



Phenotyping, Genome-wide Dissection, and Prediction of Maize Root Architecture for Temperate Adaptability

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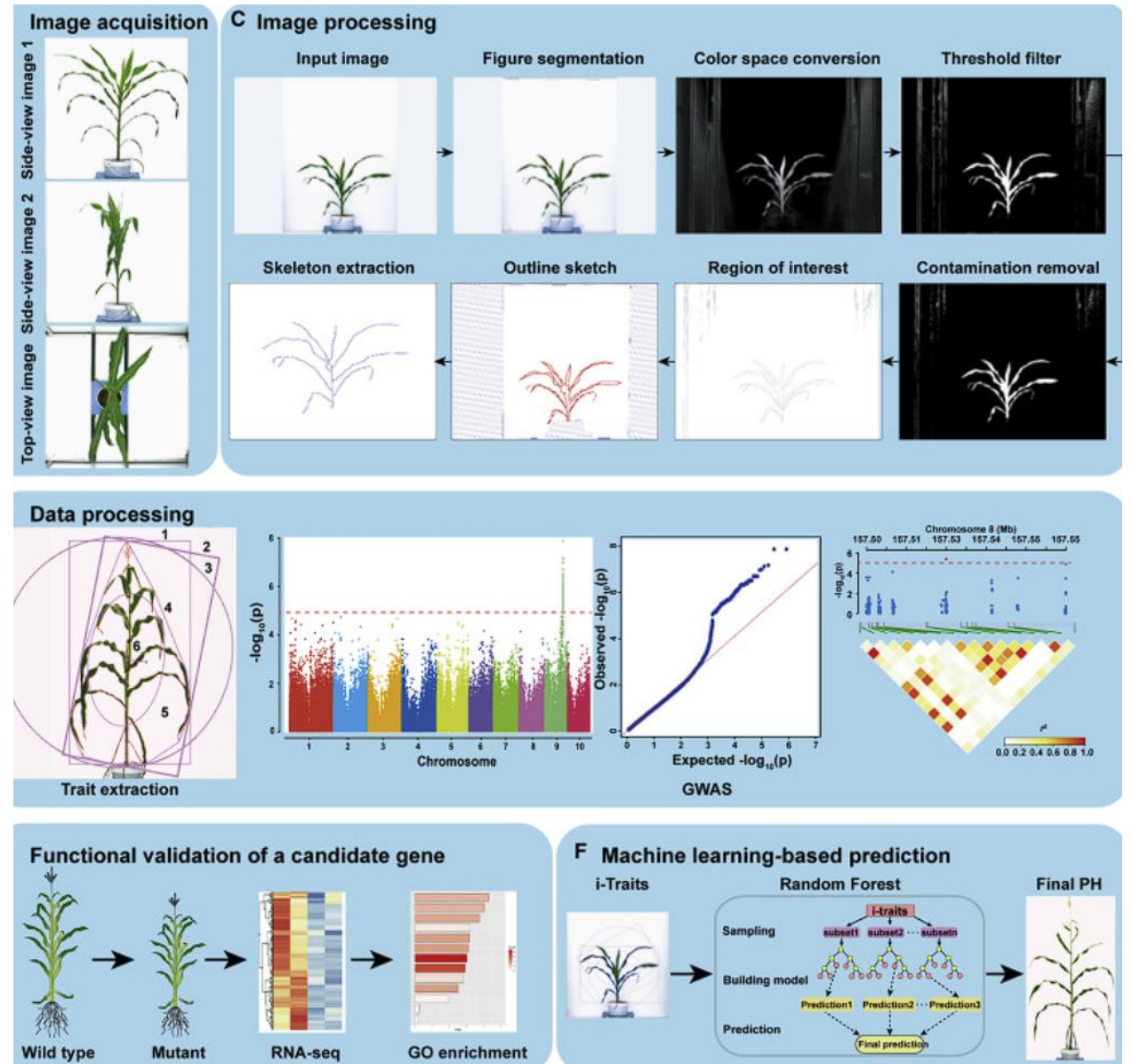
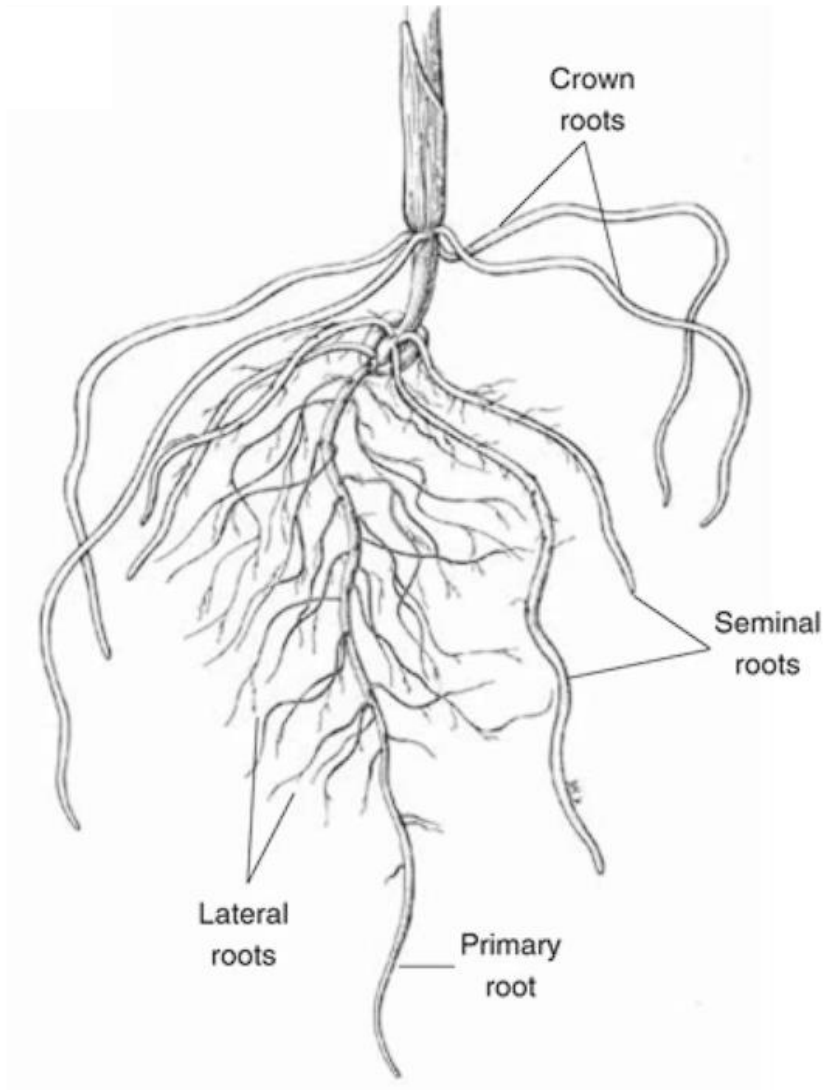


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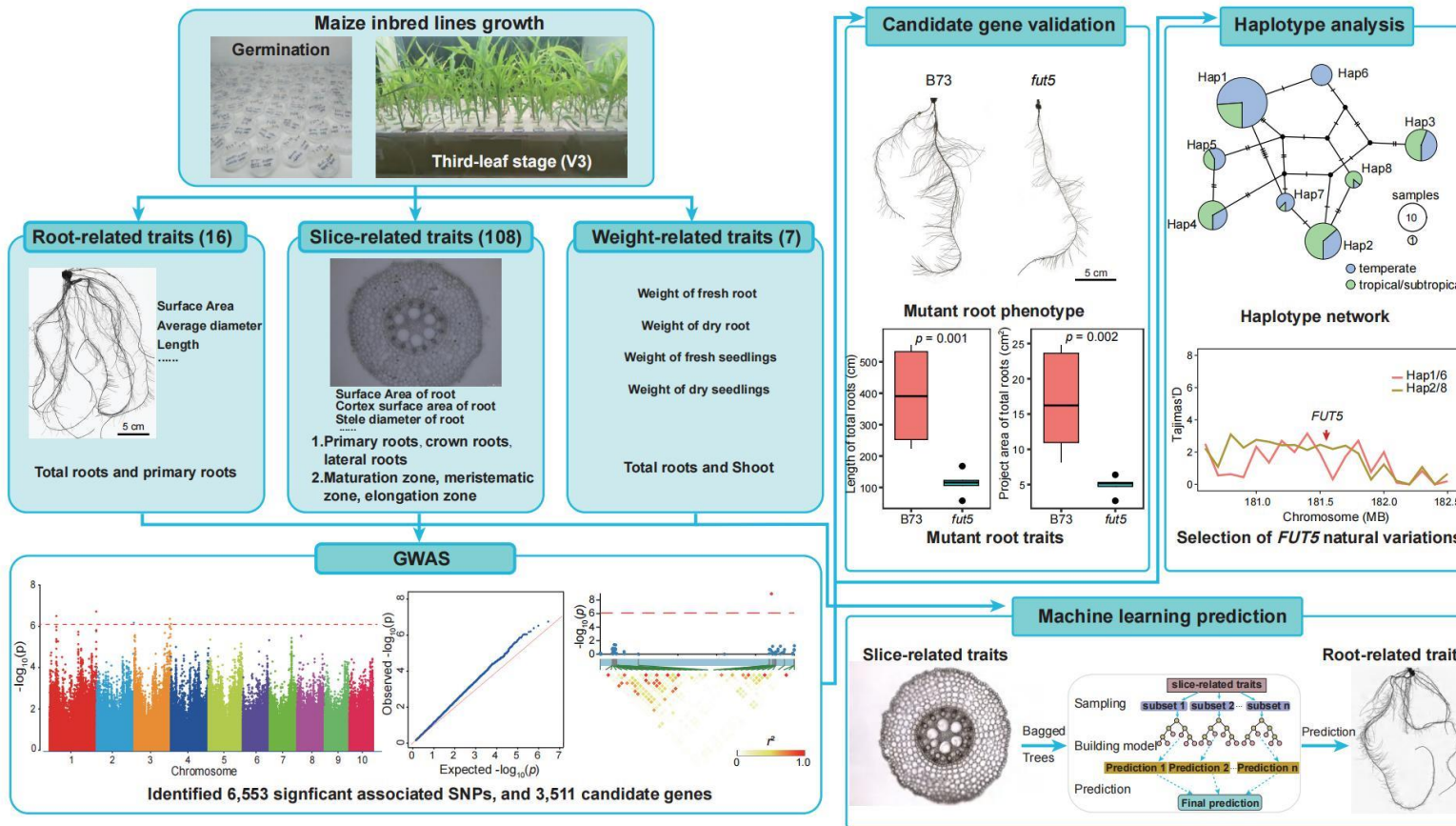
Background



Highlight



Phenomics of maize roots



- Root anatomical traits were analyzed in 316 maize lines, revealing significant differences between tropical/subtropical and temperate lines.
- GWAS identified 3,511 candidate genes for RSA.
- *FUT5* gene function was validated using EMS mutation, showing associations of different haplotypes with primary root traits.
- Machine learning models were developed using root slice traits, achieving high accuracy in predicting maize RSA.

Identification of root phenotypes in maize seedlings

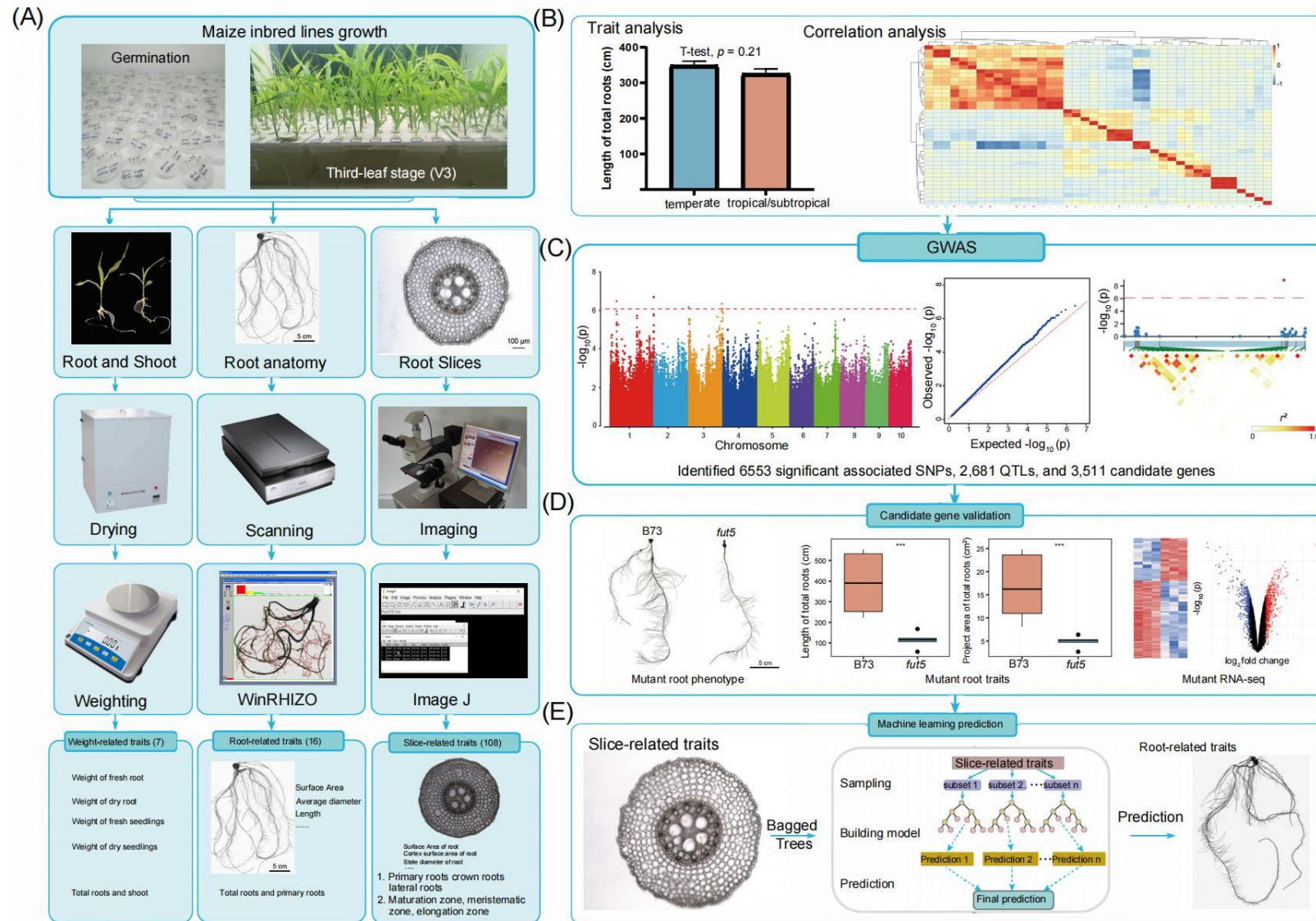


Figure 1. A flow diagram of the root architecture of maize was revealed by combining high-throughput phenotypes, GWAS, and predictive models.

Phenotypic variation of RSA traits in maize

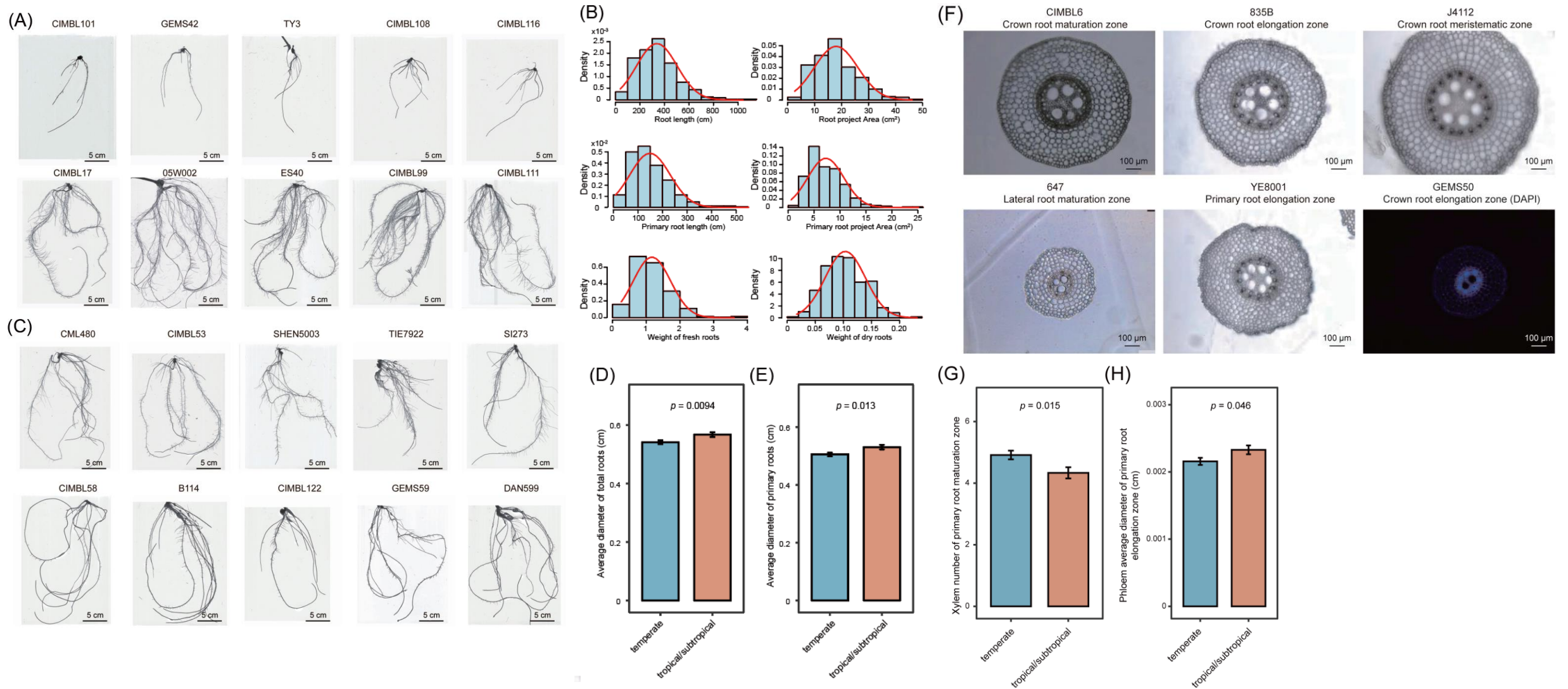


Figure 2. Root morphology and cross-sectional phenotype analysis of different maize inbred lines

Genetic basis of root architecture in maize

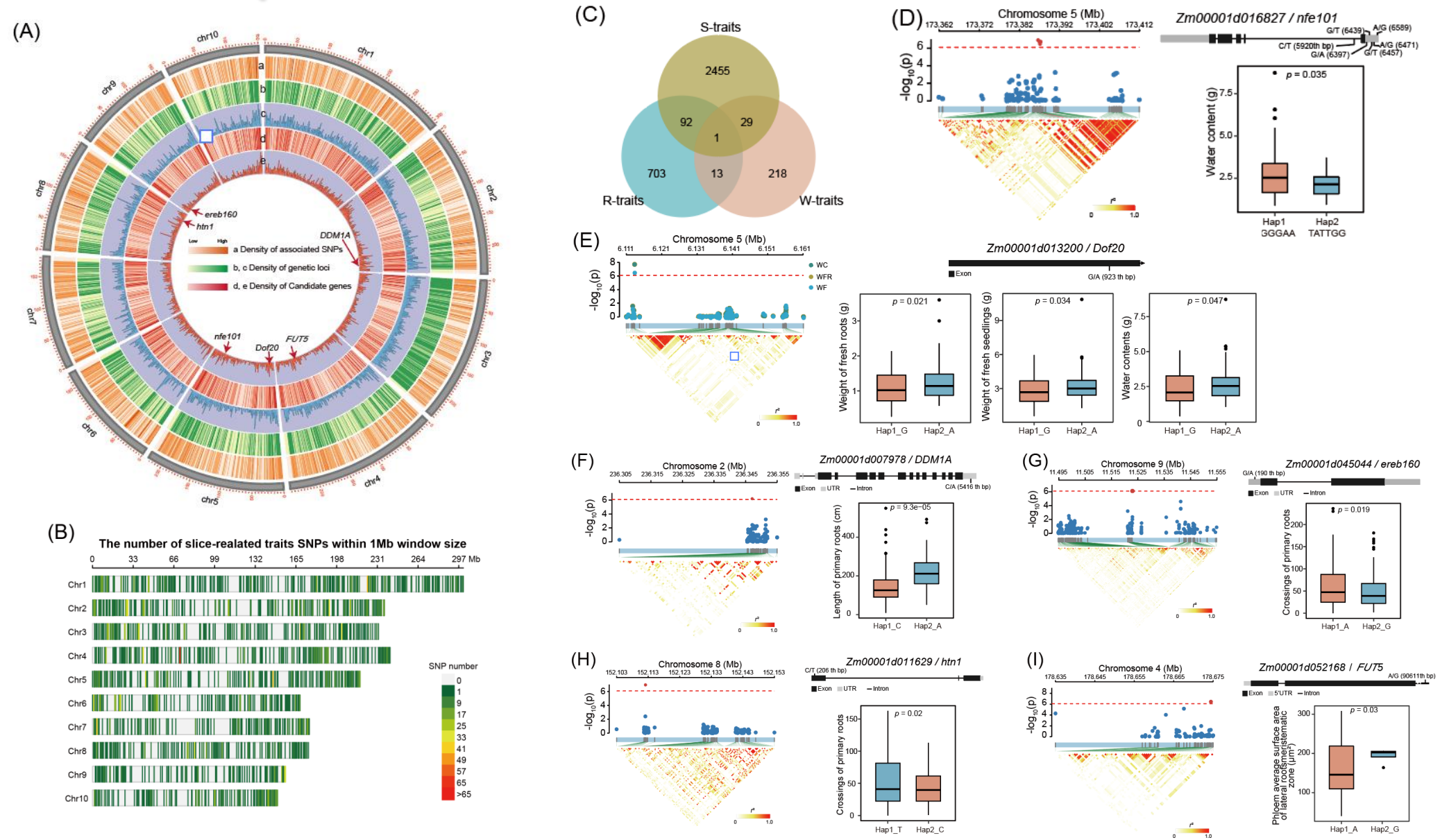


Figure 4. GWAS identification of candidate genes for variation in W-traits, R-traits, and S-traits in maize

Functional verification of the candidate root architecture gene *FUT5*

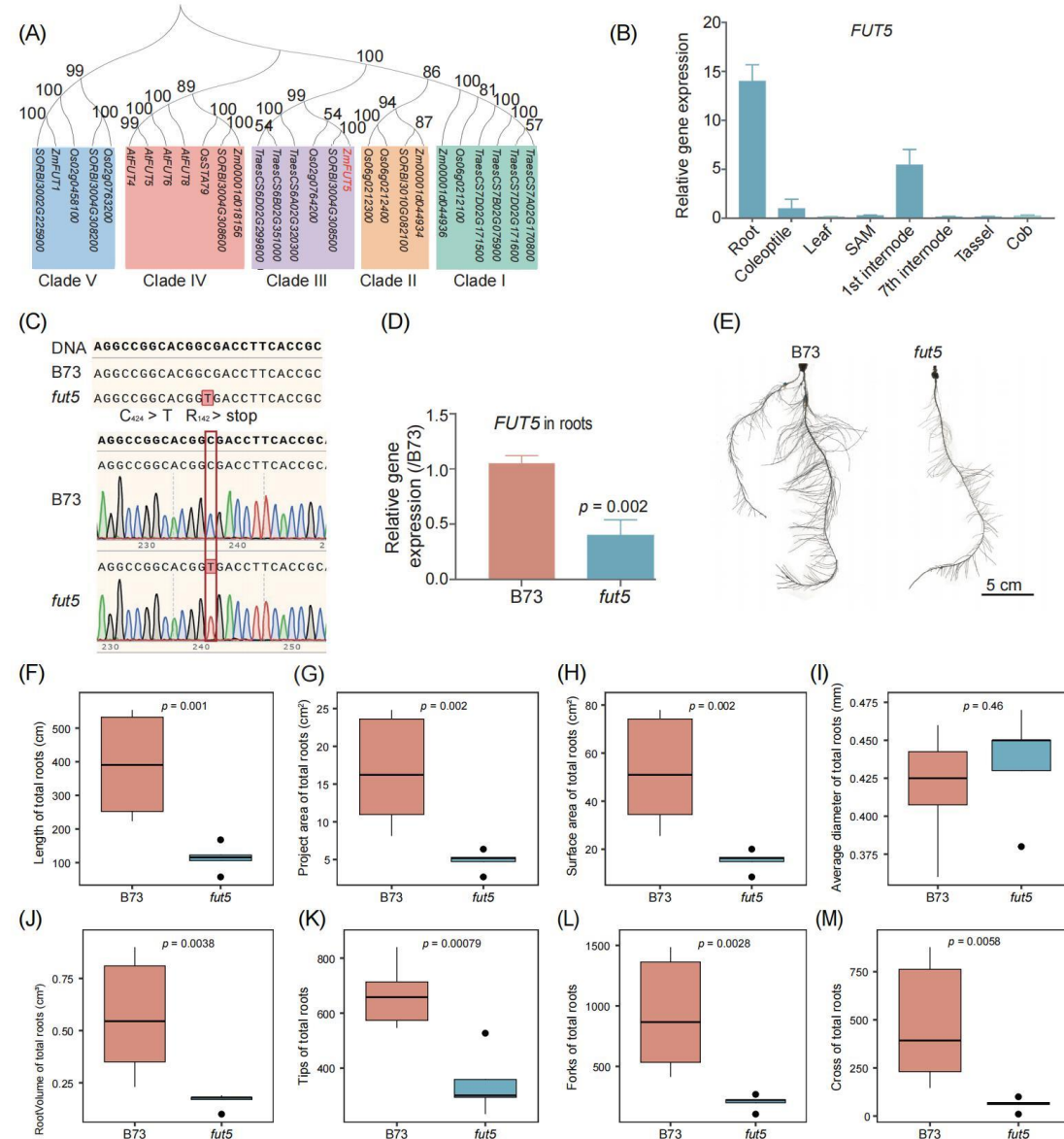


Figure 5. Effects of the *FUT5* gene on maize RSA

Functional verification of the candidate root architecture gene *FUT5*

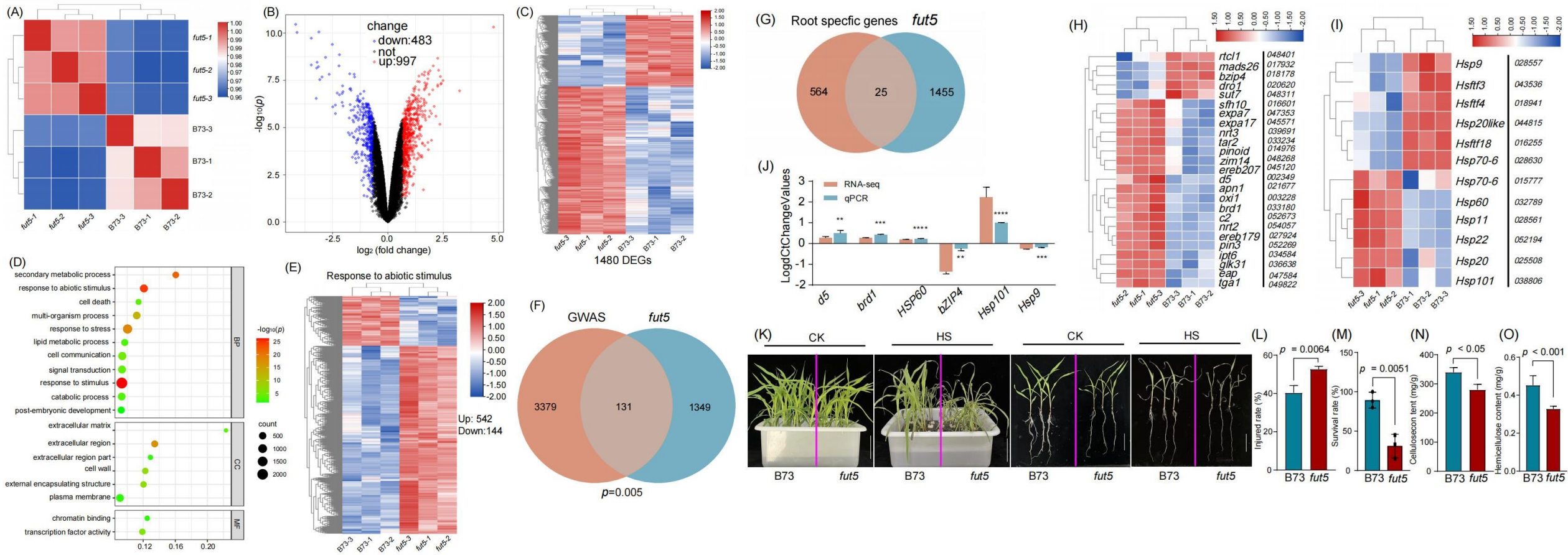


Figure 6. Transcriptome analysis of differentially expressed genes (DEGs) regulated by the *FUT5* gene

Selection of *FUT5* natural variations during the spread of maize from tropical to temperate regions

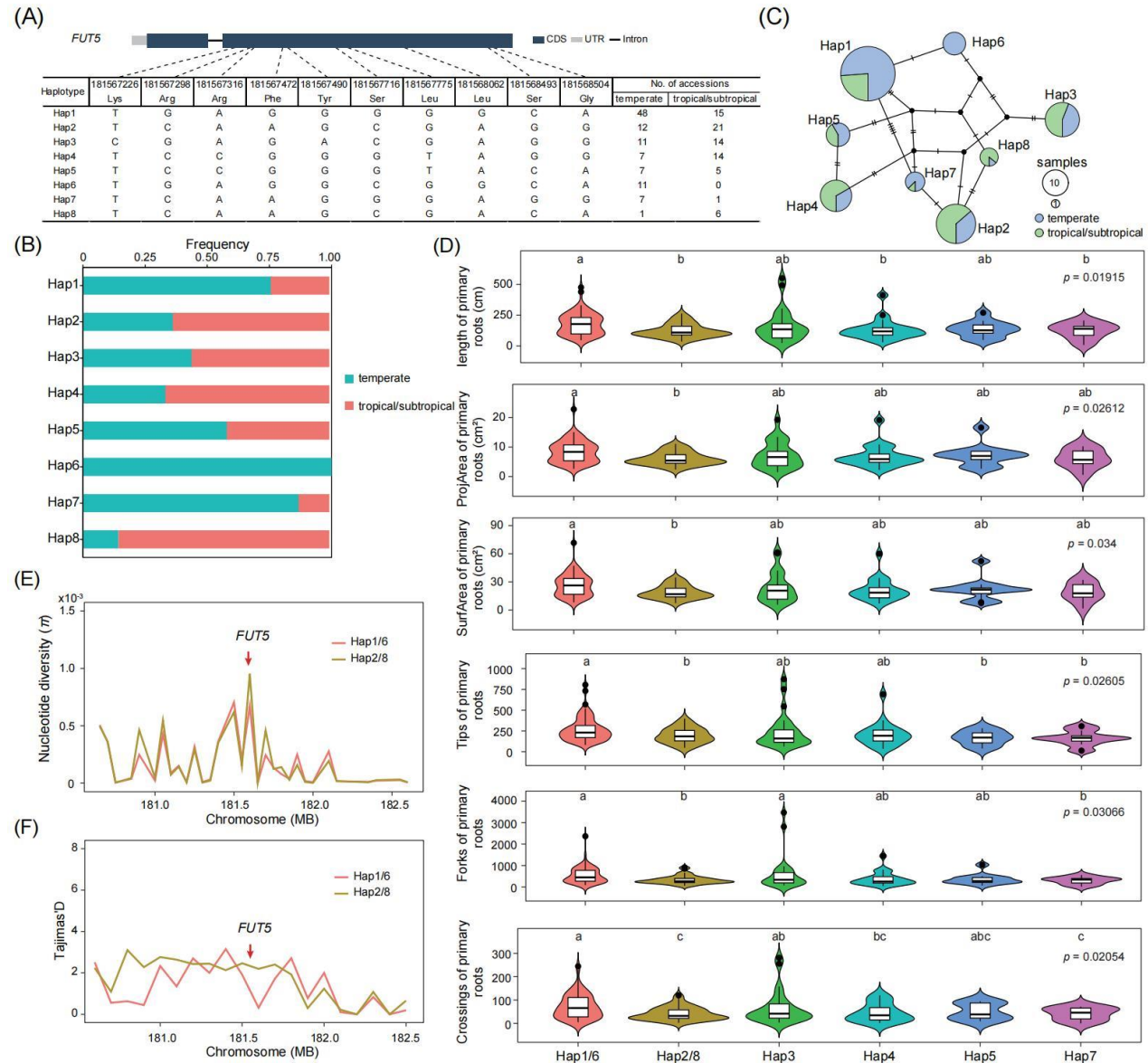


Figure 7. Selection of *FUT5* natural variations during the spread of maize from tropical to temperate regions

Machine learning-based predictive models for root architecture using cross-section traits

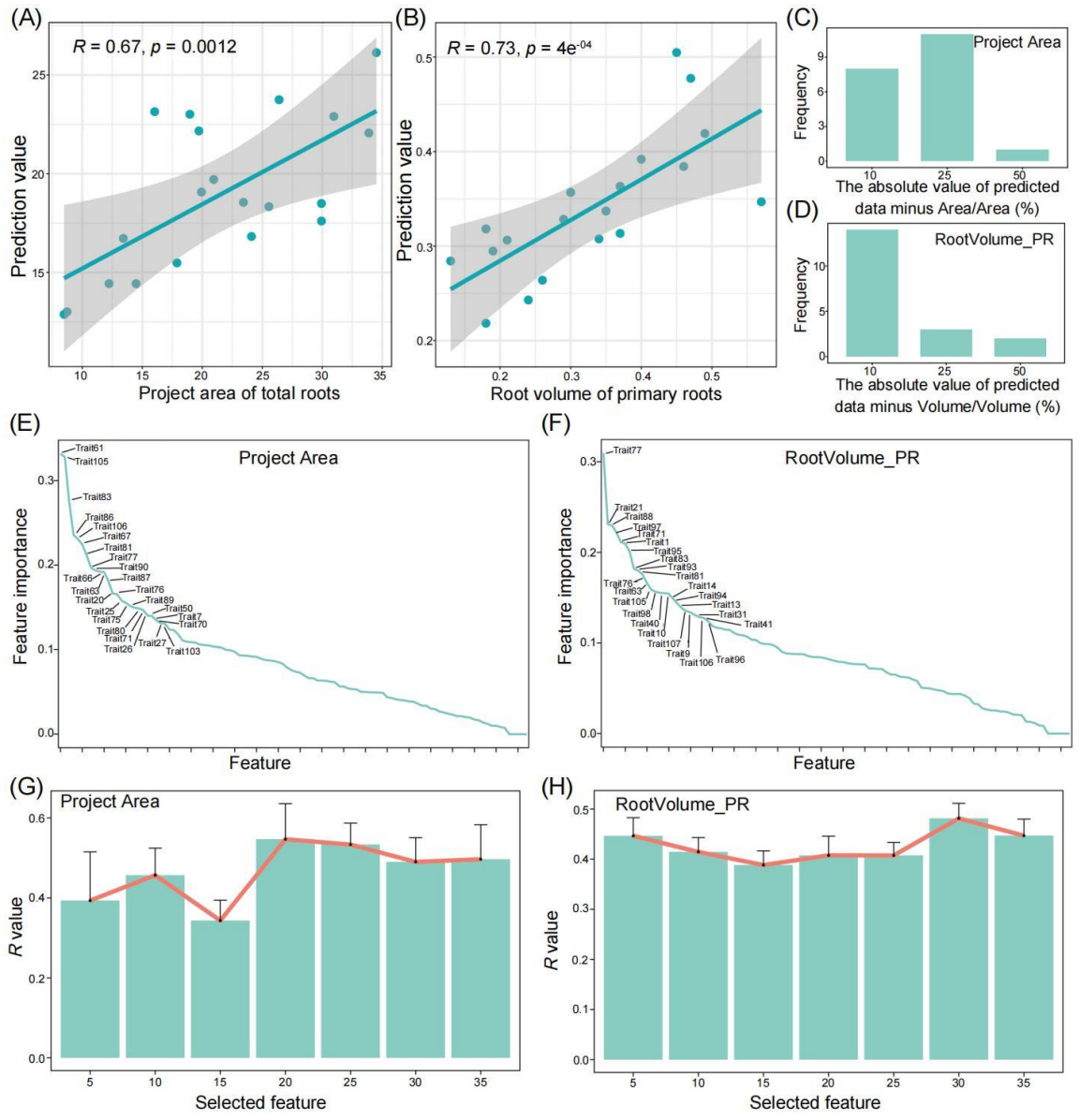


Figure 8. Prediction of R-traits using S-traits

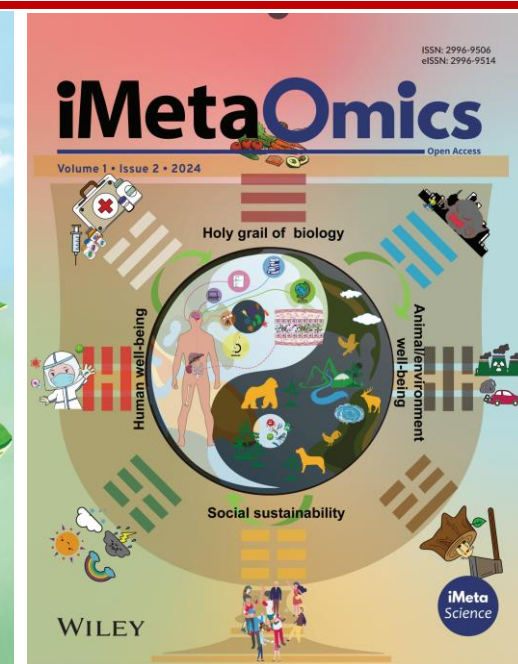
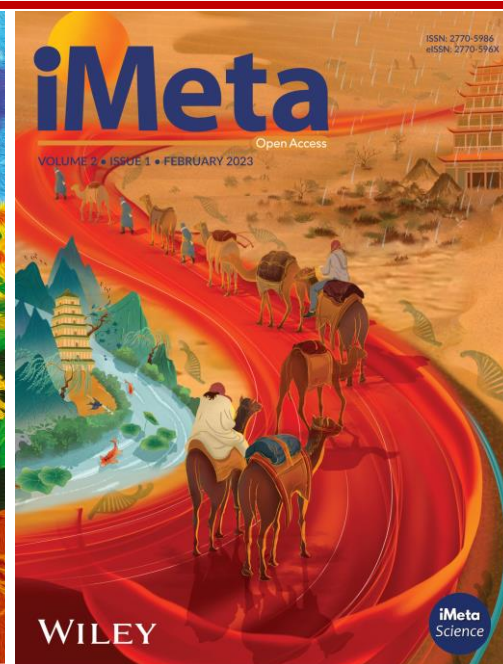


Summary

- Integrative phenomics, GWAS, and machine learning elucidate the genetic basis of temperate zone adaptation of maize roots
- The natural variation of *FUT5* is a key target for the adaptive evolution of roots
- Machine learning model provides theoretical support for root phenotype prediction and molecular design breeding



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