine, NIH/NLM grant  
2014 First Place Poster, 17th Annual Human and Molecular Genetics Symposium, GSBS, Houston, TX  
2012 Silver award of "Cup of Challenge" for College Students' Innovative Contest in Shanghai, China  
2009-2013 Model Student of Academic Records (2009, 2012, 2013, Fudan University), Shanghai, China  
2007 Second Prize of National Mathematical Modeling Contest in Heilongjiang province, Harbin, China  
2007 Social Practice Scholarship (NEAU), Harbin, China  
2006 National Encouragement Scholarship, Harbin, China  
2005-2007 Model Student of Academic Records (NEAU), Harbin, China  
2005 National Scholarship (NEAU), Harbin, China

**Ph.D. Dissertation**

Cancer Biomarker Research Based on Genome-wide DNA methylation Profile: Diagnosis and Prognosis, 2015.  
Supervisor: Dr. Li Jin, MOE Key Laboratory of Contemporary anthropology, Fudan University

**Publications**

S. Guo, S. Jiang, N. Epperla, Y. Ma, M. Maadooliat, Z. Ye, B. Olson, M. Wang, T. Kitchner, J. Joyce, R. Stenn, J.J. Mazza, J.K. Meece, W. Wu, L. Jin, J.A. Smith, J. Wang, S.J. Schrodi. A Gene-Based Recessive Diplotype Exome Scan Discovers FGF6, a Novel Hepcidin-Regulating Iron Metabolism Gene. *Blood* (Accepted)

1. Xu, X.-H., Y. Bao, X. Wang, F. Yan, **S. Guo**, Y. Ma, D. Xu, L. Jin, J. Xu, J. Wang (2018) Hypoxic-Stabilized Epas1 Proteins Transactivate Dnmt1 and Cause Promoter Hypermethylation and Transcription Inhibition of Epas1 in Non-Small Cell Lung Cancer. *The FASEB Journal*, 2018: p. fj. 201700715.
2. Wang, C., W. Pu, D. Zhao, Y. Zhou, T. Lu, S. Chen, Z. He, X. Feng, Y. Wang, C. Li, S. Li, **S. Guo**<sup>#</sup>, J Wang<sup>#</sup>, M Wang<sup>#</sup>. (2018) Identification of Hyper-Methylated Tumor Suppressor Genes-Based Diagnostic Panel for Esophageal Squamous Cell Carcinoma (Escc) in a Chinese Han Population. *Front Genet*, 9:356.

3. Feng, W., X. Guo, H. Huang, C. Xu, Y. Li, **S. Guo**, Z. Zhao, Q. Li, D. Lu, L. Jin (2018) Polymorphism Rs3819102 in Thymidylate Synthase and Environmental Factors: Effects on Lung Cancer in Chinese Population. *Current Problems in Cancer* [Jul 21, Epub ahead of print].
4. Pu, W., C. Wang, S. Chen, D. Zhao, Y. Zhou, Y. Ma, Y. Wang, C. Li, Z. Huang, L. Jin, **S. Guo**<sup>#</sup>, J. Wang<sup>#</sup>, M. Wang<sup>#</sup> (2017) Targeted Bisulfite Sequencing Identified a Panel of DNA Methylation-Based Biomarkers for Esophageal Squamous Cell Carcinoma (ESCC). *Clinical Epigenetics*, 9:129.
5. Lei, Y., L. Liu, S. Zhang, **S. Guo**, X. Li, J. Wang, B. Su, Y. Fang, X. Chen, H. Ke (2017) Hdac7 Promotes Lung Tumorigenesis by Inhibiting Stat3 Activation. *Molecular cancer*, 16(1):170.
6. He, D., J. Liu, Y. Hai, Q. Zhu, Y. Shen, **S. Guo**, W. Zhang, X. Zhou (2017) Increased Dot1l in Synovial Biopsies of Patients with Oa and Ra. *Clin Rheumatol*, 37:1327-1332
7. **Guo, S.**, Q. Zhu, T. Jiang, R. Wang, Y. Shen, X. Zhu, Y. Wang, F. Bai, Q. Ding, X. Zhou (2017) Genome-Wide DNA Methylation Patterns in Cd4+ T Cells from Chinese Han Patients with Rheumatoid Arthritis. *Mod Rheumatol*, 27:441-447.
8. **Guo, S\***, D. Diep\*, N. Plongthongkum, H.-L. Fung, K. Zhang, K. Zhang (2017) Identification of Methylation Haplotype Blocks Aids in Deconvolution of Heterogeneous Tissue Samples and Tumor Tissue-of-Origin Mapping from Plasma DNA. *Nature Genetics*, 49(4):635-642.
9. Geng, X., W. Pu, Y. Tan, Z. Lu, A. Wang, L. Tan, S. Chen, **S. Guo**<sup>#</sup>, J. Wang<sup>#</sup>, X. Chen<sup>#</sup> (2017) Quantitative Assessment of the Diagnostic Role of Fhit Promoter Methylation in Non-Small Cell Lung Cancer. *Oncotarget*, 8(4):6845.
10. Fan, L., L. Chen, X. Ni, **S. Guo**, Y. Zhou, C. Wang, Y. Zheng, F. Shen, V.K. Kolluri, M. Muktiali (2017) Genetic Variant of Mir-4293 Rs12220909 Is Associated with Susceptibility to Non-Small Cell Lung Cancer in a Chinese Han Population. *PLoS One*, 12(4):e0175666.
11. Ding, W., W. Pu, L. Wang, S. Jiang, X. Zhou, W. Tu, L. Yu, J. Zhang, **S. Guo**, Q. Liu (2017) Genome-Wide DNA Methylation Analysis in Systemic Sclerosis Reveals Hypomethylation of IFN-Associated Genes in Cd4+ and Cd8+ T Cells. *Journal of Investigative Dermatology*, 138:1069-1077.
12. Zhang, X., J. Zhang, R. Wang, **S. Guo**, H. Zhang, Y. Ma, Q. Liu, H. Chu, X. Xu, Y. Zhang (2016) Hypermethylation Reduces the Expression of Pnpla7 in Hepatocellular Carcinoma. *Oncology letters*, 12(1):670-674.
13. Suzuki, K., Y. Tsunekawa, R. Hernandez-Benitez, J. Wu, ..., **S. Guo**, ...K. Zhang, J.C. Belmonte (2016) In Vivo Genome Editing Via Crispr/Cas9 Mediated Homology-Independent Targeted Integration. *Nature*, 540(7631):144-149.
14. Shen, F., J. Chen, **S. Guo**, Y. Zhou, Y. Zheng, Y. Yang, J. Zhang, X. Wang, C. Wang, D. Zhao (2016) Genetic Variants in Mir-196a2 and Mir-499 Are Associated with Susceptibility to Esophageal Squamous Cell Carcinoma in Chinese Han Population. *Tumor Biology*, 37(4):4777-4784.
15. Pu, W., X. Geng, S. Chen, L. Tan, Y. Tan, A. Wang, Z. Lu, **S. Guo**, X. Chen, J. Wang (2016) Aberrant Methylation of Cdh13 Can Be a Diagnostic Biomarker for Lung Adenocarcinoma. *J Cancer*, 7(15):2280.
16. **Guo, S.**, Y. Li, Y. Wang, H. Chu, Y. Chen, Q. Liu, G. Guo, W. Tu, W. Wu, H. Zou (2016) Copy Number Variation of Hla-Dqa1 and Apobec3a/3b Contribute to the Susceptibility of Systemic Sclerosis in the Chinese Han Population. *J Rheumatol*, 43(5):880-886.
17. Zhang, P., J. Wang, T. Lu, X. Wang, Y. Zheng, **S. Guo**, Y. Yang, M. Wang, V.K. Kolluri, L. Qiu (2015) Mir-449b Rs10061133 and Mir-4293 Rs12220909 Polymorphisms Are Associated with Decreased Esophageal Squamous Cell Carcinoma in a Chinese Population. *Tumor Biology*, 36(11):8789-8795.
18. Wang, J., J. Li, J. Gu, J. Yu, **S. Guo**, Y. Zhu, D. Ye (2015) Abnormal Methylation Status of Fbxw10 and Smpd3, and Associations with Clinical Characteristics in Clear Cell Renal Cell Carcinoma. *Oncology letters*, 10(5):3073-3080.
19. Pan, L.I., Y.M. Huang, M. Wang, X.E. Zhuang, D.F. Luo, **S. Guo**, Z.S. Zhang, Q. Huang, S.L. Lin, and S.Y. Wang (2015) Positional Cloning and Next-Generation Sequencing Identified a Tgm6 Mutation in a Large Chinese Pedigree with Acute Myeloid Leukaemia. *European Journal of Human Genetics*, 23(2):218-223.
20. Lin, N., J. Jiang, **S. Guo**, M. Xiong (2015) Functional Principal Component Analysis and Randomized Sparse Clustering Algorithm for Medical Image Analysis. *PLoS One*, 10(7):e0132945.

21. Jiang, J., N. Lin, **S. Guo**, J. Chen, M. Xiong (2015) Multiple Functional Linear Model for Association Analysis of Rna-Seq with Imaging. *Quantitative biology* (Beijing, China), 3(2):90.
22. **Guo, S.**, F. Yan, J. Xu, Y. Bao, J. Zhu, X. Wang, J. Wu, Y. Li, W. Pu, Y. Liu (2015) Identification and Validation of the Methylation Biomarkers of Non-Small Cell Lung Cancer (NSCLC). *Clinical Epigenetics*, 7(1):3.
23. **Guo, S.**, T. Jiang, R. Wang, Y. Shen, X. Zhu, F. Bai, Q. Ding, G. Chen, D. He (2105) Genome-Wide Dna Methylation Patterns in Cd4+ T Reveal Significant Contribution of Dna Methylation to Rheumatoid Arthritis. *Arthritis & Rheumatology*, 67:1596-1597.
24. Dong, Z., **S. Guo**, Y. Yang, J. Wu, M. Guan, H. Zou, L. Jin, J. Wang (2015) Association between Abcg2 Q141k Polymorphism and Gout Risk Affected by Ethnicity and Gender: A Systematic Review and Meta-Analysis. *Int J Rheum Dis*, 18(4):382-391.
25. Zhao, Y., F. Xue, J. Sun, **S. Guo**, H. Zhang, B. Qiu, J. Geng, J. Gu, X. Zhou, W. Wang (2014) Genome-Wide Methylation Profiling of the Different Stages of Hepatitis B Virus-Related Hepatocellular Carcinoma Development in Plasma Cell-Free DNA Reveals Potential Biomarkers for Early Detection and High-Risk Monitoring of Hepatocellular Carcinoma. *Clinical Epigenetics*, 6(1):30.
26. Zhao, Y., J. Sun, H. Zhang, **S. Guo**, J. Gu, W. Wang, N. Tang, X. Zhou, J. Yu (2014) High-Frequency Aberrantly Methylated Targets in Pancreatic Adenocarcinoma Identified Via Global DNA Methylation Analysis Using Methylcap-Seq. *Clinical Epigenetics*, 6(1):18.
27. Xiao, Q., S. Gao, H. Luo, W. Fan, **S. Guo**, H. Yao, S. Leng, Z. Xu, T. Tao, X. Liu (2014) 9q33.3, a Stress-Related Chromosome Region, Contributes to Reducing Lung Squamous Cell Carcinoma Risk. *Journal of Thoracic Oncology*, 9(7):1041-1047.
28. Wang, R., J. Zhang, Y. Ma, L. Chen, **S. Guo**, X. Zhang, Y. Ma, L. Wu, X. Pei, S. Liu (2014) Association Study of Mir-149 Rs2292832 and Mir-608 Rs4919510 and the Risk of Hepatocellular Carcinoma in a Large -Scale Population. *Molecular Medicine Reports*, 10(5):2736-2744.
29. Song, X., **S. Guo**, Y. Chen, C. Yang, H. Ji, F. Zhang, Z. Jiang, Y. Ma, Y. Li, L. Jin (2014) Association between Hla-Dqa1 Gene Copy Number Polymorphisms and Susceptibility to Rheumatoid Arthritis in Chinese Han Population. *Journal of Genetics*, 93(1): 215-218.
30. Huang, L\*, Y. Li\*, **S. Guo\***, Y. Sun, C. Zhang, Y. Bai, S. Li, F. Yang, M. Zhao, B. Wang (2014) Different Hereditary Contribution of the Cfh Gene between Polypoidal Choroidal Vasculopathy and Age-Related Macular Degeneration in Chinese Han Peoplehereditary Contribution of Cfh in Pcv and Amd. *Investigative Ophthalmology & Visual Science*, 55(4):2534-2538.
31. He, D., J. Wang, L. Yi, X. Guo, **S. Guo**, G. Guo, W. Tu, W. Wu, L. Yang, R. Xiao (2014) Association of the Hla-Drb1 with Scleroderma in Chinese Population. *PLoS One*, 9(9):e106939.
32. **Guo, S.**, Y.L. Wang, Y. Li, L. Jin, M. Xiong, Q.H. Ji, J. Wang (2014) Significant Snps Have Limited Prediction Ability for Thyroid Cancer. *Cancer Med*, 3(3):731-735.
33. **Guo, S.**, L. Tan, W. Pu, J. Wu, K. Xu, J. Wu, Q. Li, Y. Ma, J. Xu, L. Jin (2014) Quantitative Assessment of the Diagnostic Role of Apc Promoter Methylation in Non-Small Cell Lung Cancer. *Clinical Epigenetics*, 6(1):5.
34. Zhao, Y., H. Zhou, K. Ma, J. Sun, X. Feng, J. Geng, J. Gu, W. Wang, H. Zhang, Y. He, **S. Guo**, X. Zhou, J. Yu, Q. Lin (2013) Abnormal Methylation of Seven Genes and Their Associations with Clinical Characteristics in Early Stage Non-Small Cell Lung Cancer. *Oncology Letters*, 5(4):1211-1218.
35. Wu, L., **S. Guo**, D. Yang, Y. Ma, H. Ji, Y. Chen, J. Zhang, Y. Wang, L. Jin, and J. Wang (2013) Copy Number Variations of Hla-Drb5 Is Associated with Systemic Lupus Erythematosus Risk in Chinese Han Population. *Acta Biochim Biophys Sin*, 46(2):155-160.
36. Wang, Y.L., S.H. Feng, **S. Guo**, W.J. Wei, D.S. Li, Y. Wang, X. Wang, Z.Y. Wang, Y.Y. Ma, L. Jin (2013) Confirmation of Papillary Thyroid Cancer Susceptibility Loci Identified by Genome-Wide Association Studies of Chromosomes 14q13, 9q22, 2q35 and 8p12 in a Chinese Population. *J Med Genet*, p. jmedgenet-2013-101687.
37. Wang, X., L. Wang, **S. Guo**, Y. Bao, Y. Ma, F. Yan, K. Xu, Z. Xu, L. Jin, D. Lu (2013) Hypermethylation Reduces Expression of Tumor-Suppressor Plzf and Regulates Proliferation and Apoptosis in Non-Small-Cell Lung Cancers. *The FASEB Journal*, 27(10):4194-4203.

38. Wang, J., Y. Yang, **S. Guo**, Y. Chen, C. Yang, H. Ji, X. Song, F. Zhang, Z. Jiang, Y. Ma (2013) Association between Copy Number Variations of Hla-Dqa1 and Ankylosing Spondylitis in the Chinese Han Population. *Genes Immun*, 14(8):500-503.
39. Lin, S., L. Pan, **S. Guo**, J. Wu, L. Jin, J.C. Wang, S. Wang (2013) Prognostic Role of MicroRNA-181a/B in Hematological Malignancies: A Meta-Analysis. *PLoS One*, 8(3):e59532.
40. Zhao, Y., **S. Guo**, J. Sun, Z. Huang, T. Zhu, H. Zhang, J. Gu, Y. He, W. Wang, K. Ma (2012) Methylcap-Seq Reveals Novel DNA Methylation Markers for the Diagnosis and Recurrence Prediction of Bladder Cancer in a Chinese Population. *PLoS One*, 7(4):e35175.
41. Wu, J., J. Liu, Y. Zhou, J. Ying, H. Zou, **S. Guo**, L. Wang, N. Zhao, J. Hu, D. Lu (2012) Predictive Value of Xrcc1 Gene Polymorphisms on Platinum-Based Chemotherapy in Advanced Non-Small Cell Lung Cancer Patients: A Systematic Review and Meta-Analysis. *Clinical Cancer Research*, 18(14):3972-3981.
42. Wu, J., J. Wu, Y. Zhou, H. Zou, **S. Guo**, J. Liu, L. Lu, H. Xu (2011) Quantitative Assessment of the Variation in Igfbp2 Gene and Type 2 Diabetes Risk. *Acta Diabetologica*, 49 Suppl 1:S87-97.
43. He, Y., Y. Cui, W. Wang, J. Gu, **S. Guo**, K. Ma, X. Luo (2011) Hypomethylation of the Hsa-Mir-191 Locus Causes High Expression of Hsa-Mir-191 and Promotes the Epithelial-to-Mesenchymal Transition in Hepatocellular Carcinoma. *Neoplasia*, 13(9):841-853.
44. Zhou, X., J. Sun, Y. He, H. Zhang, J. Yu, **S. Guo**, Y. Cai, X. Hu, J. Zhu (2010) Correlation of the Methylation Status of CpG Islands in the Promoter Region of 10 Genes with the 5-Fu Chemoresensitivity in 3 Breast Cancer Cell Lines. *Zhonghua zhong liu za zhi [Chinese journal of oncology]*, 32(5):328.
45. Xiang, H., J. Zhu, Q. Chen, F. Dai, X. Li, M. Li, H. Zhang, G. Zhang, D. Li, Y. Dong, L. Zhao, Y. Lin, D. Cheong, J. Yu, J. Sun, X. Zhou, K. Ma, Y. He, Y. Zhao, **S. Guo**, M. Ye, G. Guo, Y. Li, R. Li, X. Zhang, L. Ma, K. Kristiansen, Q. Guo, J. Jiang, S. Beck, Q. Xia, W. Wang, J. Wang (2010) Single Base-Resolution Methylome of the Silkworm Reveals a Sparse Epigenomic Map. *Nature Biotechnology*, 28(5):516-520.
46. Li, Y., J. Zhu, G. Tian, N. Li, Q. Li, M. Ye, H. Zheng, J. Yu, H. Wu, J. Sun, H. Zhang, Q. Chen, R. Luo, M. Chen, Y. He, X. Jin, Q. Zhang, C. Yu, G. Zhou, J. Sun, Y. Huang, H. Zheng, H. Cao, X. Zhou, **S. Guo**, X. Hu, X. Li, K. Kristiansen, L. Bolund, J. Xu, W. Wang, R. Li, S. Beck, J. Wang, X. Zhang (2010) The DNA Methylome of Human Peripheral Blood Mononuclear Cells. *PLoS Biol*, 8(11):e1000533.
47. Ao, J.X., X.J. Gao, Y.B. Yu, B. Qu, X.H. Yuan, Y. Liu, **S. Guo** (2009) Construction of a General Standard Molecule for the Qualitative Detection in Different Transgenic Foodcrops. *Journal of Northeast Agricultural University (English Edition)*, 16(2):37-41.
48. Ao, J., X. Gao, Y. Qiu, **S. Guo** (2009) Real-Time Quantitative PCR and the Application in the Detection of Genetically Modified Plants [J]. *Journal of Northeast Agricultural University*, 6:033.
49. Ao, J.X., X.J. Gao, B. Qu, X.H. Yuan, Y. Liu, Y.W. Qiu, **S. Guo** (2008) Construction of a Standard Reference Plasmid for Detecting Exogenous Genes in Transgenic Soybean, Maize and Rice [J]. *Journal of China Agricultural University*, 6:005.

## Books and book Chapters

Tumor Suppressor Genes Mediated by DNA Hypermethylation, Tumor Suppressor Genes, IntechOpen (**preparing**)

## Conference

### Oral Presentation:

1. DNA Methylation Research in Rheumatology Arthritis: Promising and Challenging, AMRBSA, 2018, Shanghai

### Poster Presentation

2. **Guo S**, Li L, Jiang J, Lin N., Chen M. Jin L, Xiong M. (2014) A novel approach to methylation-Seq data analysis based on functional principle component analysis (FPCA) 2014, ASHG
3. **Guo S**, Xiong M, Jin L, Wang J. (2014). Epigenetic Approaches for non-small cell lung cancer diagnosis based on DNA methylation, HGV2014, Sep 17- Sep 19, Belfast, Northern Ireland, UK
4. Lin N, Jiang J, Guan X, Yu X, **Guo S** and Xiong MM. (2014). A novel method for ultrasound image analysis. NCI-NIBIB Point of Care Technologies for Cancer Conference. January 8-10, 2014, Natcher Center, NIH campus- Building 45, Bethesda, Maryland.
5. Lin N, Jiang J, **Guo S**, Yu X, Ma L and Xiong MM. (2014). Classification Analysis of Big Image Data. Statistical and Computational Theory and Methodology for Big Data Analysis. Feb 9-Feb 14, 2014, Calgary, AB Canada.

6. Yu J, Lin N, Ma L, **Guo S** and Xiong MM. (2014). Cloud computing for joint big genetic, epigenetic and image data analysis. Keystone Symposia: Big Data in Biology, March 23-25, 2014. Fairmont San Francisco, San Francisco, California.
7. **Guo S**, Wang J, Li Jin. (2012) A Panel of Epigenetic Biomarkers of NSCLC identified by genome-wide DNA methylation microarray, 2012, ASHG

### **Ad hoc Reviewer**

Journals: Clinical Epigenetics  
Epigenetics  
Scientific Report  
BMC Genetics  
Genes and Immunity  
Frontiers in Genetics  
Journal of Genetics and Genomics  
Epigenomics  
Cancer investigation  
Biomarker  
Frontiers in Oncology  
Functional & Integrative Genomics  
Frontiers in Cell and Developmental Biology

Conferences: BIBM 2014: Bioinformatics and Biomedicine