



Integrated high-throughput phenomics and transcriptomics uncover the transcriptional mechanisms underlying rice responses to elevated CO₂ concentration and cadmium stress

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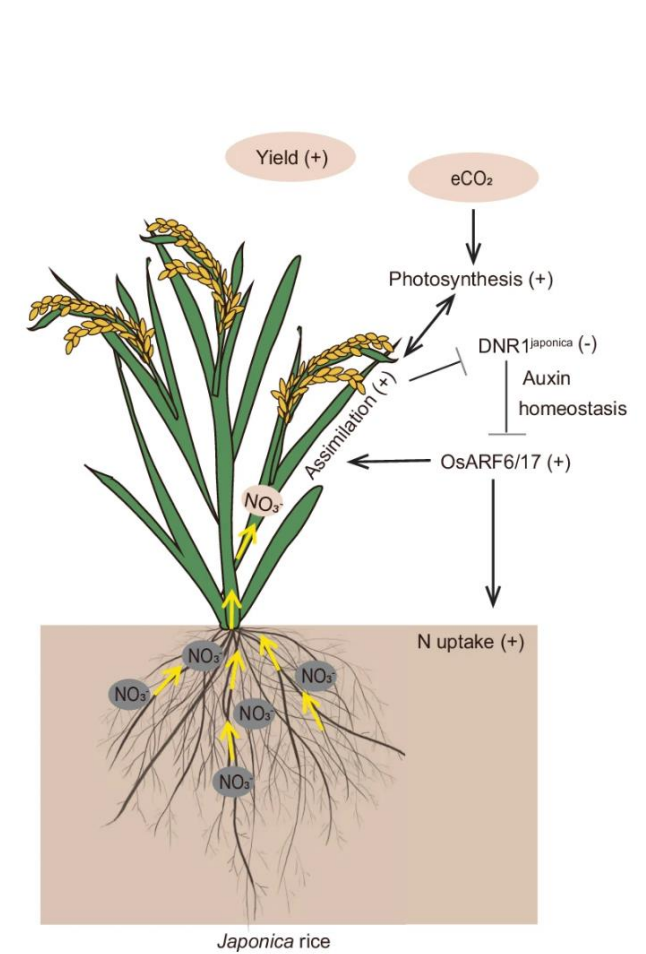
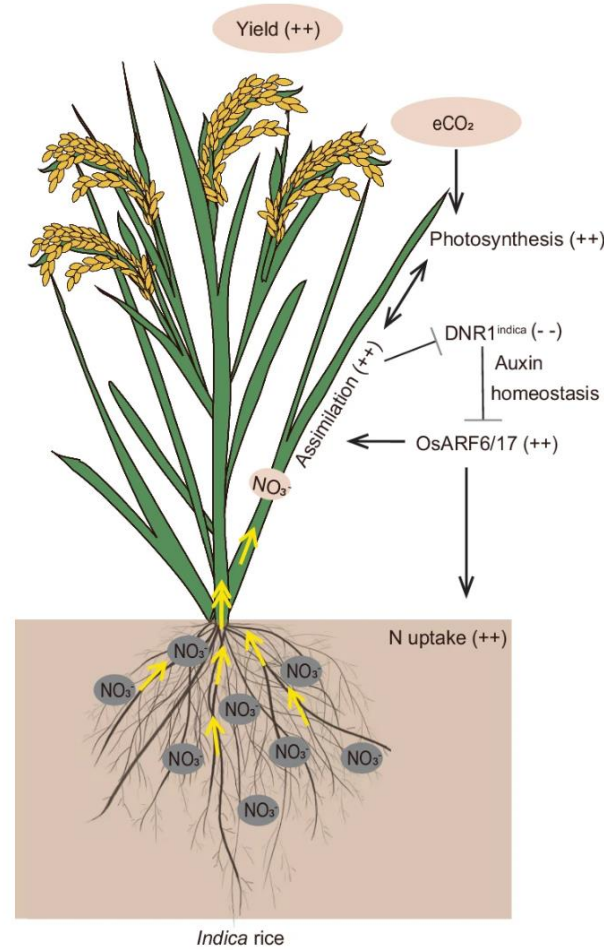
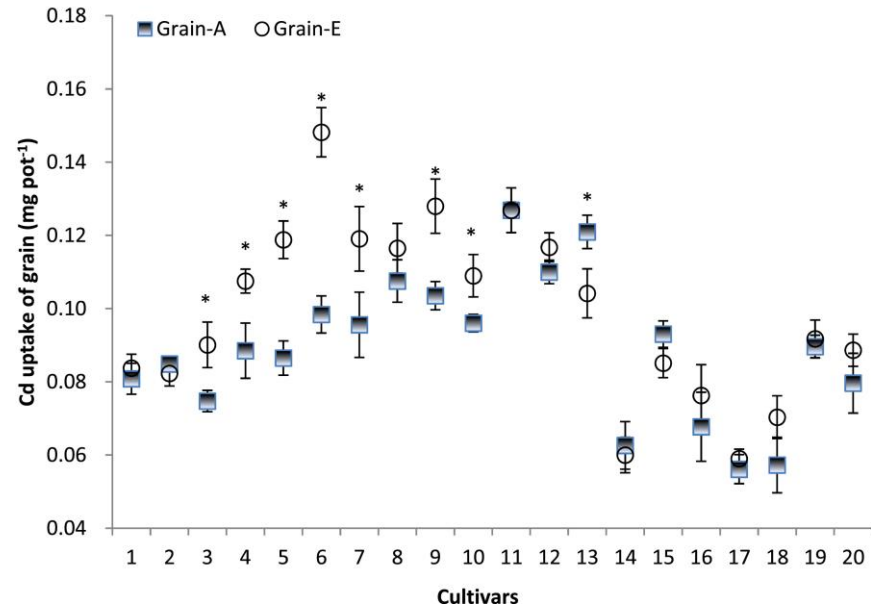
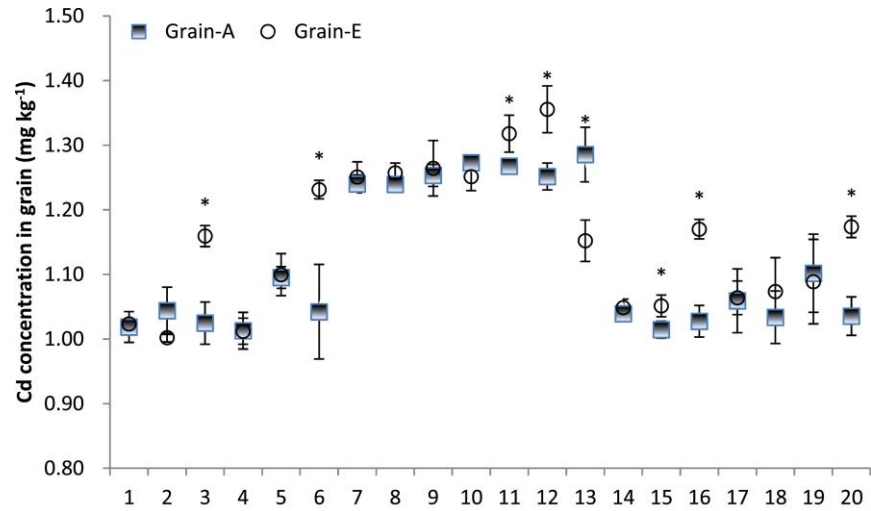
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Background

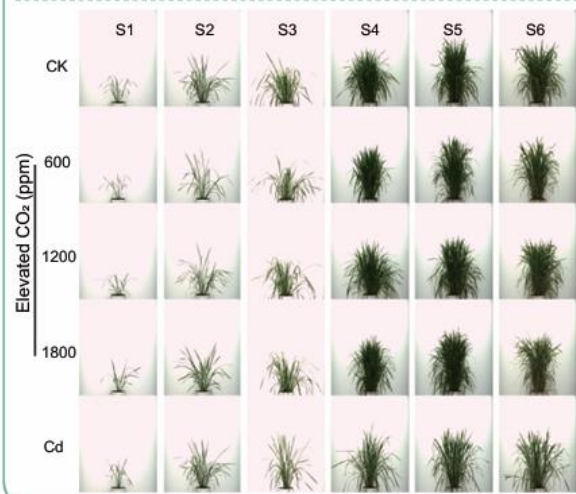




Highlight

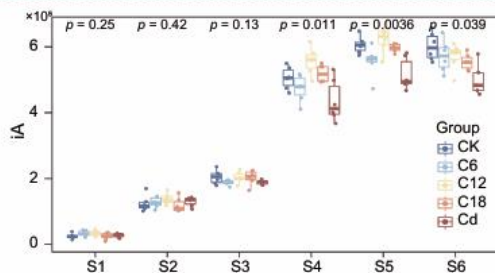
High-throughput phenomics

High-throughput phenomics of rice cultivar Nip under eCO₂ and Cd stress



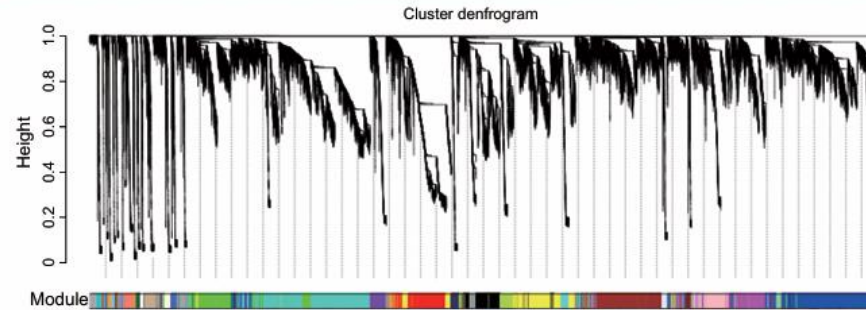
Dynamic change of phenotype

Dynamic change pattern analysis of traits from phenomics

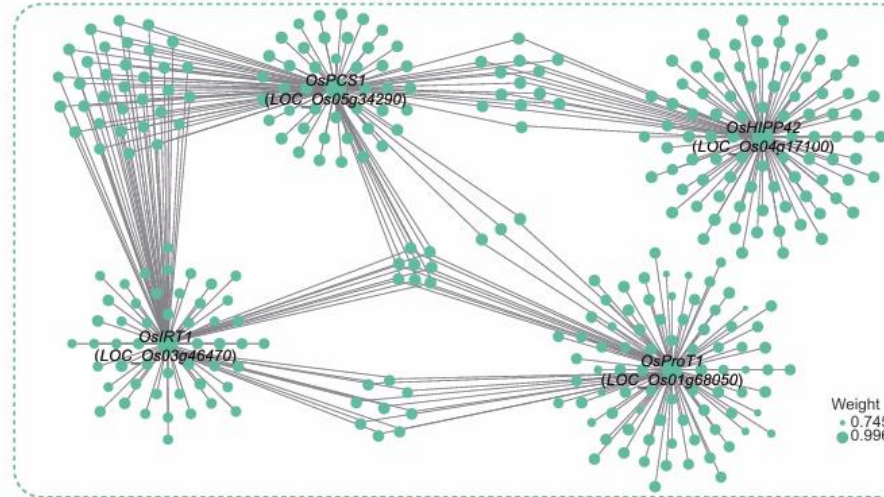


Integrative network analysis

Weight co-expression gene co-expression network in rice responses to eCO₂ and Cd stress



Identification key subnetworks and hub genes in response to eCO₂ and Cd stress in rice



- Acquisition of high-throughput phenomics covering six key growth stages of rice cultivar Nipponbare under eCO₂ and Cd stress.
- Differentially expressed genes and hormone-related genes exhibit a similar expression pattern under Cd and eCO₂ using multi-tissue transcriptome analysis.
- We constructed an integrative co-expression network and identified five stress-responsive subnetworks.
- Haplotype 2 frequency of hub gene OsMSR3 decreases from low- to high-latitude regions and from southern to northeastern China, mirroring the geographic distribution of Cd-contaminated soils.

Dynamic phenotypic changes in rice under Cd and eCO₂ conditions

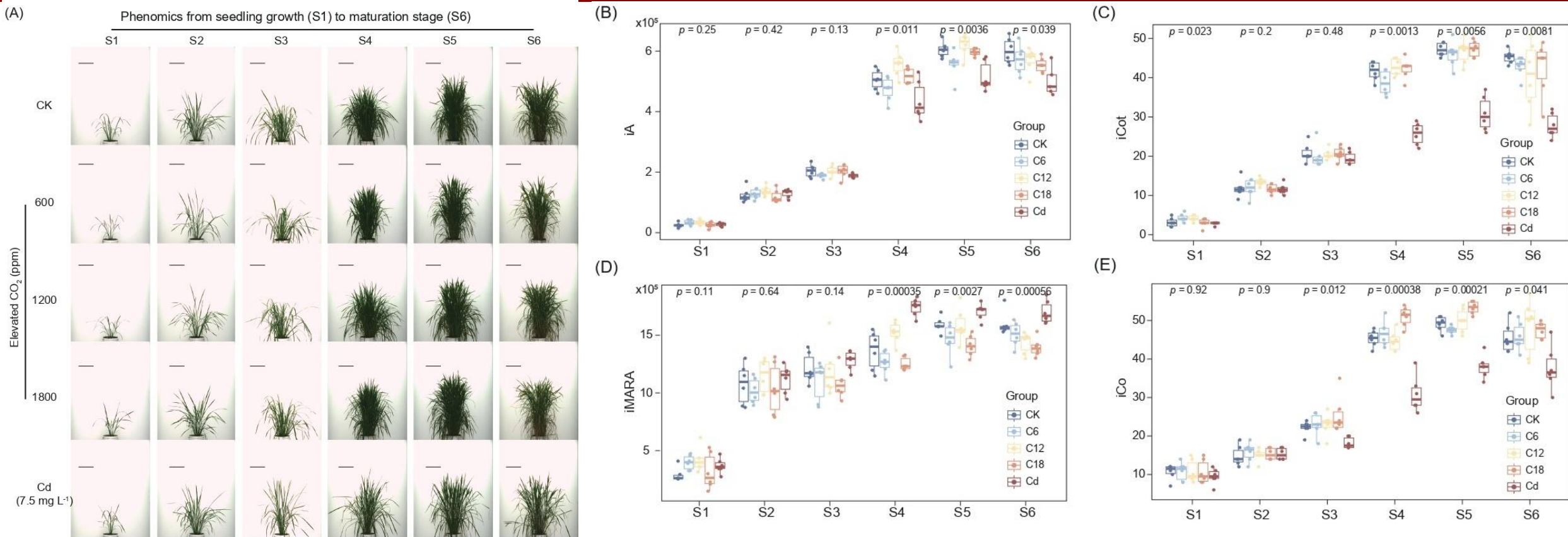
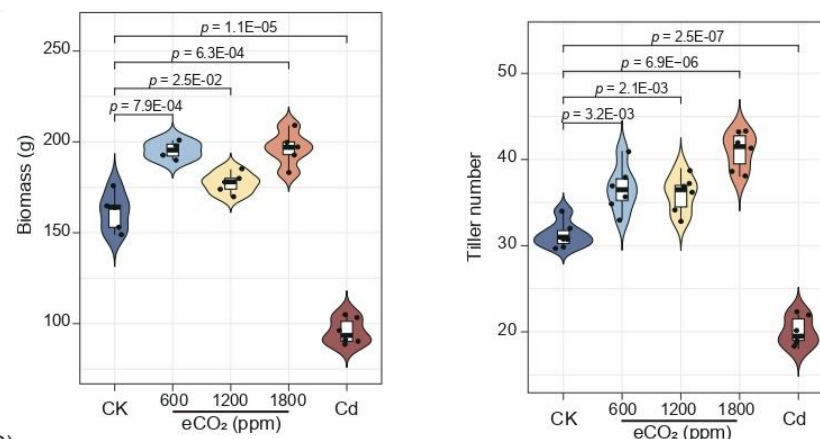


Figure 1. High-throughput phenomics of rice under elevated carbon dioxide (eCO₂) concentration and cadmium (Cd) stress



Multi-tissue transcriptomes reveal shared transcriptional functions in response to Cd and eCO₂

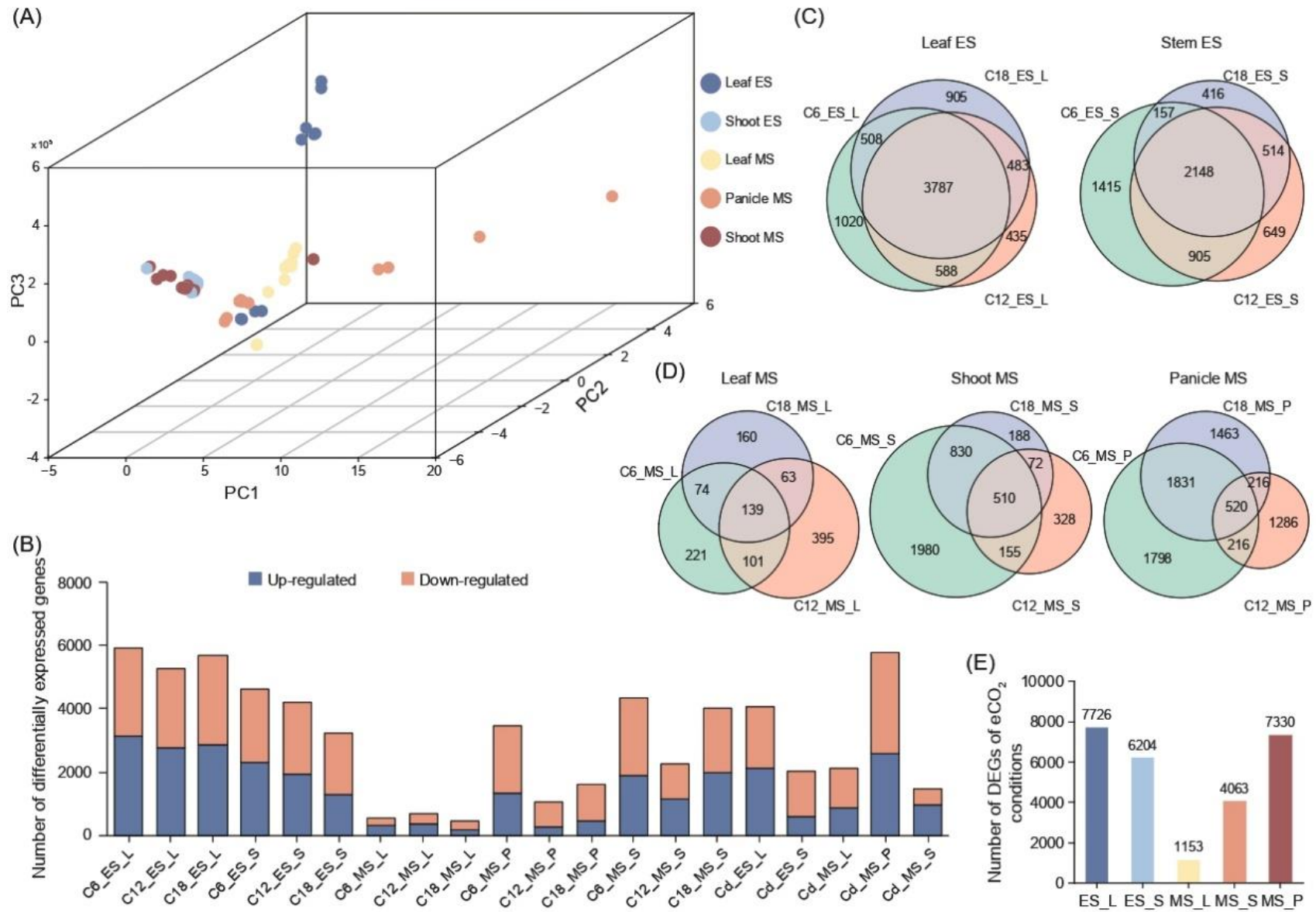


Figure 2. Tissue-specific transcriptomic profile of rice in response to eCO₂ and Cd stress

Multi-tissue transcriptomes reveal shared transcriptional functions in response to Cd and eCO₂

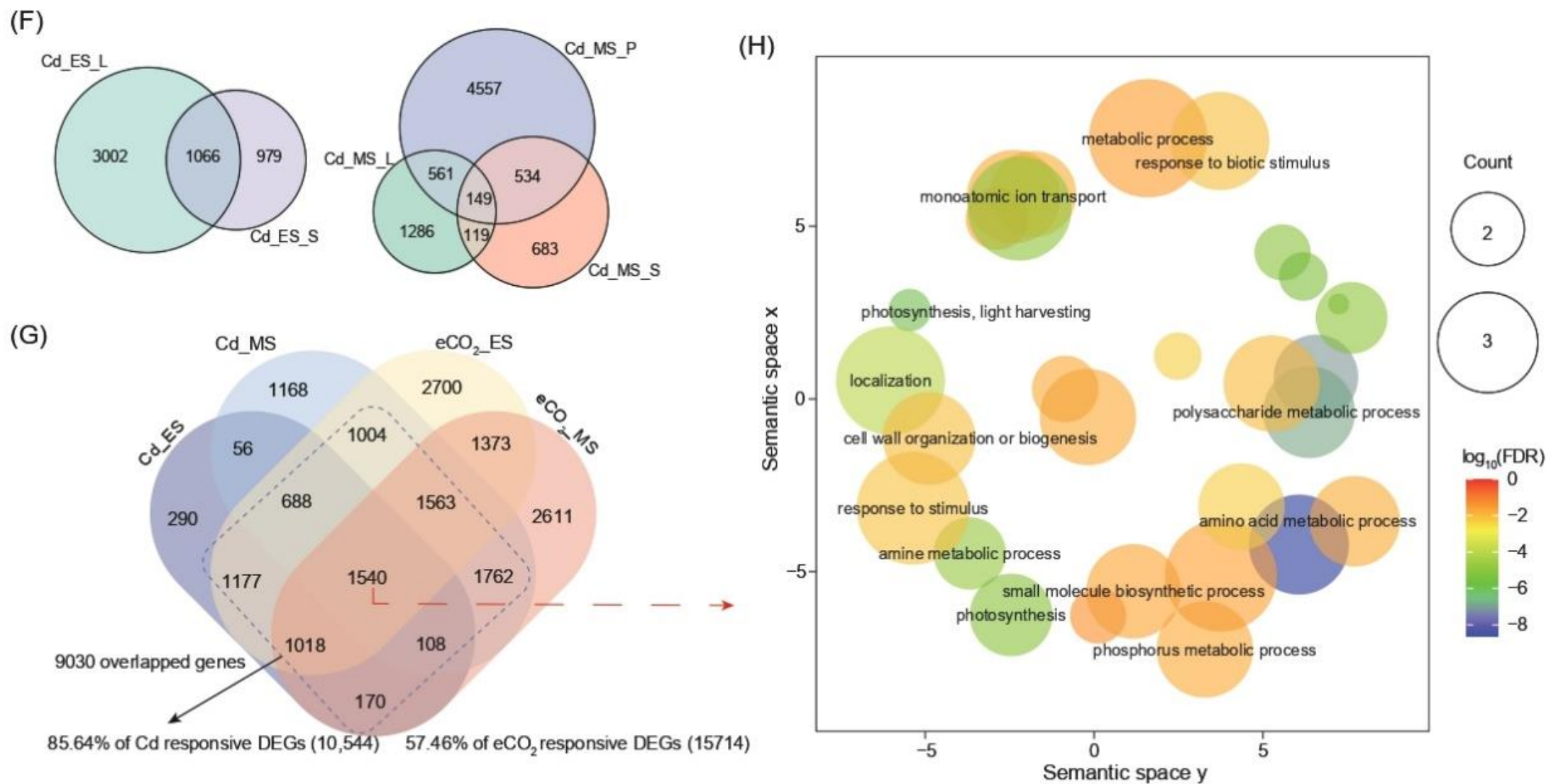


Figure 2. Tissue-specific transcriptomic profile of rice in response to eCO₂ and Cd stress

Dynamic changes in hormone-related genes under Cd and eCO₂ conditions

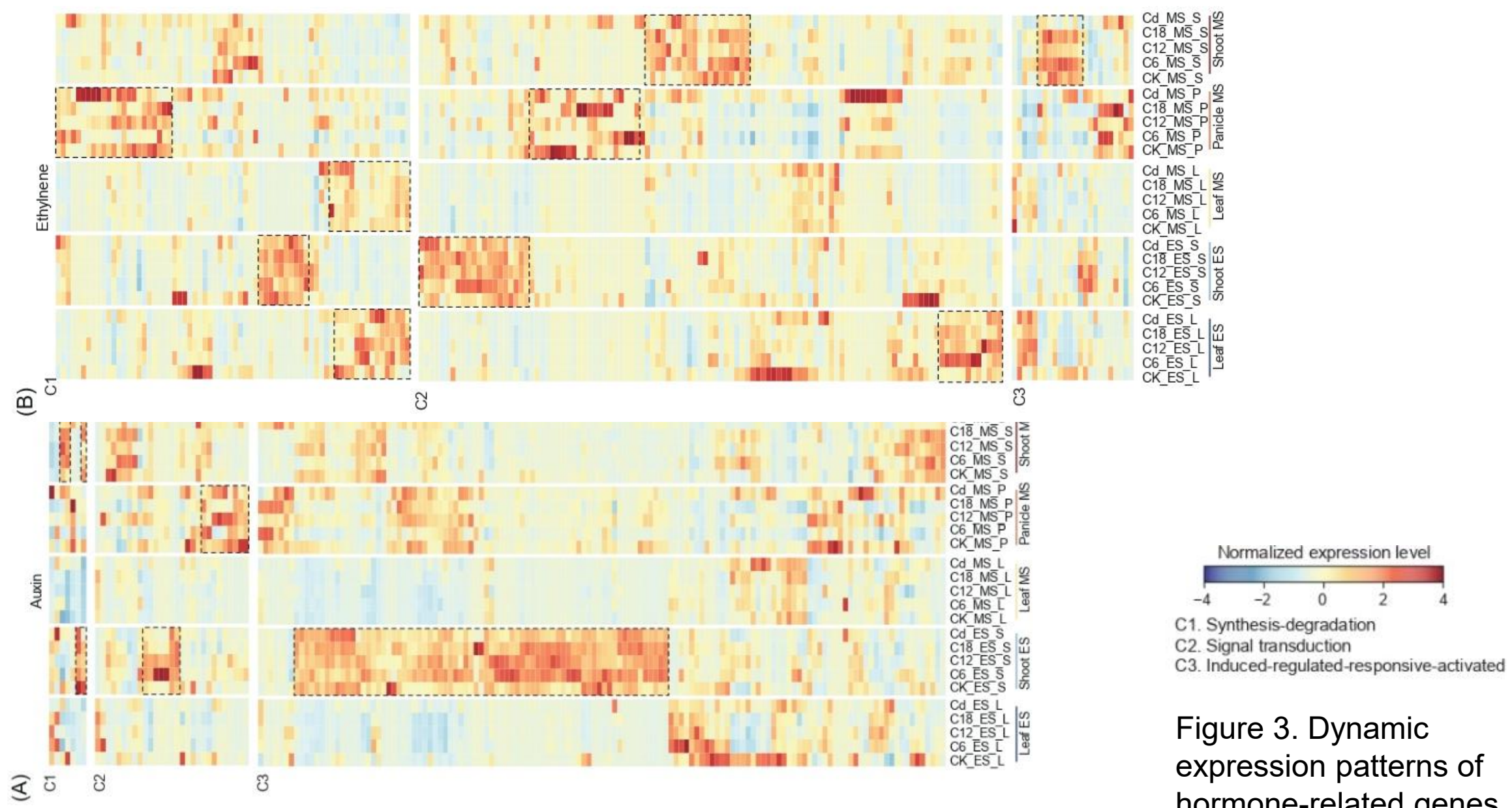


Figure 3. Dynamic expression patterns of hormone-related genes

Dynamic changes in hormone-related genes under Cd and eCO₂ conditions

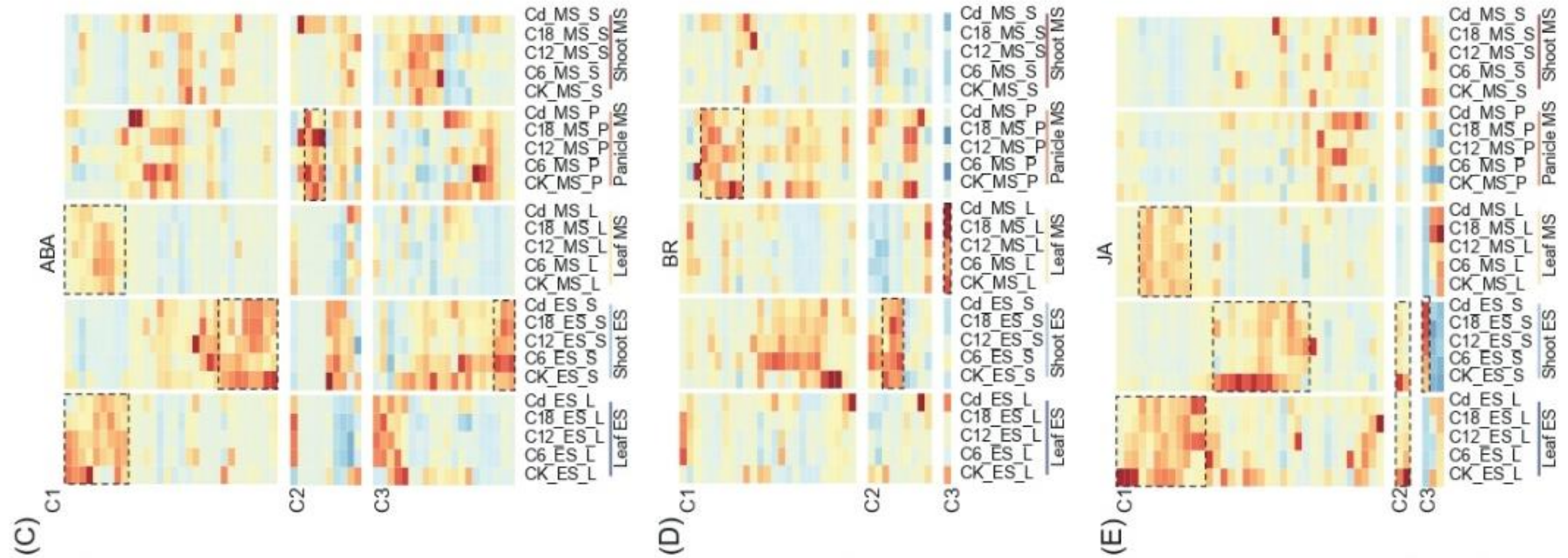
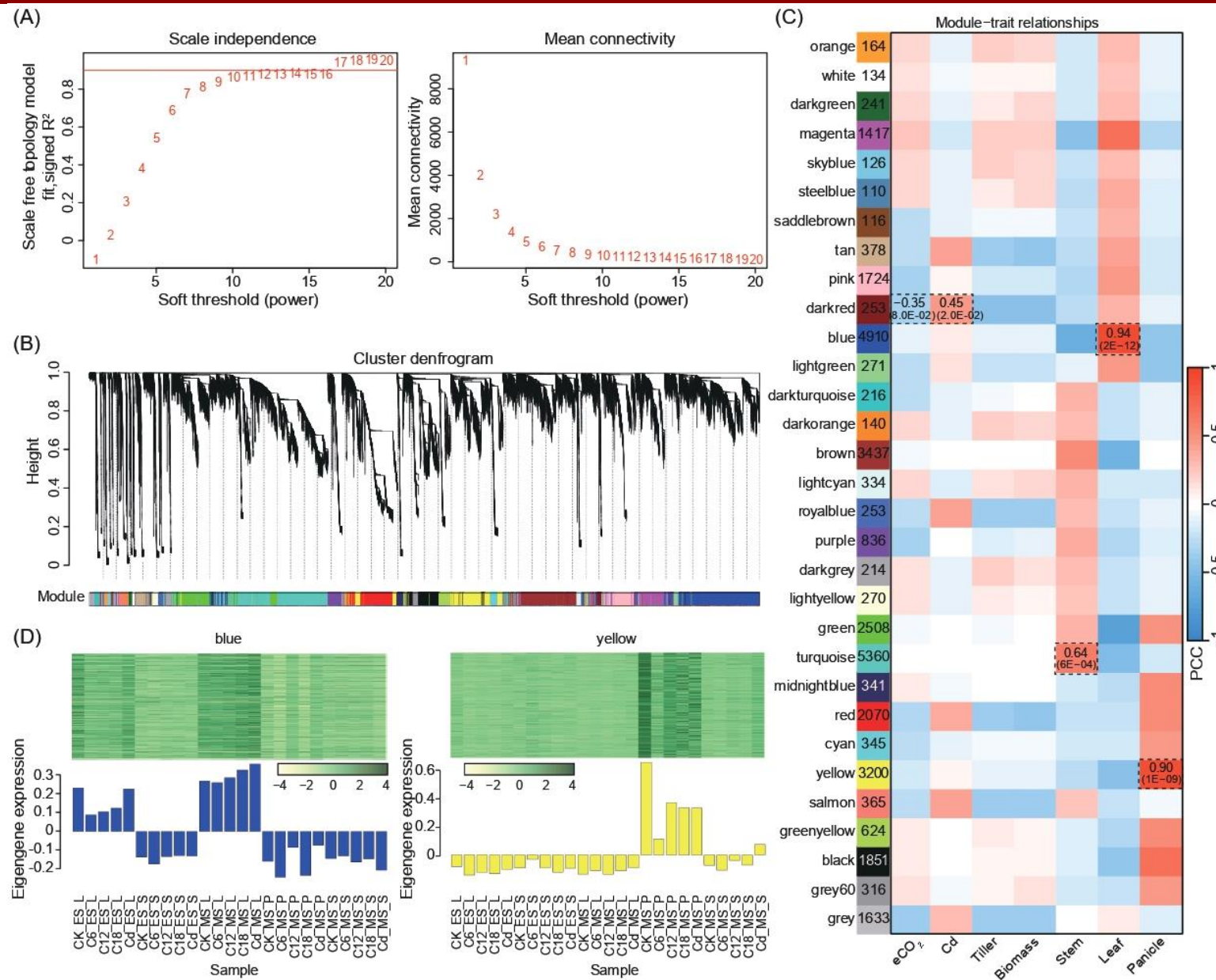


Figure 3. Dynamic expression patterns of hormone-related genes

Construction of an integrative network in response to Cd and eCO₂ in rice



Transcriptional regulatory subnetworks of rice respond to Cd and eCO₂

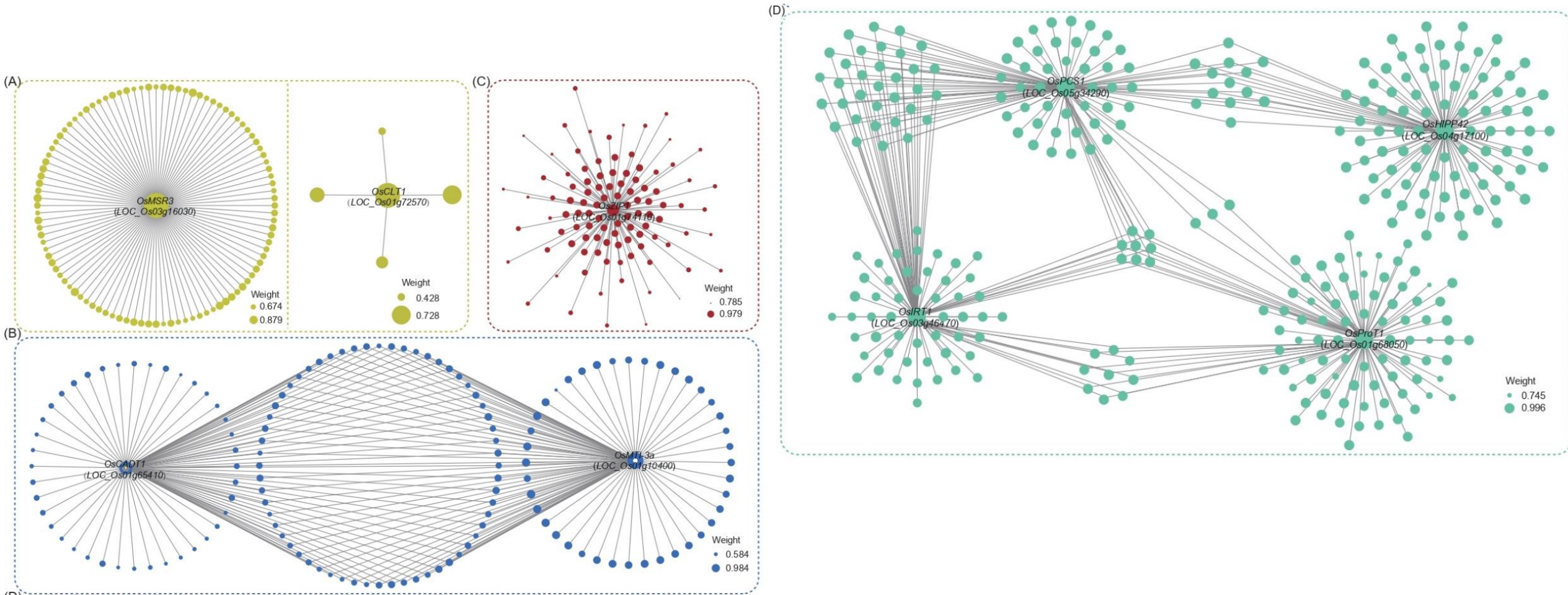


Figure 5. Effects of the *FUT5* gene on maize RSA

Population analysis of *OsMSR3* identifies a potential breeding target for low-Cd rice under rising CO₂

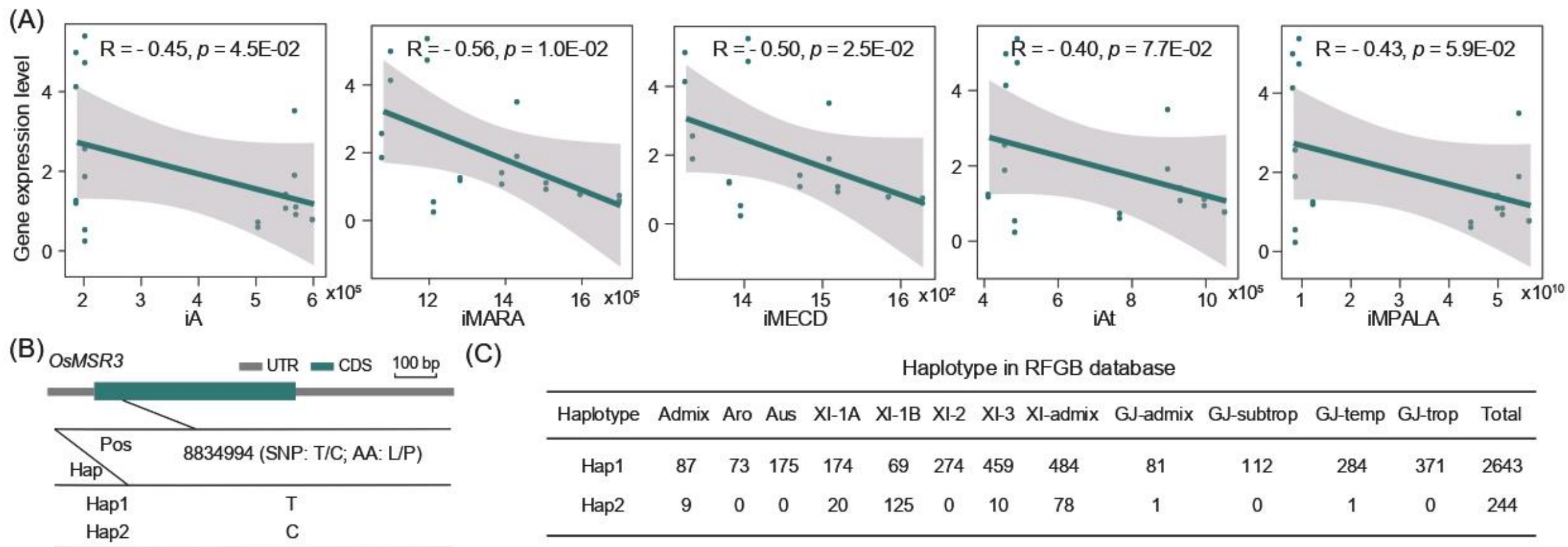


Figure 6. Haplotype analysis of *OsMSR3*

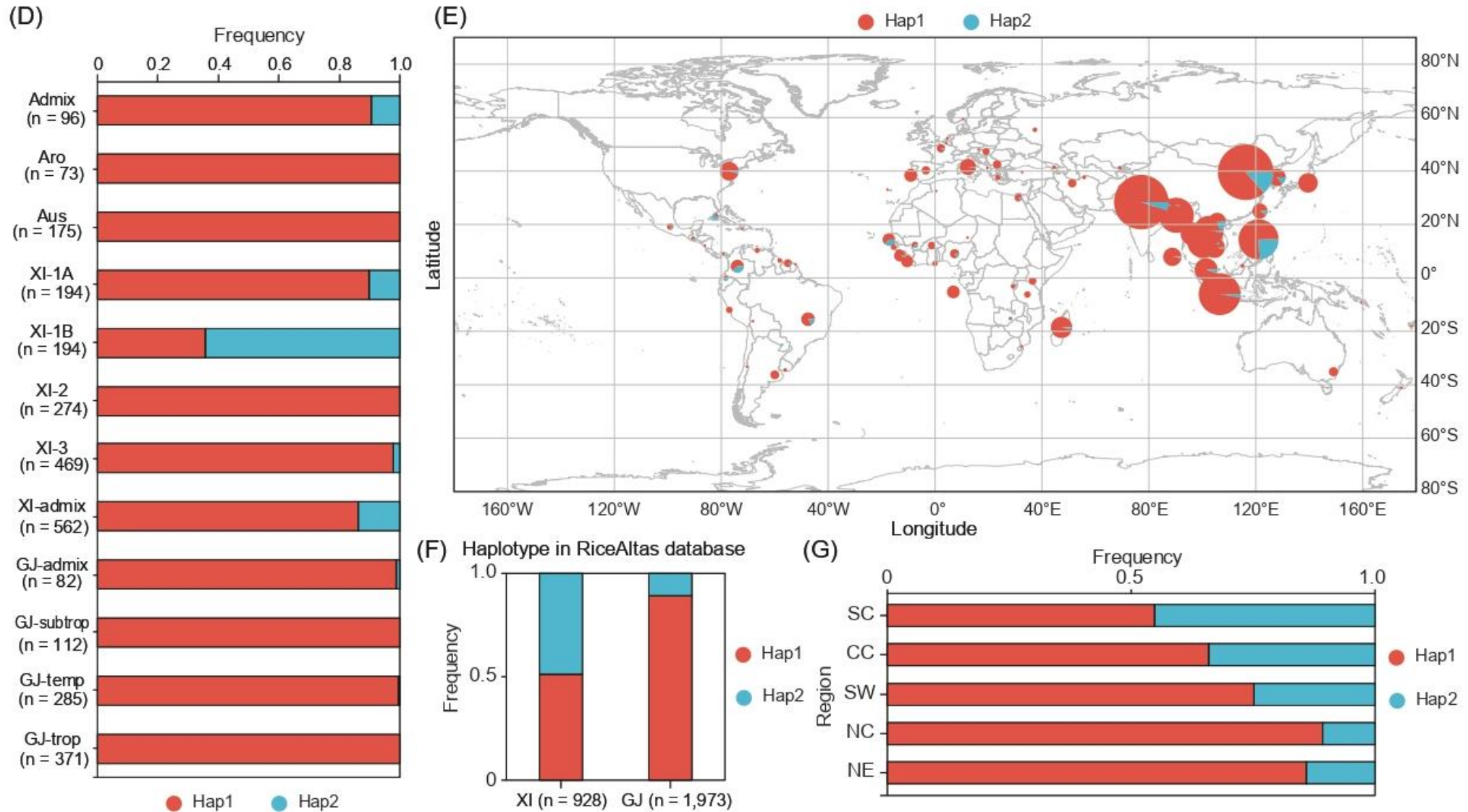


Figure 6. Haplotype analysis of *OsMSR3*



Summary

- ❑ Constructing an integrative phenotype-transcriptome network in rice under Cd and eCO₂ conditions
- ❑ High-throughput phenomics analysis reveals phenotypic similarities and differences in rice responses to Cd and eCO₂
- ❑ Differentially expressed genes and hormone-related genes show a similar expression pattern in response to both Cd and eCO₂
- ❑ Population analysis of OsMSR3 identifies a potential breeding target for low-Cd rice under rising CO₂

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