

# Huanwei Wang

5/222 Carmody Road, St Lucia  
Brisbane, Queensland, Australia

(+61)431626350  
zju.whw@gmail.com

## Education

University of Queensland, Australia	Apr/2017-present (thesis submitted)
Ph.D., Quantitative Genetics	
Shanghai Jiao Tong University, China	Sep/2012-Dec/2015
M.S., Biochemistry and Molecular Biology	
Zhejiang University, China	Sep/2008-Jun/2012
B.S., Pharmaceutical Sciences	

## Work Experience

University of Queensland, Australia	Mar/2021-present
Research officer	
Westlake university, China	Aug/2020-Dec/2020
Visiting PhD student	
GeneDock Inc., China	Apr/2016-Mar/2017
Bioinformatics engineer	

## Publications

1. Jian Zeng, Angli Xue, Longda Jiang, Luke R. Lloyd-Jones, Yang Wu, **Huanwei Wang**, Zhili Zheng, Loic Yengo, Kathryn E. Kemper, Michael E. Goddard, Naomi R. Wray, Peter M. Visscher, Jian Yang. Widespread signatures of natural selection across human complex traits and functional genomic categories. Nature communications, 2021, 12, p. 1164.
2. Joana A. Revez, Tian Lin, Zhen Qiao, Angli Xue, Yan Holtz, Zhihong Zhu, Jian Zeng, **Huanwei Wang**, Julia Sidorenko, Kathryn E. Kemper, Anna A. E. Vinkhuyzen, Julianne Frater, Darryl Eyles, Thomas H. J. Burne, Brittany Mitchell, Nicholas G. Martin, Gu Zhu, Peter M. Visscher, Jian Yang, Naomi R. Wray, John J. McGrath. Genome-wide association study identifies 143 loci associated with 25 hydroxyvitamin D concentration. Nature communications, 2020, 11(1), p. 1647.

Update: 22/Jun/2021

3. Yang Wu, Ting Qi, **Huanwei Wang**, Futao Zhang, Zhili Zheng, Jennifer E. Phillips-Cremins, Ian J. Deary, Allan F. McRae, Naomi R. Wray, Jian Zeng, Jian Yang. Promoter-anchored chromatin interactions predicted from genetic analysis of epigenomic data. *Nature communications*, 2020. 11(1): p. 2061.
4. Luke R. Lloyd-Jones, Jian Zeng, Julia Sidorenko, Loic Yengo, Gerhard Moser, Kathryn E. Kemper, **Huanwei Wang**, Zhili Zheng, Reedik Magi, Tonu Esko, Andres Metspalu, Naomi R. Wray, Michael E. Goddard, Jian Yang, Peter M. Visscher. Improved polygenic prediction by Bayesian multiple regression on summary statistics. *Nature communications*, 2019, 10(1), pp. 5086.
5. **Huanwei Wang**, Futao Zhang, Jian Zeng, Yang Wu, Kathryn E. Kemper, Angli Xue, Min Zhang, Joseph E. Powell, Michael E. Goddard, Naomi R. Wray, Peter M. Visscher, Allan F. McRae, Jian Yang. Genotype-by-environment interactions inferred from genetic effects on phenotypic variability in the UK Biobank. *Science Advances*, 2019, 5(8), p.eaaw3538. (first author)
6. Yizhen Li, **Huanwei Wang**, Xiaoling Wang, Wen Jin, Yun Tan, Hai Fang, Saijuan Chen, Zhu Chen, and Kankan Wang. Genome-wide studies identify a novel interplay between AML1 and AML1/ETO in t(8;21) acute myeloid leukemia. *Blood*, 2015; 127(2): 233-242. (co-first author).
7. Hui Zhang, Jianqing Mi, Hai Fang, Zhao Wang, Chun Wang, Lin Wu, Bin Zhang, Mark Minden, Wentao Yang, **Huanwei Wang**, Junmin Li, Xiaodong Xi, Saijuan Chen, Ji Zhang, Zhu Chen, and Kankan Wang. Preferential eradication of acute myelogenous leukemia stem cells by fenretinide. *Proc. Natl. Acad. Sci. U. S. A.*, 2013; 110: 5606-5611.

Google scholar: <https://scholar.google.com/citations?user=B8z18fgAAAAJ&hl=en>

## **Conferences**

1. Quantifying the inflation in test-statistics for epistasis due to imperfect tagging using whole-genome sequence data (lightning talk). GeneMappers Conference 2018. Queensland, Australia.
2. Genotype-by-environment interactions inferred from genetic effects on phenotypic variability in the UK Biobank (Poster presentation). Gordon Research Conference Quantitative Genetics and Genomics 2019. Tuscany, Italy.

3. Integrating the genetic and environmental information to improve the phenotype prediction for body mass index (Poster presentation). The 6th International Conference of Quantitative Genetics Virtual 2020.
4. Quantification of the contribution of ultra-rare coding variants to trait heritability (oral presentation). GeneMappers Conference 2021. Queensland, Australia.