

# Content

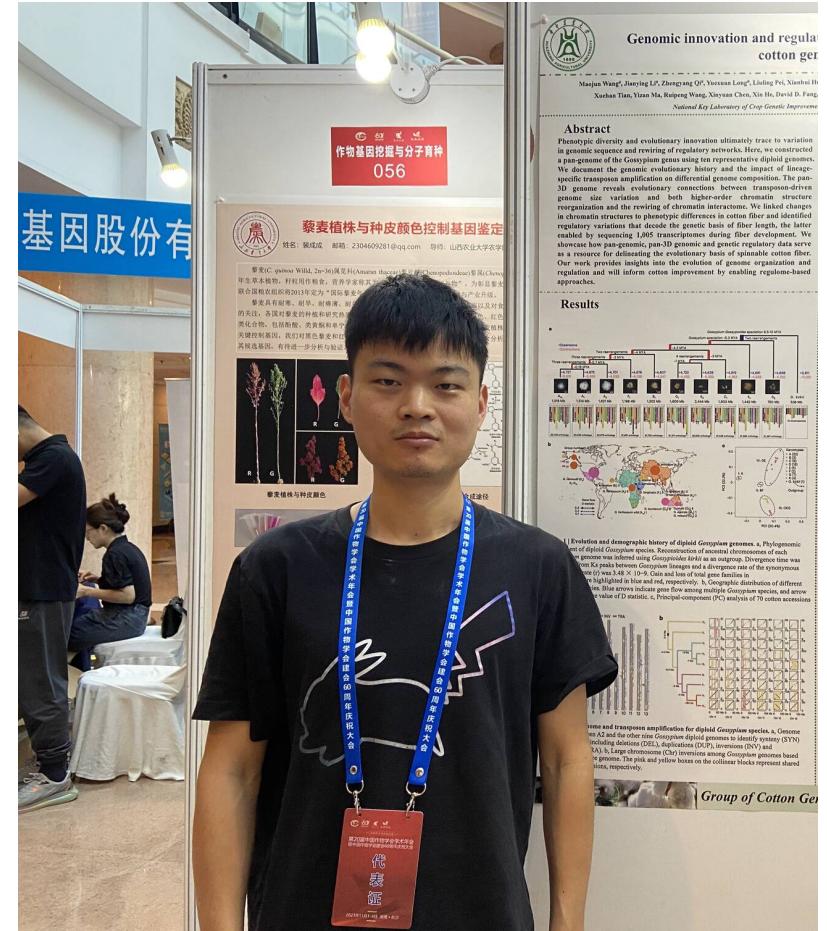
- Education background
- Current research achievement
- Future research interests

# Education

2020 - present, HZAU, Ph.D.  
candidate

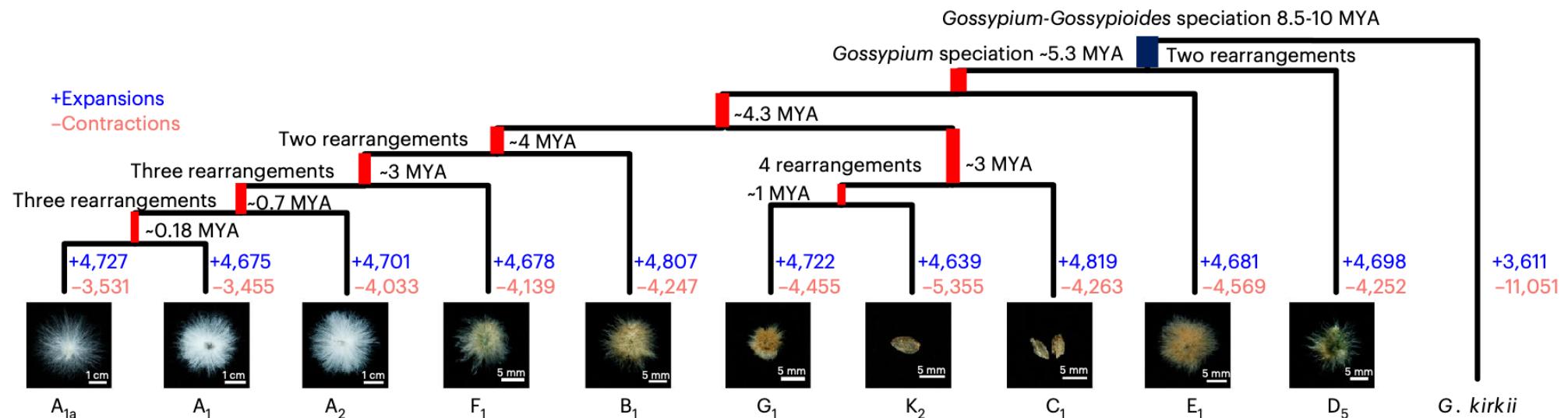
2016 - 2019, HZAU, Master's Degree

2012 - 2016, HZAU, Bachelor's  
Degree



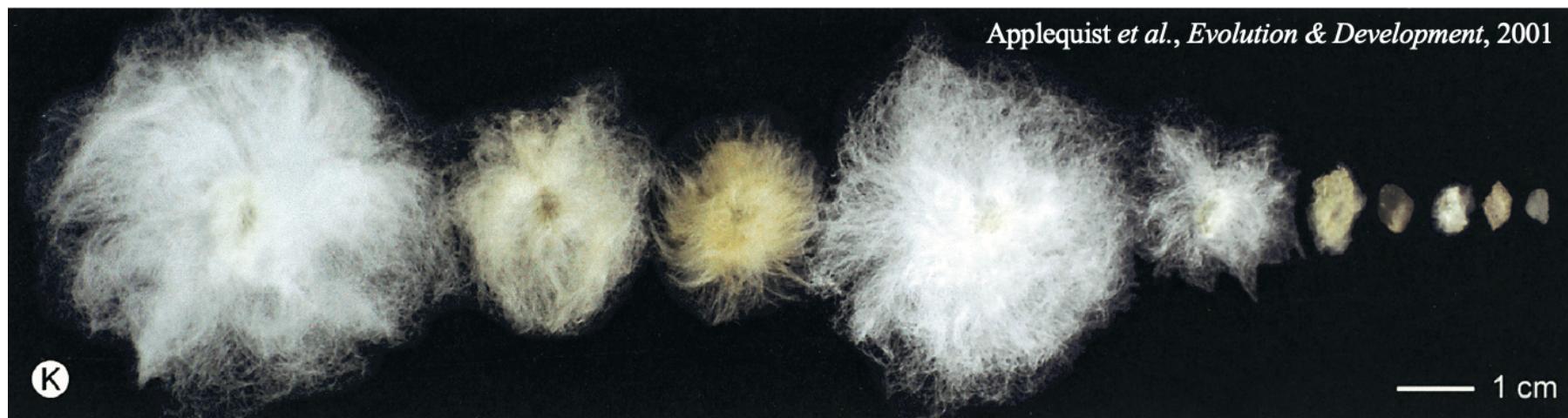
# Background

- Cotton contains 45 diploids and 7 allopolyploids (AD)
- 4 species were domesticated as cultivars (A1, A2, AD1 and AD2)



# Questions

1. What genetic factors influence the fiber quality of upland cotton?
2. Why only A genome has spinnable fibers in diploids?
3. Why allotetraploids have better fiber quality than diploids?



# Project 1

<https://doi.org/10.1038/s42003-022-03022-7>

OPEN

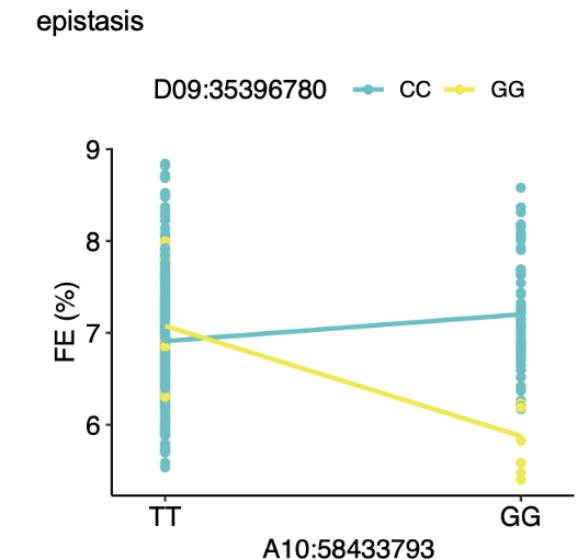
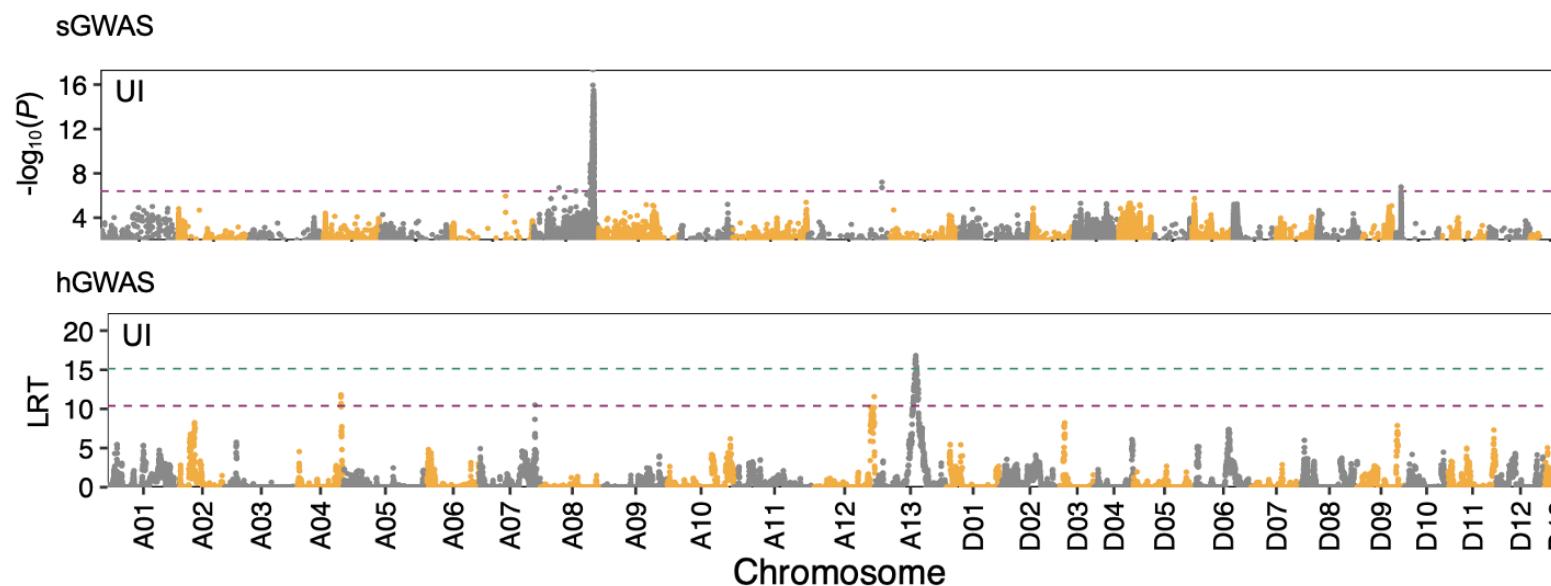
Genomic interrogation of a MAGIC population highlights genetic factors controlling fiber quality traits in cotton

Maojun Wang  <sup>1,2,4</sup>, Zhengyang Qi<sup>2,4</sup>, Gregory N. Thyssen<sup>1</sup>, Marina Naoumkina<sup>1</sup>, Johnie N. Jenkins  <sup>3</sup>, Jack C. McCarty  <sup>3</sup>, Yingjie Xiao<sup>2</sup>, Jianying Li<sup>2</sup>, Xianlong Zhang<sup>2</sup>  & David D. Fang  <sup>1</sup> 

I performed data analysis and wrote the manuscript.

# Main results

1. Performed two complementary GWAS method
2. Detect prevalent epistatic interactions



# What I have learnt

The main approaches for studying complex traits

- GWAS and linkage mapping
- IBD inference
- genome-wide epistasis analysis
- heritability and the breeder's equation

# Project 2

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nature genetics

Article

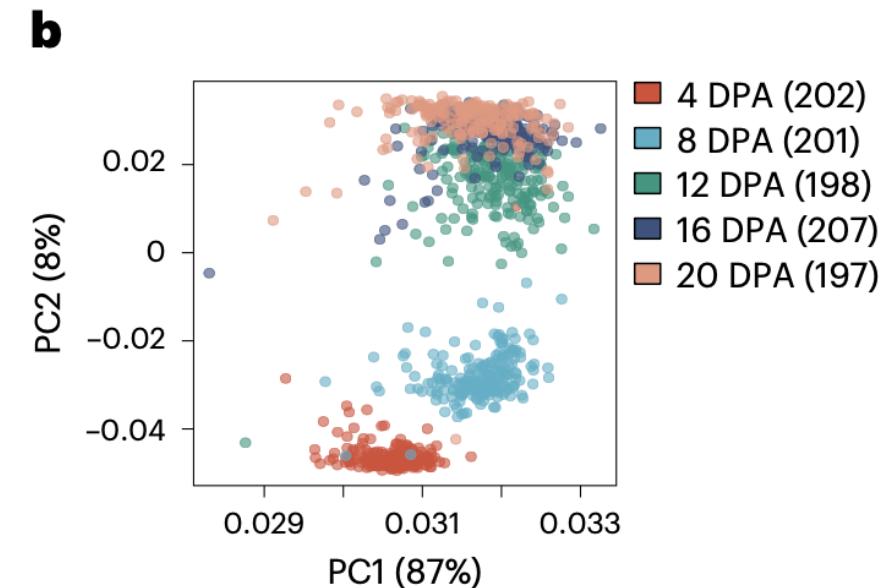
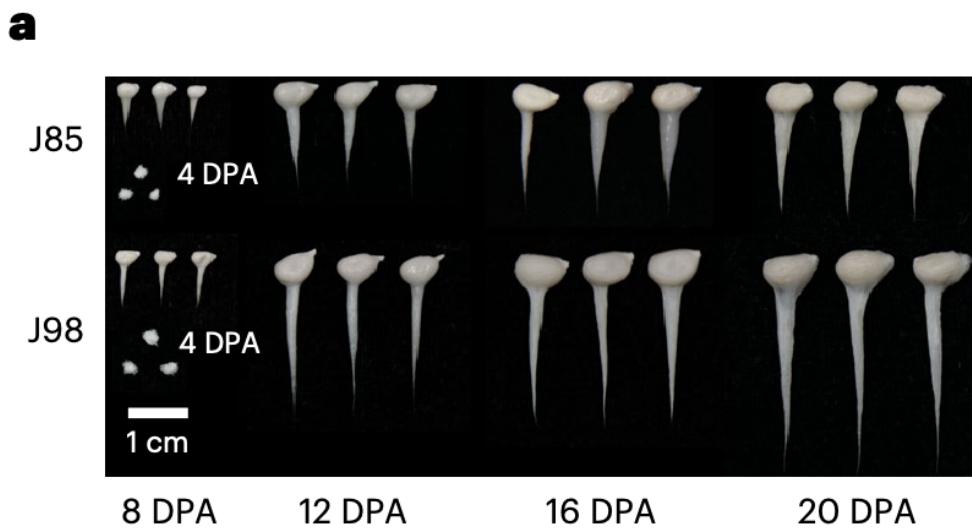
<https://doi.org/10.1038/s41588-022-01237-2>

## **Genomic innovation and regulatory rewiring during evolution of the cotton genus *Gossypium***

Contribution: 1/3 analysis tasks (figs 5,6)

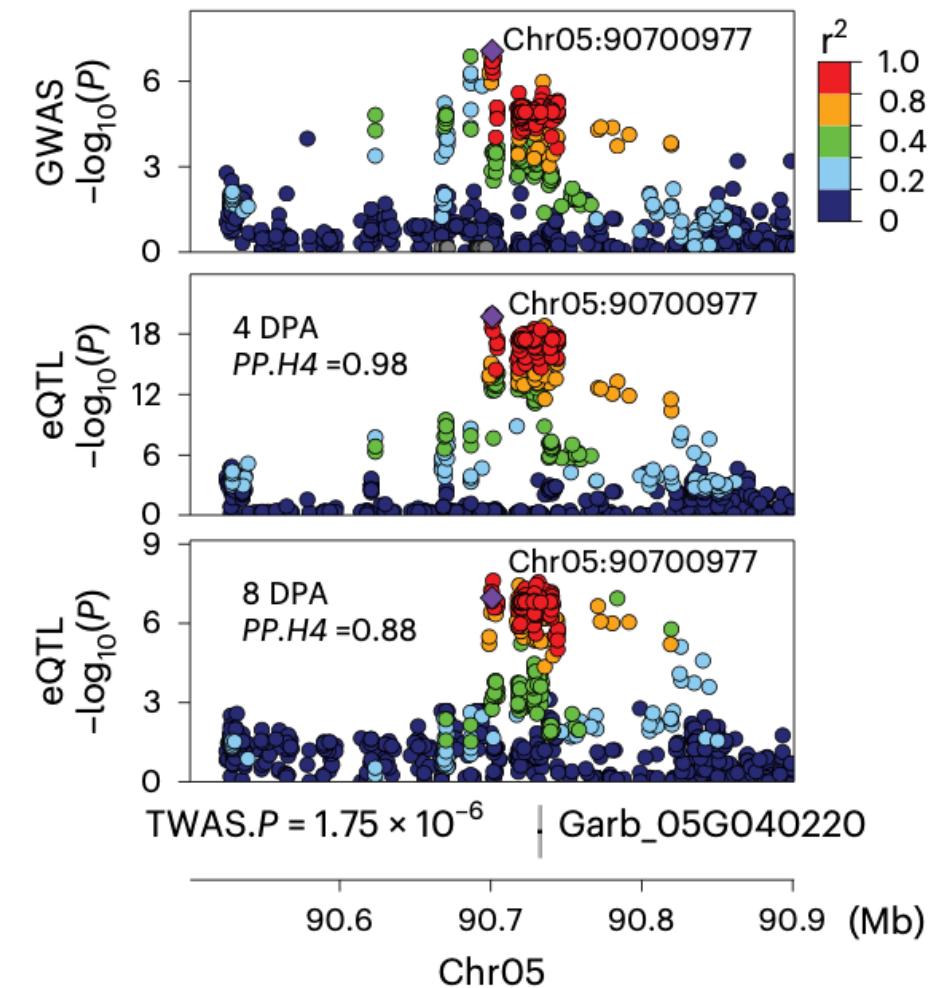
# Experimental design

- Re-sequence 216 diploid cotton accessions
- RNA-seq for 5 time-points for each accession
- Perform GWAS and eQTL analysis



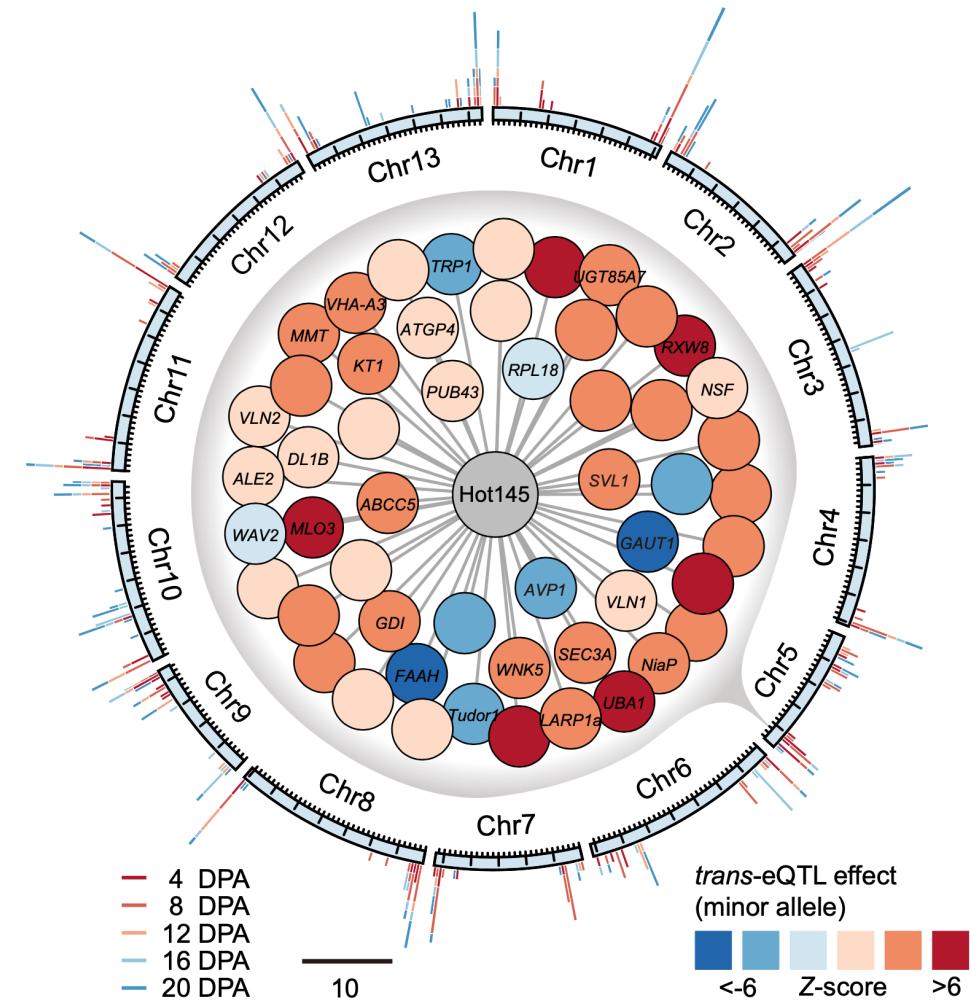
# Why perform eQTL analysis?

- Provide a reliable molecular link between DNA variants and complex phenotypes
- Prioritize causal genes at GWAS loci



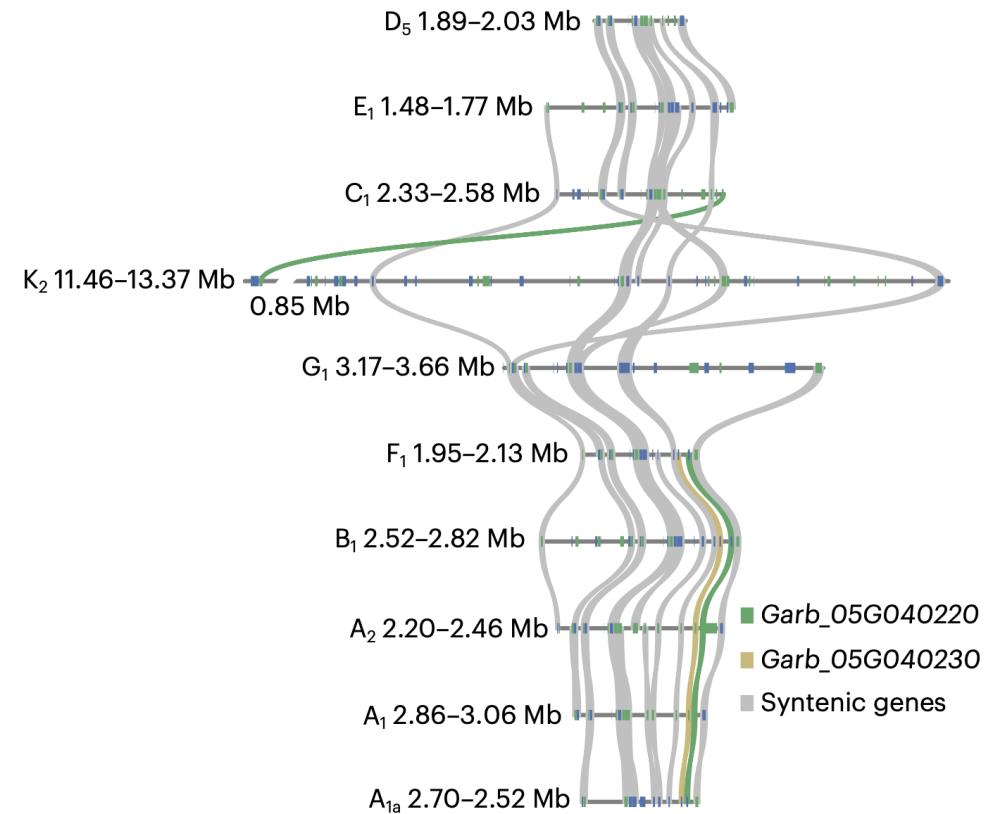
# Networking of genes

- A regulatory hotspot overlapped with a GWAS locus of FL
- The 52 genes regulated by the hotspot were involved in the processes of plant-type cell wall organization and protein transport



# Why A genome has spinnable fibers?

- Performed syntenic analysis of 195 putative functional genes
- The left figure serves as an example, illustrating the PAV of two tandem duplication genes was associated with fiber evolution



# Project 3

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nature genetics



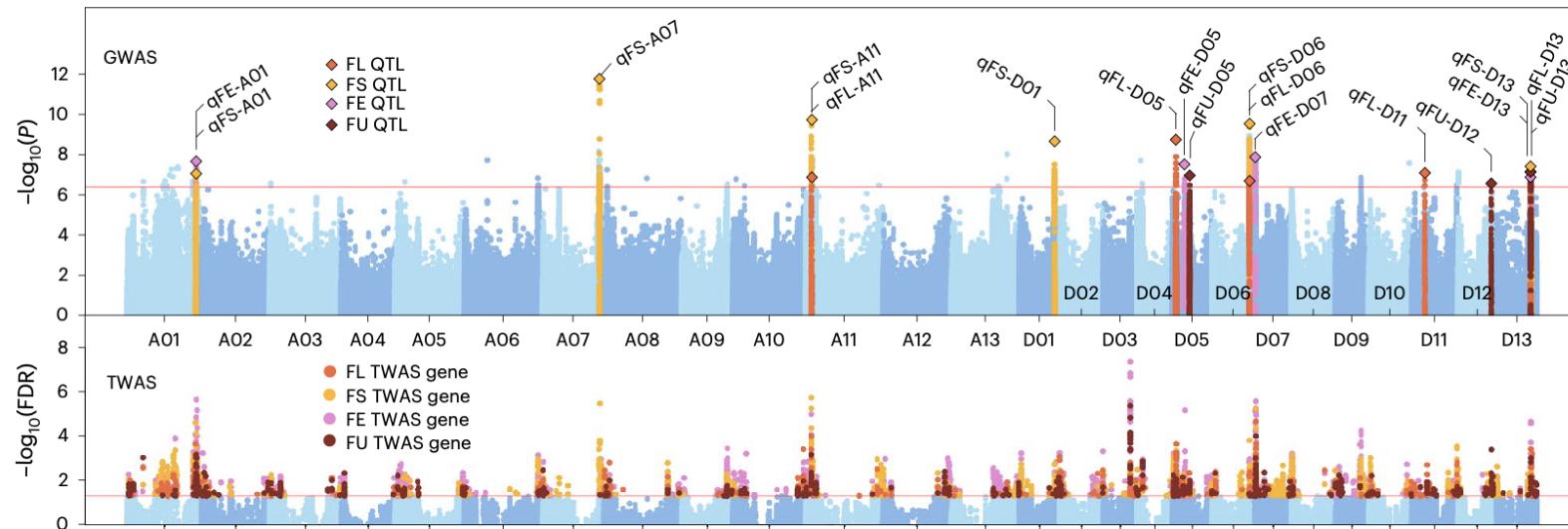
Article

<https://doi.org/10.1038/s41588-023-01530-8>

## **Regulatory controls of duplicated gene expression during fiber development in allotetraploid cotton**

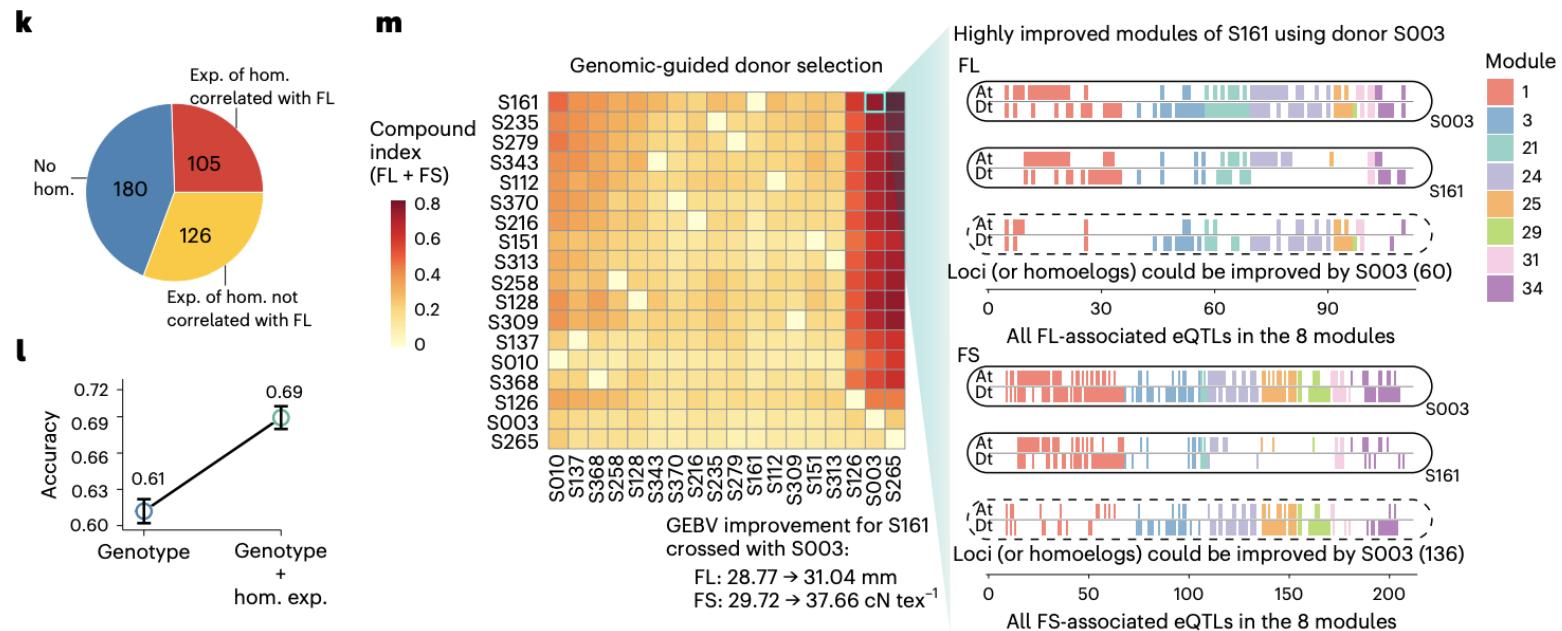
Contribution: 1/3 analysis tasks (part of figs.2,3, and entire fig.6)

# GWAS and TWAS analysis



- Conducted GWAS of fiber quality and found 18 QTLs
- Performed TWAS and found 1255 genes associated with fiber quality

# Cotton breeding strategy



- We can further improve fiber quality by targeting one of the less favourably expressed gene in the homologous gene pairs.

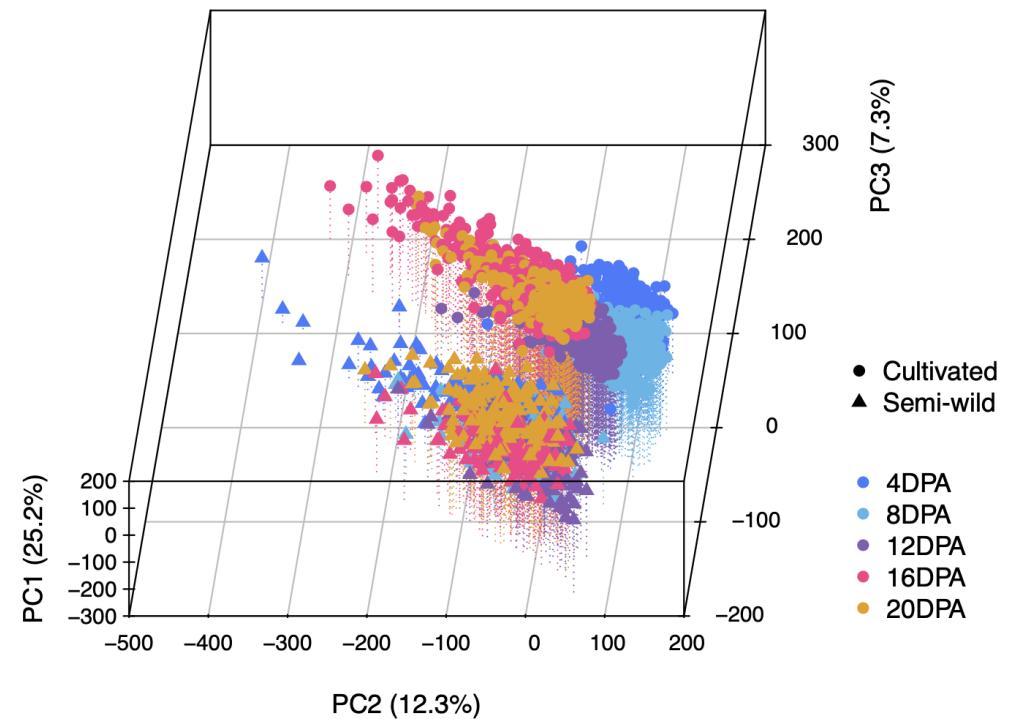
# What I have learnt

## Post-GWAS analysis

- Inferring Causal Associations between Genes and Disease via the Mapping of Expression Quantitative Trait Loci
- Inferring gene regulatory networks
- Construction of genomic prediction model

# Two more projects

- Domestication/breeding history of upland cotton
- Pan-genome analysis of 75 accessions (15 diploids and 60 tetraploids)



# Skills

- I know many details about quantitative genetics.
- I am good at bioinformatics workflow construction and downstream analysis.



# Future research interests

- Understand the evolution of interesting phenotypes by employing a state-of-the art multi-omics approach
- Decipher the genetics basis of key agronomic traits by using statistical genetics and functional case-studies

# Acknowledgement

- National Key Laboratory of Crop Genetic Improvement
- High-performance computing platform in HZAU
- Dr. Wang's research group



# Thanks

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