

# Yafei Mao, Ph.D.

Associate Professor  
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## EDUCATION

2019 Ph.D. Okinawa Institute of Science and Technology Graduate University  
*Evolutionary Genomics* (Advisors: [Dr. Noriyuki Satoh](#) and [Dr. Evan Economo](#))

2014 B.Sc. Nanjing University (with honor)  
*Life Sciences*

### Other Training:

May 2018 - Oct 2018    Princeton University  
Visiting Student (Advisor: [Dr. Ricardo Mallarino](#))  
Oct 2013 - Mar 2014    Hong Kong University of Science and Technology  
Visiting Student (Advisor: [Dr. Mingjie Zhang](#))

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## APPOINTMENTS

### Shanghai Jiao Tong University

May 2022 - present    Associate Professor

### University of Washington

Jun 2019 - May 2022    Postdoctoral Fellow (Advisor: [Dr. Evan Eichler](#))

### Okinawa Institute of Science and Technology Graduate University

Apr 2019 - Jun 2019    Junior Researcher  
(Advisors: [Dr. Noriyuki Satoh](#) and [Dr. Evan Economo](#))

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## PUBLICATIONS

### Journal Articles

25. Zhang, S., Xu, N., Fu, L., Yang, X., Li, Y., Yang, Z., ..., Sun, Q.\* & **Mao, Y.\*** (2024). Comparative genomics of macaques and integrated insights into genetic variation and population history. [bioRxiv](#), 2024-04.
24. **Mao, Y.\***, Harvey, W. T., Porubsky, D., Munson, K. M., Hoekzema, K., Lewis, A. P., ... & Eichler, E. E.\* (2024). Structurally divergent and recurrently mutated regions of primate genomes. [Cell](#).
23. Mao, Y., Li, Y., Yang, Z., Xu, N., Zhang, S., Wang, X., ... & **Mao, Y.\*** (2024). Comparative transcriptome analysis between rhesus macaques (*Macaca mulatta*) and crab-eating macaques (*M. fascicularis*). [Zoological Research](#), 45(2): 299-310.
22. Logsdon, G.A., Rozanski, A.N., Ryabov, F., ... **Mao, Y.** ... & Eichler, E. E.\* (2024). The variation and evolution of complete human centromeres. [Nature](#), 1-10.
21. Yang X., Wang X., Zou Y.,... & **Mao, Y.\*** (2023). Characterization of large-scale genomic differences in the first complete human genome. [Genome Biology](#), 24, 157.
20. He, Y.\* & **Mao, Y.\*** (2023). Exploring the primate genome: Unraveling the mysteries of evolution and human disease. [The Innovation](#), 4(4).
19. Okhovat, M.\* & VanCampen, J., Nevenon, K. A., ... **Mao, Y.** ... & Carbone, L.\* (2023). TAD Evolutionary and functional characterization reveals diversity in mammalian TAD boundary properties and function. [Nature Communications](#), 14(1), 8111.
18. Yang, X., **Mao, Y.**, Wang, X., ..., Li, Z.\* & Takahashi, E.\* & Li, W.\* (2023). Population genetics of marmosets in Asian primate research centers and loci associated with epileptic risk revealed by whole-genome sequencing. [Zoological Research](#), 44(5), 837–847.
17. Li, Z.\* & Liu, X., Wang, C., ... **Mao, Y.** ..., & Chen, Y.\* (2023). The pig pangenome provides insights into the roles of coding structural variations in genetic diversity and adaptation. [Genome Research](#), 33(10), 1833-1847.
16. Yang, C., Zhou, Y., Song, Y., ... **Mao, Y.** ... & Zhang, G.\* (2023). The complete and fully-phased diploid genome of a male Han Chinese. [Cell Research](#), 1-17.
15. **Mao, Y.\***, Zhang, G.\* (2022) A complete, telomere-to-telomere human genome sequence presents new opportunities for evolutionary genomics. [Nature Methods](#) 19, 635–638.
14. Wang, T.\* & Kim, C. N., Bakken, T. E., Gillentine, M. A., Henning, B., **Mao, Y.**, ... & Eichler, E. E.\* (2022). Integrated gene analyses of de novo variants from 46,612 trios with autism and developmental disorders. [Proceedings of the National Academy of Sciences](#), 119(46), e2203491119.

## Before SJTU

13. Ebler, J., Ebert, P., Clarke, W. E., Rausch, T., Audano, P. A., Houwaart, T., ... **Mao, Y.** ... & Marschall, T.\* (2022). Pangenome-based genome inference allows efficient and accurate genotyping across a wide spectrum of variant classes. [\*Nature Genetics\*](#), 54(4), 518-525.
12. **Mao, Y.**, Catacchio, C.R., Hillier, L.W., Porubsky, D., Li, R., Sulovari, A., ... & Eichler, E.E.\* (2021). A high-quality bonobo genome refines the analysis of hominid evolution. [\*Nature\*](#), 594(7861), 77-81.
11. Logsdon, G.A., Vollger, M.R., Hsieh, P., **Mao, Y.**, Liskovych, M.A., Koren, S., ... & Eichler, E.E.\* (2021). The structure, function and evolution of a complete human chromosome 8. [\*Nature\*](#), 593(7857), 101-107.
10. Hsieh, P.\*, Dang, V., Vollger, M.R., **Mao, Y.**, Huang, T.H., Dishuck, P.C., ... & Eichler, E.E.\* (2021). Evidence for opposing selective forces operating on human-specific duplicated TCAF genes in Neanderthals and humans. [\*Nature Communications\*](#), 12(1), 1-14.
9. **Mao, Y.\***, Hou, S., Shi, J., & Economo, E.P. (2020). TREEasy: an automated workflow to infer gene trees, species trees, and phylogenetic networks from multilocus data. [\*Molecular Ecology Resources\*](#), 20:832–840.
8. **Mao, Y.\*** (2020). Genomic insights into hybridization of reef corals. [\*Coral Reefs\*](#), 39(1), 61-67.
7. Warren, W.C.\*, Harris, R.A., Haukness, M., ... **Mao, Y.** ... , Rogers, J.\* & Eichler, E.E.\* (2020). Sequence diversity analyses of an improved rhesus macaque genome enhance its biomedical utility. [\*Science\*](#), 370(6523).
6. Cantsilieris, S., Sunkin, S.M., Johnson, M.E., Anaclerio, F., Huddleston, J., Baker, C., ... **Mao, Y.**, ... & Eichler, E.E.\* (2020). An evolutionary driver of interspersed segmental duplications in primates. [\*Genome Biology\*](#), 21(1), 1-35.
5. Maggiolini, F.A.M., Sanders, A.D., Shew, C.J., Sulovari, A., **Mao, Y.**, Puig, M., ... & Antonacci, F.\* (2020). Single-cell strand sequencing of a macaque genome reveals multiple nested inversions and breakpoint reuse during primate evolution. [\*Genome Research\*](#), 30(11), 1680-1693.
4. **Mao, Y.\***, & Satoh, N. (2019). A likely ancient genome duplication in the speciose reef-building coral genus, *Acropora*. [\*iScience\*](#), 13, 20-32.
3. **Mao, Y.\*** (2019). GenoDup Pipeline: a tool to detect genome duplication using the dS-based method. [\*PeerJ\*](#), 7, e6303.
2. **Mao, Y.\***, Economo, E.P.\*, & Satoh, N.\* (2018). The roles of introgression and climate change in the rise to dominance of *Acropora* corals. [\*Current Biology\*](#), 28(21), 3373-3382.
1. Zhang, Y., Shao, Z., Yang, L., Sun, X., **Mao, Y.**, Chen, J.\* & Wang, B.\* (2013). Non-random arrangement of synonymous codons in archaea coding sequences. [\*Genomics\*](#), 101(6), 362-367.

NOTE: \*Corresponding author

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## PRESENTATIONS

2024	CSHA: DNA Metabolism, Genomic Stability and Human Disease (Oral talk)	Suzhou, China
2024	Frontiers of Biotechnology Forum (Invited)	Shenzhen, China
2024	China Primatological Society Conference 2024 (Invited speaker)	Zhengzhou, China
2024	National Genome Informatics Conference (Invited speaker)	Wuhan, China
2023	The 3rd AsiaEvo Conference (Oral talk)	Singapore
2023	International Symposium on Human Cultural and Genetic Diversity in Southeast Asia and Southwest China (Invited speaker)	Kunming, China
2023	GSC2023 (Invited speaker)	Wuhan, China
2023	The Innovation Webinar No.66 (Invited speaker)	Virtual Meeting
2023	School of Life Sciences, Southwest University (Invited speaker)	Chongqing, China
2023	Chengdu Institute of Biology, Chinese Academy of Sciences	Chengdu, China
2023	School of Life Sciences, Southern University of Science and Technology (Invited speaker)	Shenzhen, China
2023	School of Life Sciences, Nanjing University (Invited speaker)	Nanjing, China
2023	Neuroscience Research Institute, Peking University (Invited speaker)	Virtual Meeting
2022	Institute of Neuroscience, Chinese Academy of Sciences Center for Excellence in Brain Science and Intelligence Technology, Chinese Academy of Sciences (Invited speaker)	Shanghai, China
2022	Department of Anthropology and Human Genetics, Fudan University (Invited speaker)	Shanghai, China
2022	Structural Variants and DNA Repeats	Virtual Meeting
2022	School of Medicine, Zhejiang University(Invited speaker)	Hangzhou, China
2022	CAS, Kunming Institute of Zoology (Invited speaker)	Kunming, China
2021	Biodiversity Genomics 2021 (Invited speaker)	Virtual Meeting
2021	Structural Variants and DNA Repeats	Virtual Meeting
2021	Bold Predictions for Human Genomics by 2030	Virtual Meeting
2020	T2T/HPRC Symposium	Virtual Meeting
2019	The Use of Big Data in Quantitative Genetics	Lucca, Italy
2018	The 1st AsiaEvo Conference (Invited speaker)	Shenzhen, China
2017	Agricultural Genomics 2017	Wuhan, China
2017	Speciation (Selected for Oral Presentation)	Lucca, Italy

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## GRANTS AND FELLOWSHIPS

- 2024 Natural Science Foundation of Chongqing, China  
2024 General Program of National Natural Science Foundation of China  
2024 National Natural Science Fund for Excellent Young Scientists Fund Program (Overseas)  
2022 Shanghai Pujiang Program (A-type)  
2022 Shanghai Jiao Tong University 2030 Program (C-type)  
2022 Opening research fund from Shanghai Key Laboratory of Stomatology, Shanghai Ninth People's Hospital  
2017 Japan Society for the Promotion of Science (JSPS) Fellow, DC1
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## AWARDS AND HONORS

- 2024 Excellent Young Job Expert of Shanghai Jiao Tong University  
2023 Shanghai Young Talent Program  
2022 CUHK Vice-Chancellor Assistant Professorship (withdraw)  
2014 Outstanding Graduates of Nanjing University  
2013 Gold Medal of iGEM (team leader)  
2010, 2011, 2012 Cyrus Tang Scholarship  
2012 National Scholarship  
2011, 2013 National Motivational Scholarships  
2011 Outstanding Students of Nanjing University
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## MENTORSHIP

<b>Shanghai Jiao Tong University</b>		<b>Nanjing University</b>
Xiangyu Yang	Dan Meng	Shuke Xiao
Kaiyue Ma	Xuankai Wang	Kun Lv
Shilong Zhang	Lianting Fu	Yuanyuan Wang
Xinrui Jiang	Junmin Han	Jianchen Yang
Da Lian	Feifei Zhou	

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## ACADEMIC SERVICE

### Society Memberships

Society for Molecular Biology & Evolution  
Human Pangenome Reference Consortium  
Chinese Society of Biotechnology  
Genetics Society of China

### Subject/Associate Editor/Review Editor

2024-present *Genome Biology*  
2022-present *BMC Biology*  
2021-present *eLife (Early-Career Reviewers Pool)*

### Peer Reviewer

*Cell Genomics, Cell Reports, eLife, Genome Research, Nature Communications, PLoS Genetics, Science Bulletin* and others

### Grant Review

Research Grants Council (RGC) of Hong Kong, Funding Scheme: GRF / ECS

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## REFERENCES

### Evan P. Economo

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### Evan E. Eichler

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