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EDUCATION

2014.09 - 2018.06	**Ph.D.**	Genetics	HUST
2016.10 - 2017.10	**Visiting Scholar**	Computational Biology and Bioinformatics	UTHealth
2010.09 - 2014.06	**B.S.**	Bioinformatics	HUST

RESEARCH EXPIERENCE

2018.06 – 2021.10	**Postdoctoral Fellow**	HUST	Advisor: An-Yuan Guo
2021.10 – present	**Postdoctoral Fellow**	CHOP	Advisor: Yi Xing

RESEARCH INTERESTS

Tumor immunotherapy and biomarkers

✧ Tumor diagnosis of RNA signatures based on tumor educated platelet.

✧ Mining immunotherapy response biomarkers and building prediction model.

Non-coding RNA in cancer

✧ Non-coding RNA (snoRNA, tRNA, circRNA) in cancer subtype and prognosis.

✧ Data portal of non-coding construction, including LNCRediting and miRNASNP.

Bioinformatic tools

✧ Cancer analysis tools, including GSCALite, GEDS and SEGtool.

✧ Building genomic and immunogenomic pipelines.

FUNDINGS

2019.06	China Postdoctoral Science Foundation	2019M652623	¥80,000
2016.06	Innovative Interdisciplinary Ph.D. Student Foundation	-	¥50,000

PUBLICATIONS

Contributed equally as first author

1. Gao, Y.[†], **Liu, C.J.**[†], Li, H.[†], Liu J.H., … Guo, A.Y., Gao, Q. (2022). A 61-platelet mRNA classifier for early and accurate detection of ovarian cancer: a retrospective, multicenter, biomarker identification study. ***Protein & Cell***, **Under review**.

2. **Liu, C.J.,** Li, H., Gao, Y. … Guo, A.Y., Gao Q. (2022). Platelet RNA signature independently predicts ovarian cancer prognosis by a deep learning neural network model. ***Protein & Cell***, **Under review**.

3. **Liu, C.J.**, Hu, F.F., Zeng, Yan, Guo, A.Y. (2022). GSCA: an integrated genomic and immunogenomic web-based platform for gene set cancer research. ***Briefings in Bioinformatics***, **Under Review**.

4. Xie, G.Y., **Liu, C.J**.[#], Guo A.Y.[#] (2022). EVAtool: an optimized reads assignment tool for small ncRNA quantification and its application in extracellular vesicle datasets. ***Briefings in Bioinformatics, Online.***

5. **Liu C.J.**, Xie, G.Y., Miao, Y., Xia, M., Wang, Y., Zhang, Q., Guo, A.Y. (2022). EVAtlas: a comprehensive database for expression profiles of eight ncRNAs in extracellular vesicles of human. ***Nucleic acids research, 50(D1), pp.D111-D117.***

6. Xie, G.Y.[‡], **Liu, C.J.**[†], Miao, Y. R., Xia, M., Zhang, Q., & Guo, A. Y. (2022). A comprehensive platelet expression atlas (PEA) resource and platelet transcriptome landscape. ***American journal of hematology***, **97(1), E18-E21.**

7. **Liu C.J.**, Fu, X., Xia, M., Zhang, Q., Gu, Z. Guo, A.Y. (2021). miRNASNP-v3: a comprehensive database for SNPs and disease-related variations in miRNAs and miRNA targets. ***Nucleic acids research***, **49(D1), D1276-D1281**.

8. Hu, F.F.,[†], **Liu, C.J.**[†], Lan-Lan Liu, Qiong Zhang, An-Yuan Guo. (2021). Expression profile of immune checkpoint genes and its role in predicting immunotherapy response. ***Briefings in bioinformatics***, **22(3), bbaa176.**

9. Chen, S.Y.[†], **Liu, C.J.**[†], Zhang, Q., Guo, A.Y. (2020). An ultra-sensitive T-cell receptor detection method for TCR-Seq and RNA-Seq data. ***Bioinformatics***, **36(15), 4255-4262**.

10. Gong, J.[†], **Liu, C.J.** [†], Liu, W., Xiang, Y., Diao, L., Guo, A.Y., Han, L. (2017). LNCediting: a database for functional effects of RNA editing in lncRNAs. ***Nucleic Acids Research***, **45(D1), D79-D84**.

11. Gong, J.†, Li, Y.†, **Liu, C.J.†,** Xiang, Y., Li, C., Ye, Y., Zhang, Z., Hawke, D. H., Park, P. K., Diao, L., others, NA (2017). A pan-cancer analysis of the expression and clinical relevance of small nucleolar RNAs in human cancer. ***Cell Reports***, **21(7), 1968-1981**.

12. Zhang, Z.†, Ruan, H.†, **Liu, C.J.†,** Ye, Y., Gong, J., Diao, L., Guo, A.Y., Han, L. (2019). tRic: a user-friendly data portal to explore the expression landscape of tRNAs in human cancers. ***RNA Biology***, **1-6.**

13. **Liu, C.J.,** Hu, F.F., Xia, M.X., Han, L., Zhang, Q., Guo, A.Y. (2018). GSCALite: a web server for gene set cancer analysis. ***Bioinformatics***, **34(21), 3771-3772.**

14. **Liu, C.J.,** Gao, C., Cong, R., Zhang, Q., Guo, A.Y. (2017). lncRInter: a database of experimentally validated long non-coding RNA interaction. ***Journal Of Genetics And Genomics***, **44(5), 265-268.**

15. Xia, M.†, **Liu, C.J.†,** Zhang, Q., Guo, A.Y. (2019). GEDS: a gene expression display server for mRNAs, miRNAs and proteins. ***Cells***, **8(7), 675.**

16. Gong, J.†, **Liu, C.J.†,** Liu, W., Wu, Y., Ma, Z., Chen, H., Guo, A.Y. (2015). An update of miRNASNP database for better SNP selection by GWAS data, miRNA expression and online tools. ***Database***, **2015.**

17. Gao, M.†, Zhang, S.†, **Liu, C.J.†,** Qin, Y., Archacki, S., Jin, L., Wang, Y., Liu, F., Chen, J., Liu, Y., others, NA (2016). Whole exome sequencing identifies a novel NRL mutation in a Chinese family with autosomal dominant retinitis pigmentosa. ***Molecular Vision***, **22.**

Other publications

1. Zhang, C., **Liu, C. J.,** & Feng, W. (2022). A Long‐Term Clearing Cranial Window for Longitudinal Imaging of Cortical and Calvarial Ischemic Injury through the Intact Skull. ***Advanced Science***, **2105893**.

2. Zhang, H.M., Liu, T., **Liu, C.J**., …, Xue, Y., Guo, A.Y. (2015). AnimalTFDB 2.0: a resource for expression, prediction and functional study of animal transcription factors. *Nucleic Acids Research*, 43(D1), D76-D81.

3. Gong, J., Mei, S., **Liu, C.J.,** Xiang, Y., Ye, Y., Zhang, Z., Feng, J., Liu, R., Diao, L., Guo, A.Y., others, NA (2018). PancanQTL: systematic identification of cis-eQTLs and trans-eQTLs in 33 cancer types. *Nucleic Acids Research*, 46(D1), D971-D976.

4. Shi, M.W., Zhang, N.A., Shi, C.P., **Liu, C.J.,** Luo, Z.H., Wang, D.Y., Guo, A.Y., Chen, Z.X. (2019). SAGD: a comprehensive sex-associated gene database from transcriptomes. *Nucleic Acids Research*, 47(D1), D835-D840.

5. Zhang, Q., Liu, W., **Liu, C.J.,** Lin, S.Y., Guo, A.Y. (2018). SEGtool: a specifically expressed gene detection

tool and applications in human tissue and single-cell sequencing data. *Briefings In Bioinformatics*, 19(6), 1325-1336.

6. Gong, J., Wan, H., Mei, S., Ruan, H., Zhang, Z., **Liu, C.J.**, Guo, A.Y., Diao, L., Miao, X., Han, L. (2019). Pancan-meQTL: a database to systematically evaluate the effects of genetic variants on methylation in human cancer. *Nucleic Acids Research*, 47(D1), D1066-D1072.

7. Ruan, H., Xiang, Y., Ko, J., Li, S., Jing, Y., Zhu, X., Ye, Y., Zhang, Z., Mills, T., Feng, J., **Liu. C.J.**, NA (2019). Comprehensive characterization of circular RNAs in 1000 human cancer cell lines. *Genome Medicine*, 11(1), 1-14.

8. Ye, Y., Xiang, Y., Ozguc, F. M., Kim, Y., **Liu, C.J.**, Park, P. K., Hu, Q., Diao, L., Lou, Y., Lin, C., others, NA (2018). The genomic landscape and pharmacogenomic interactions of clock genes in cancer chronotherapy. *Cell Systems*, 6(3), 314-328.

9. Zhang, Q., Hu, H., Chen, S.Y., **Liu, C.J.**, Hu, F.F., Yu, J., Wu, Y., Guo, A.Y. (2019). Transcriptome and regulatory network analyses of CD19-CAR-T immunotherapy for B-ALL. *Genomics, Proteomics & Bioinformatics*, 17(2), 190-200.

10. Lin, Y., Zhang, Q., Zhang, H.M., Liu, W., **Liu, C.J.**, Li, Q., Guo, A.Y. (2015). Transcription factor and miRNA co-regulatory network reveals shared and specific regulators in the development of B cell and T cell. *Scientific Reports*, 5.

11. Zhao, A., Kong, F., **Liu, C.J.**, Yan, G., Gao, F., Guo, H., Guo, A.Y., Chen, Z., Li, Q. (2017). Tumor cell-derived microvesicles induced not epithelial-mesenchymal transition but apoptosis in human proximal tubular (HK-2) cells: implications for renal impairment in multiple myeloma. *International Journal Of Molecular Sciences*, 18(3), 513.

12. Wang, J., Liu, Y., Liu, F., Huang, C., Han, S., Lv, Y., **Liu, C.J.**, Zhang, S., Qin, Y., Ling, L., others, NA (2016). Loss-of-function mutation in PMVK causes autosomal dominant disseminated superficial porokeratosis. *Scientific Reports*, 6(1), 1-9.

13. Zhang, Z., Ye, Y., Gong, J., Ruan, H., **Liu, C.J.**, Xiang, Y., Cai, C., Guo, A.Y., Ling, J., Diao, L., others, NA (2018). Global analysis of tRNA and translation factor expression reveals a dynamic landscape of translational regulation in human cancers. *Communications Biology*, 1(1), 1-11.