

# Yafei Mao, Ph.D.

Associate Professor  
Evo-Geno-Disease Lab (<https://yafmao.org/>)

Shanghai, 200030  
CHINA

+86-(021)-62932151  
yafmao@sjtu.edu.cn

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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

15. 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.
14. **Mao, Y.**, Zhang, G. A complete, telomere-to-telomere human genome sequence presents new opportunities for evolutionary genomics. *[Nature Methods](#)* 19, 635–638 (2022).
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](#)*, 2020;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., Fiddes, I.T., Murali, S.C., Fernandes, J.,... **Mao, Y.** ... & 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.M., Shao, Z.Q., Yang, L.T., Sun, X.Q., **Mao, Y.F.**, Chen, J.Q., & 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

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	Fudan University, Department of Anthropology and Human Genetics (Invited speaker)	Shanghai, China
2022	Structural Variants and DNA Repeats	Virtual Meeting
2022	Zhejiang University, School of Medicine (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

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

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

### Shanghai Jiao Tong University

Xiangyu Yang  
Dan Meng  
Xuankai Wang  
Shilong Zhang  
Lianting Fu

### Nanjing University

Shuke Xiao  
Kun Lv  
Yuanyuan Wang  
Jianchen Yang

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## ACADEMIC SERVICE

### Society Memberships

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

### Subject/Associate Editor/Review Editor

2022-present *BMC Biology*  
2022-present *Frontiers in Bioinformatics*  
2021-present *eLife (Early-Career Reviewers Pool)*

### Peer Reviewer

*Genome Research, BMC Biology, eLife, GigaScience, Scientific Reports, Frontier in Plant Science, Frontiers in Marine Science, Frontier in Bioinformatics*

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## REFERENCES

### **Evan P. Economo**

Professor  
Biodiversity and Biocomplexity Unit  
Okinawa Institute of Science and  
Technology Graduate University  
+1 (617) 386-6669 (US)  
+81 (098) 982-3328 (JP)  
economo@oist.jp

### **Douglas E. Soltis**

Distinguished Professor  
Florida Museum of Natural History  
Department of Biology

### **Evan E. Eichler**

Principal Investigator  
Professor of Genome Sciences  
Department of Genome Sciences,  
University of Washington  
(206) 543-9526  
eee@gs.washington.edu

### University of Florida

(352) 273-1963  
dsoltis@ufl.edu