16th INTERNATIONAL RAPESEED CONGRESS

華中農業大學
HUAZHONG AGRICULTURAL UNIVERSITY

Combining Physio-Biochemical Characterization and Transcriptome Analysis Reveal the Responses to Varying Degrees of Drought Stress in *Brassica napus*

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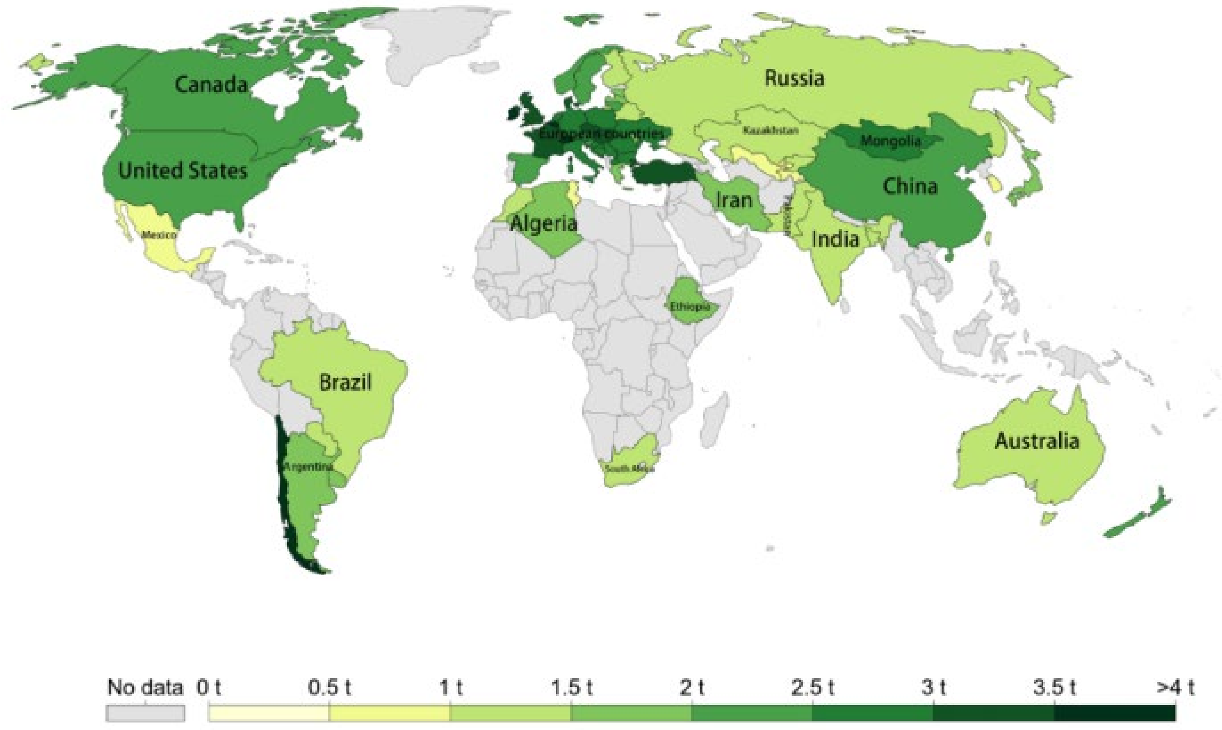
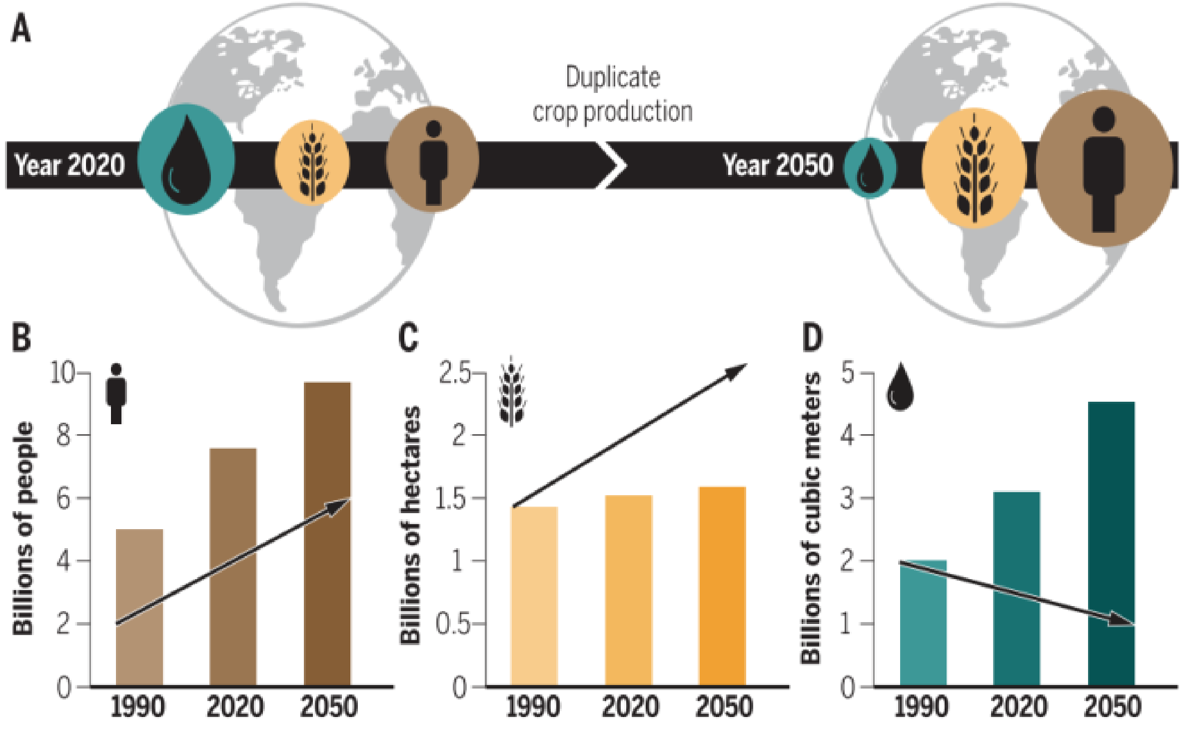
- Background
- Combining physio-biochemical characterization and transcriptome analysis reveal the Responses to Varying Degrees of Drought Stress in *B.napus*
- Genome-wide association studies of stomatal conductance under mild drought stress

Drought seriously affected the distribution of rapeseed

- **Rapeseed is a valuable, economically essential, and widely growing oilseed crop globally (Maria Batool, et al 2022) .**
- **Over the past decade, drought has cost the world USD 30 billion in crop production losses.**



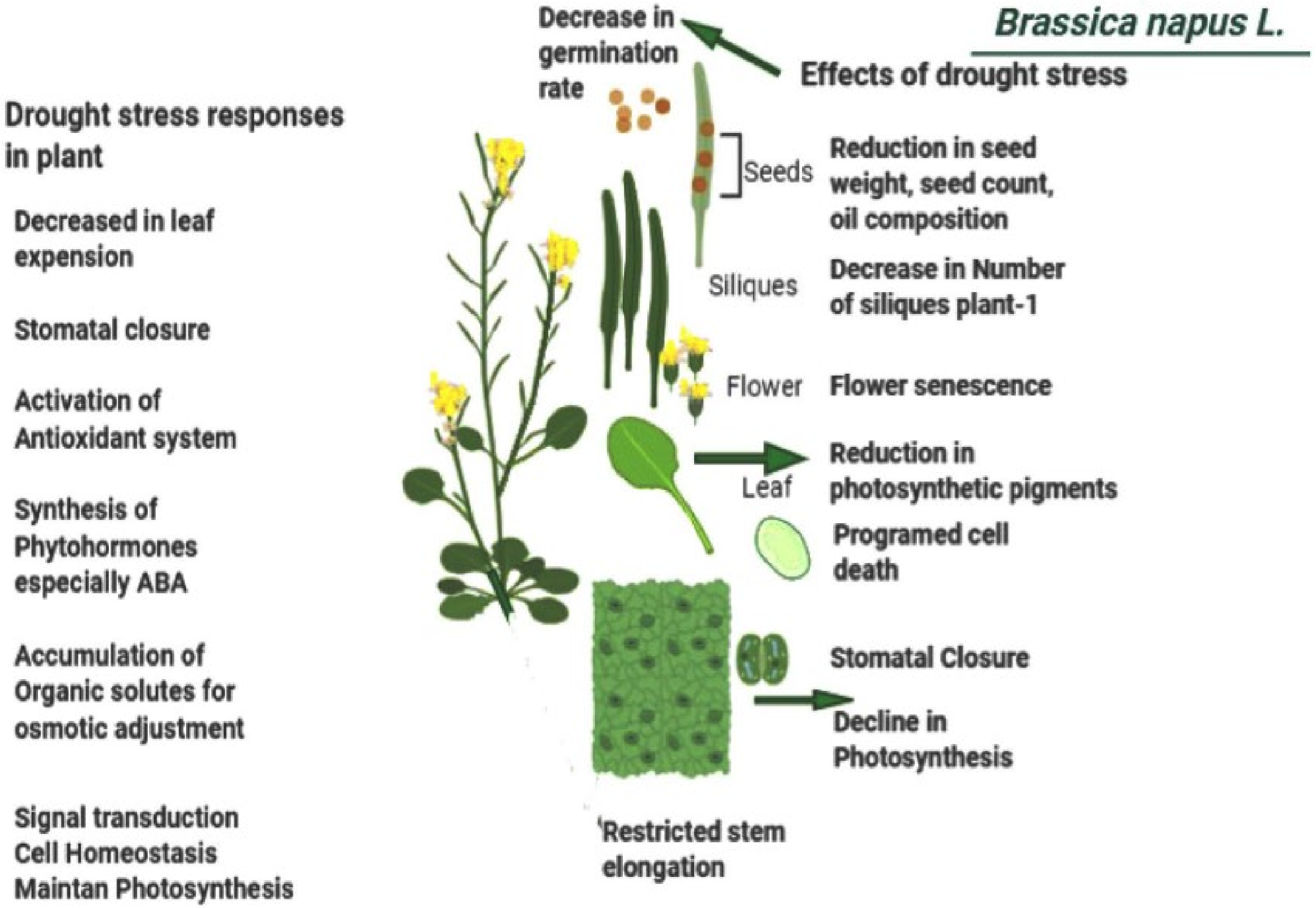
Batool et al, *J Plant Growth Regul*, 2022



Gupta et al, *Science*, 2020

Drought inhibits rapeseed growth and development

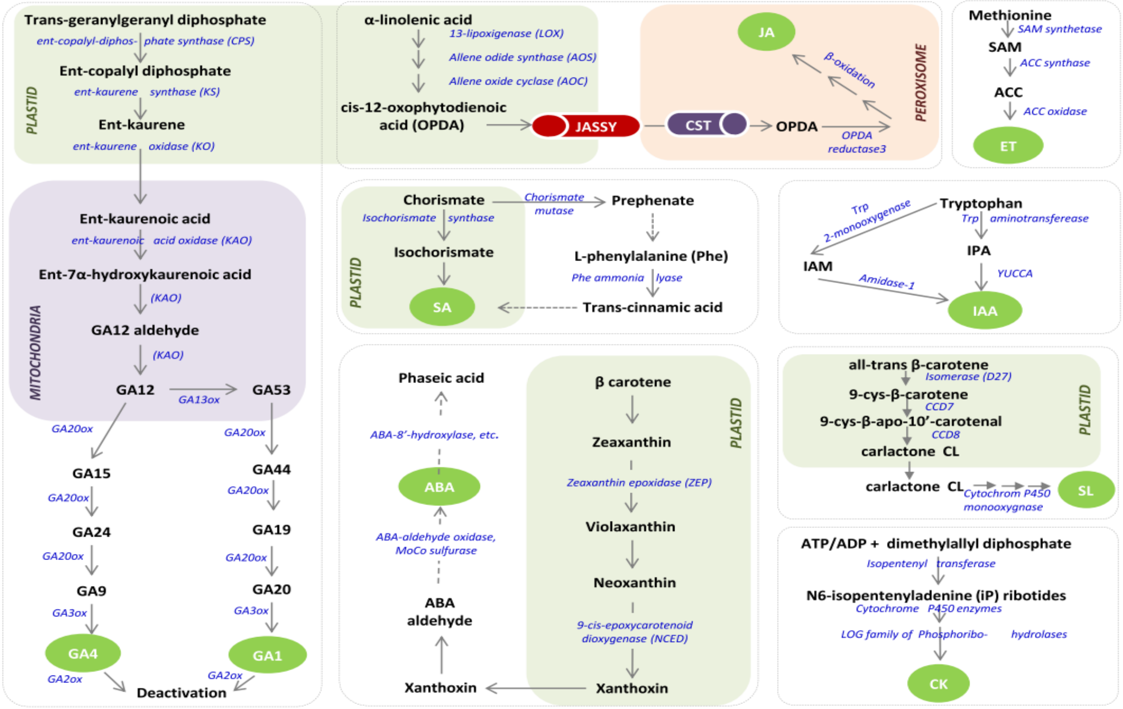
- **Drought stress causes cellular dehydration, affecting plant’ s morpho-physiological traits, reducing photosynthesis, yield-related attributes, seed germination and plant development (Maria Batool, et al 2022).**



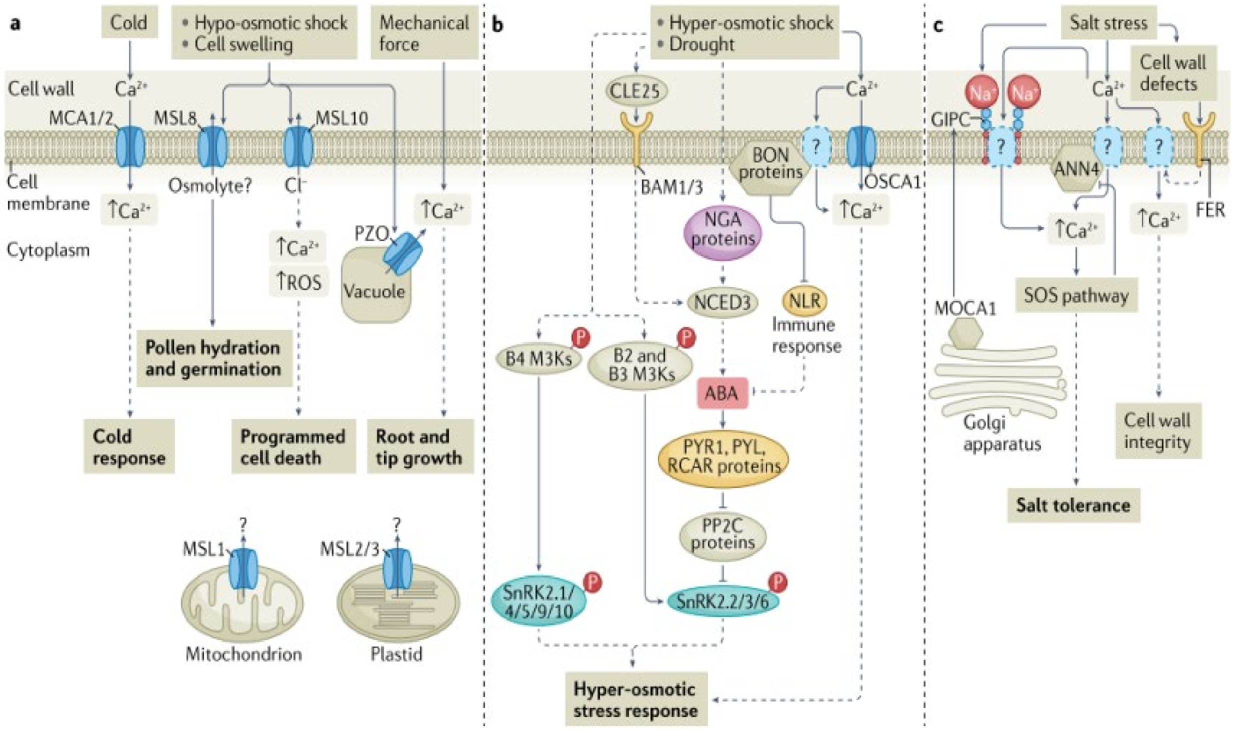
Batool et al, *J Plant Growth Regul*, 2022

Plants respond to drought stress

- **Phytohormones are ubiquitously involved in plant biological processes and regulate cellular signaling pertaining to unheralded environmental cues, such as salinity, drought, extreme temperature and nutrient deprivation (Prafull Salvi, et al 2021).**



Salvi et al, *Plant Cell Rep*, 2021

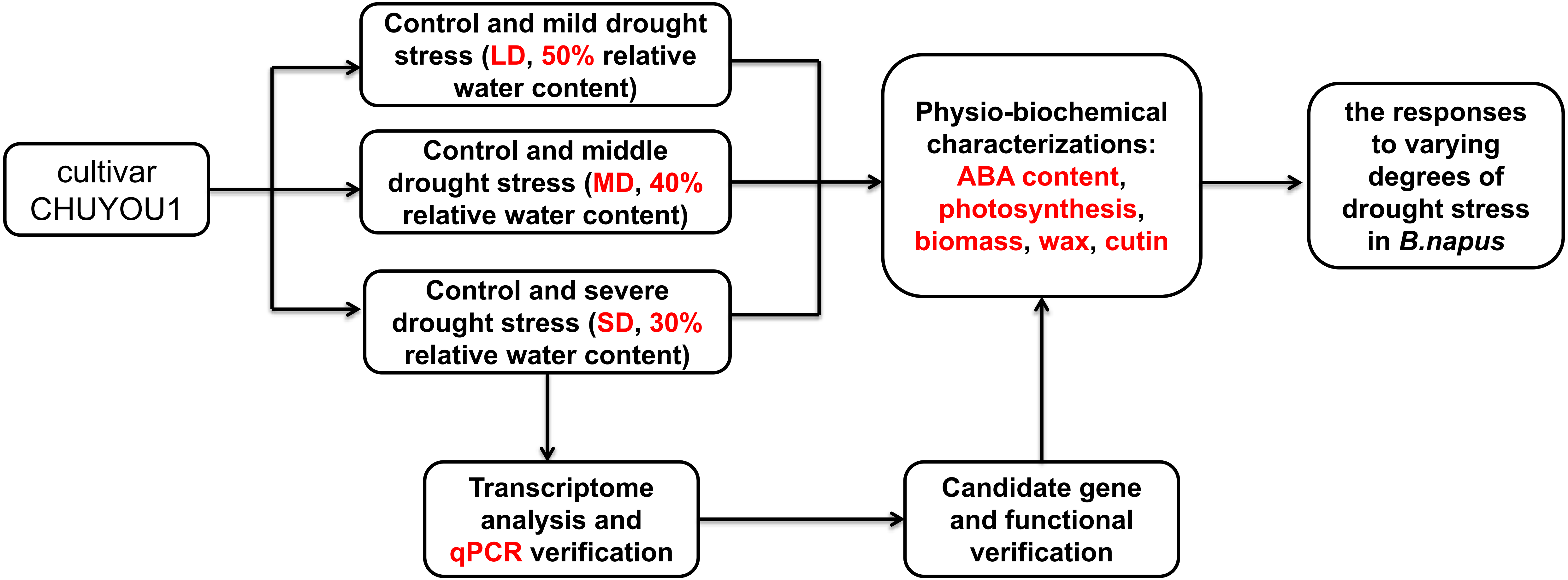


Waadt et al, *Nat. Rev. Mol. Cell Biol*, 2022

① **Combining physio-biochemical characterization and transcriptome analysis reveal the Responses to Varying Degrees of Drought Stress in *B.napus***

② Genome-wide association studies of stomatal conductance under mild drought stress

Technical route



cultivar CHUYOU1

Control and mild drought stress (LD, 50% relative water content)

Control and middle drought stress (MD, 40% relative water content)

Control and severe drought stress (SD, 30% relative water content)

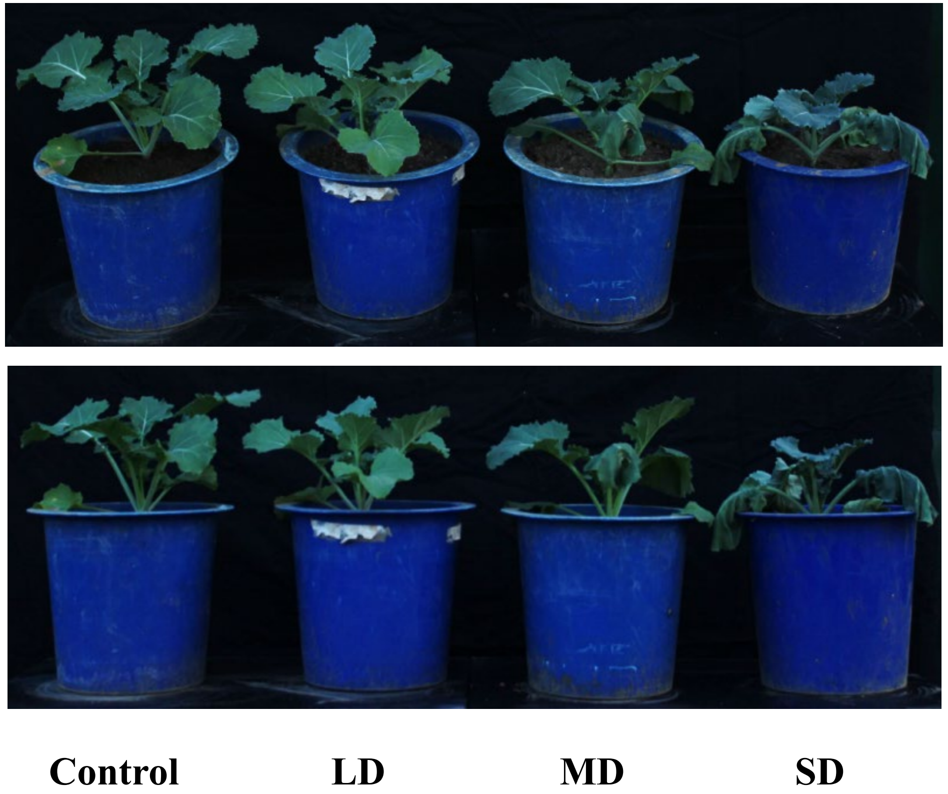
Physio-biochemical characterizations: ABA content, photosynthesis, biomass, wax, cutin

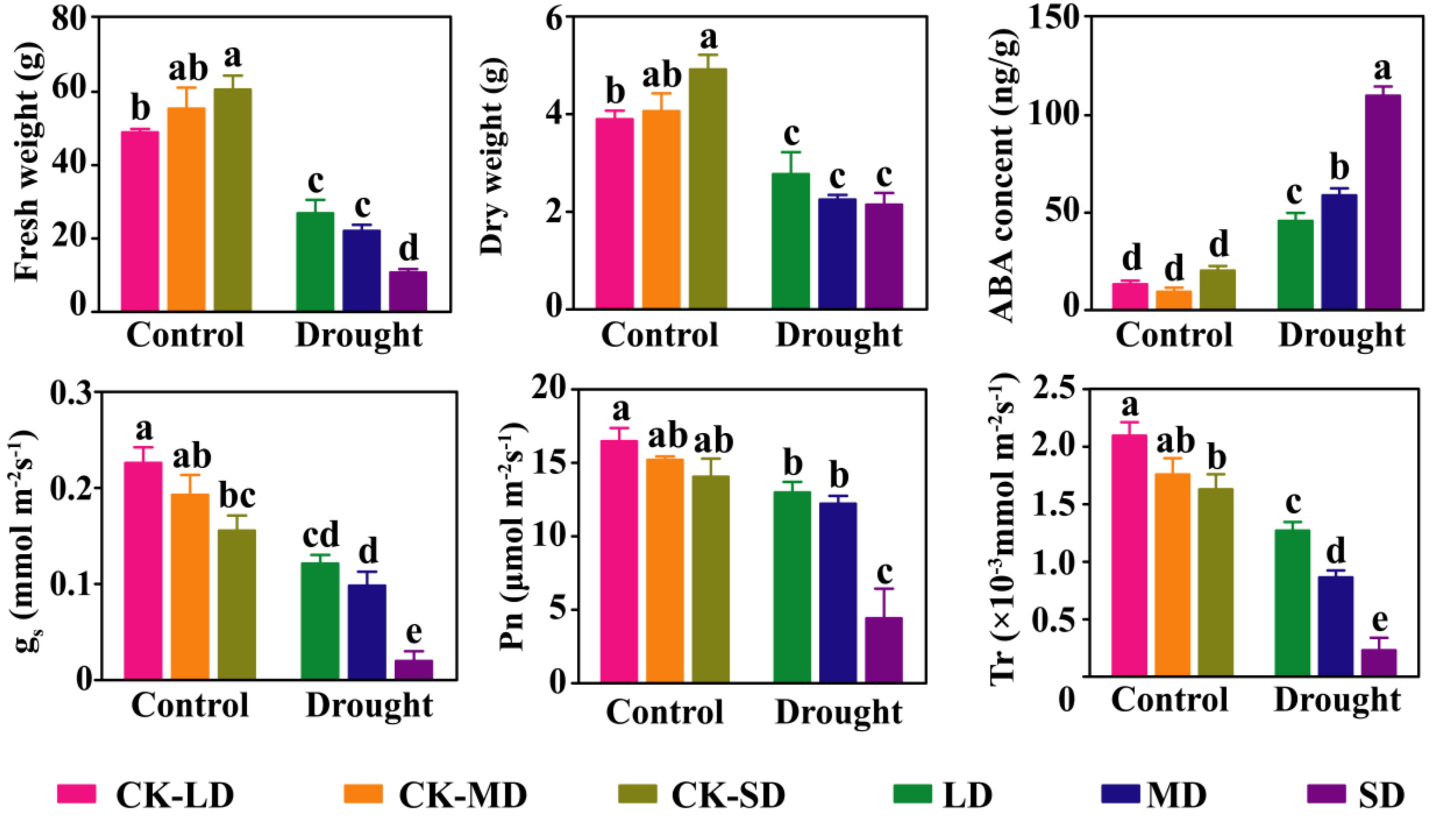
the responses to varying degrees of drought stress in *B.napus*

Transcriptome analysis and qPCR verification

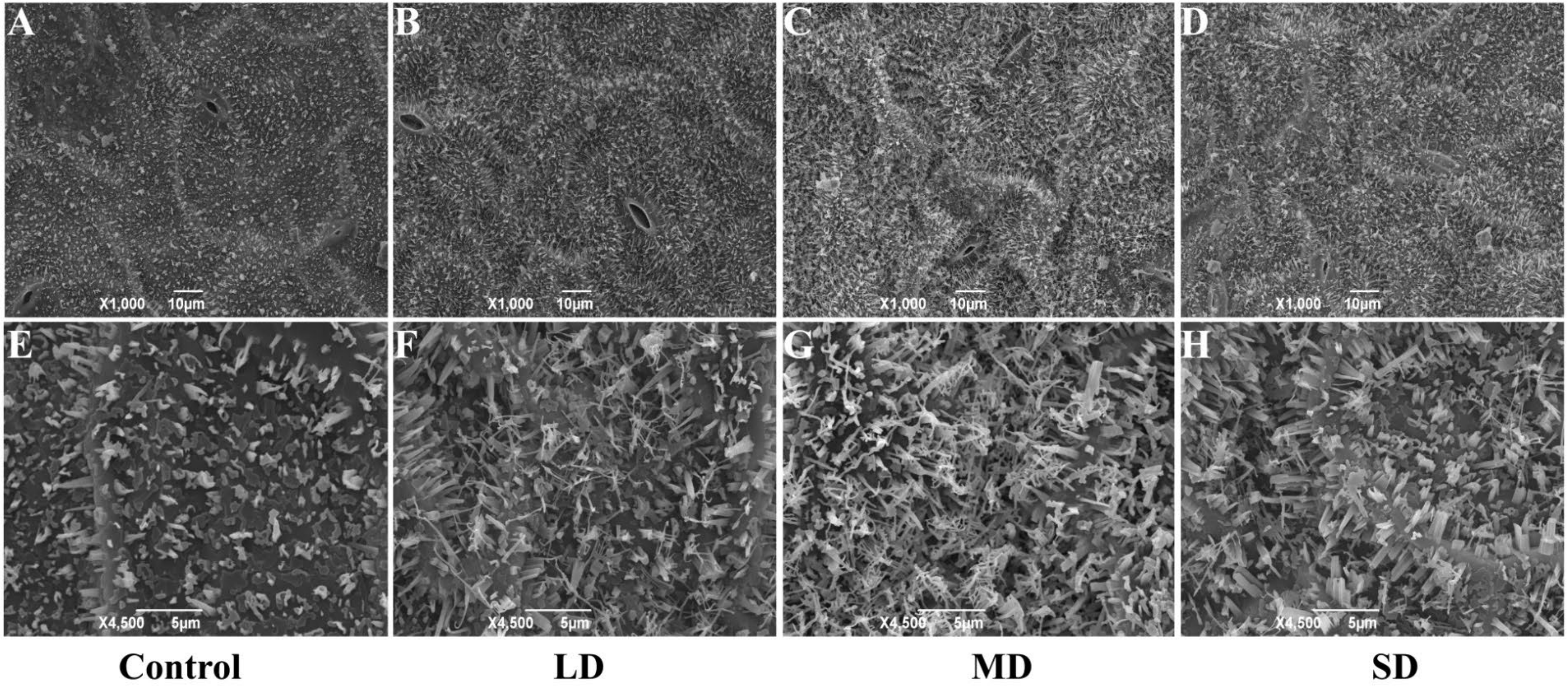
Candidate gene and functional verification

Characterization of Physio-biochemical Traits at Seedling Stage under Varying Degrees of Drought Stress in *B. napus*

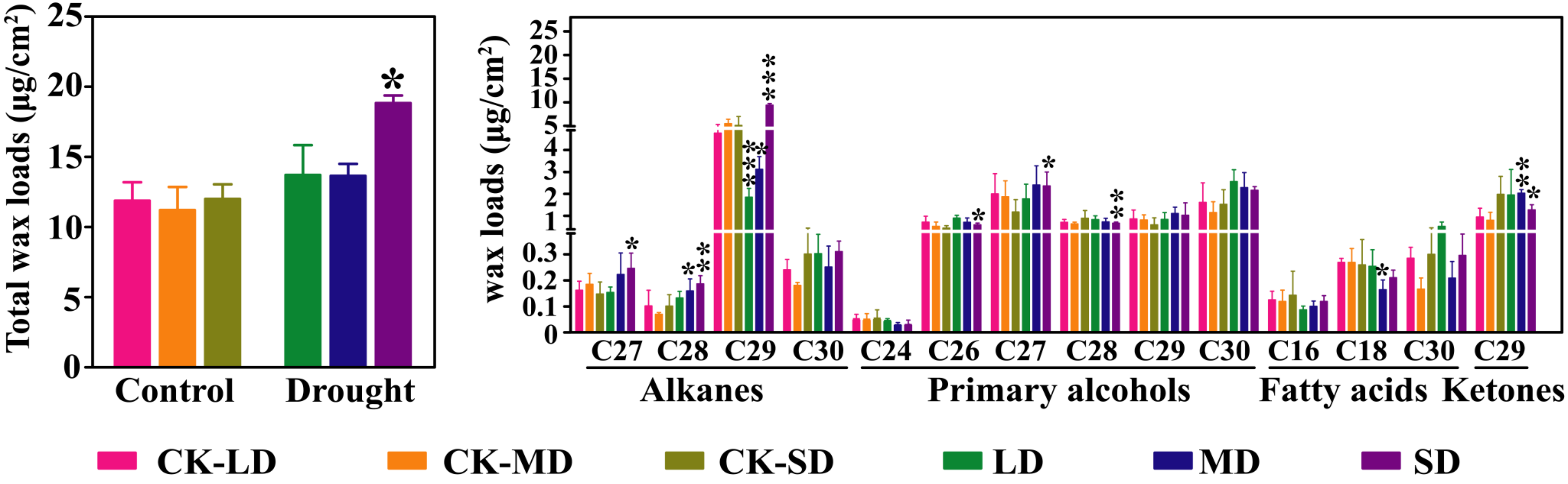




Changes in Crystal Morphology under Varying Degrees of Drought Stress in *B. napus*

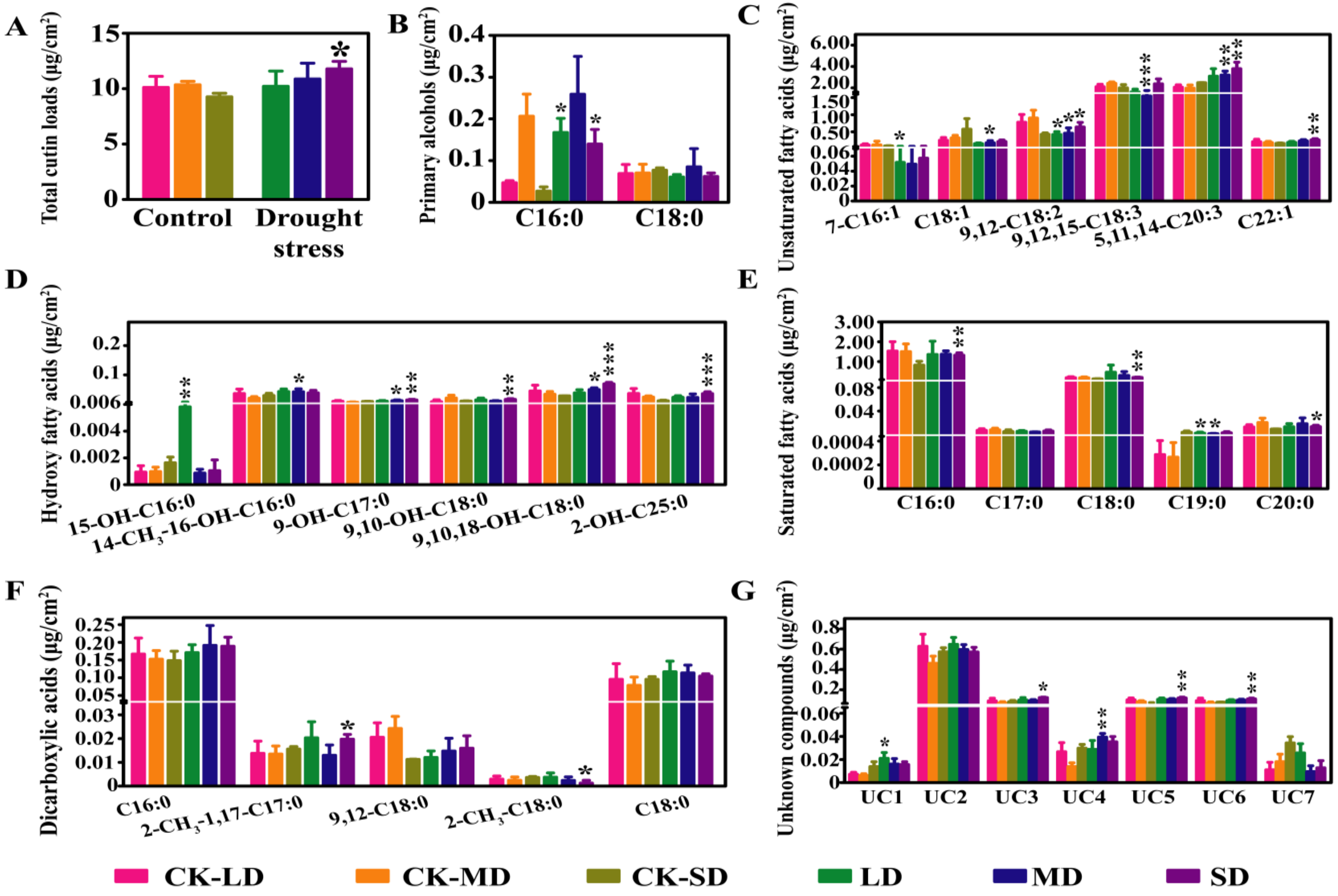


Changes in Wax Content and Composition of Epidermal Wax under Varying Degrees of Drought Stress in *B. napus*



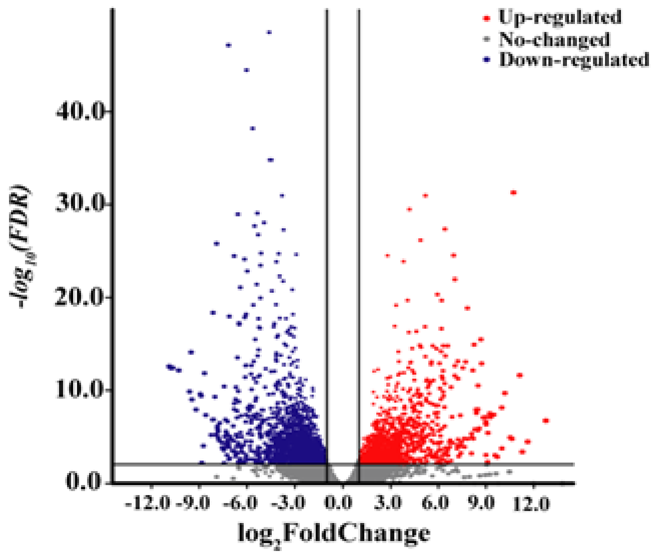
- Severe drought (SD) stress resulted in a significant increase in epidermal wax content
- The main components of surface wax are alkanes, primary alcohols, fatty acids and ketones

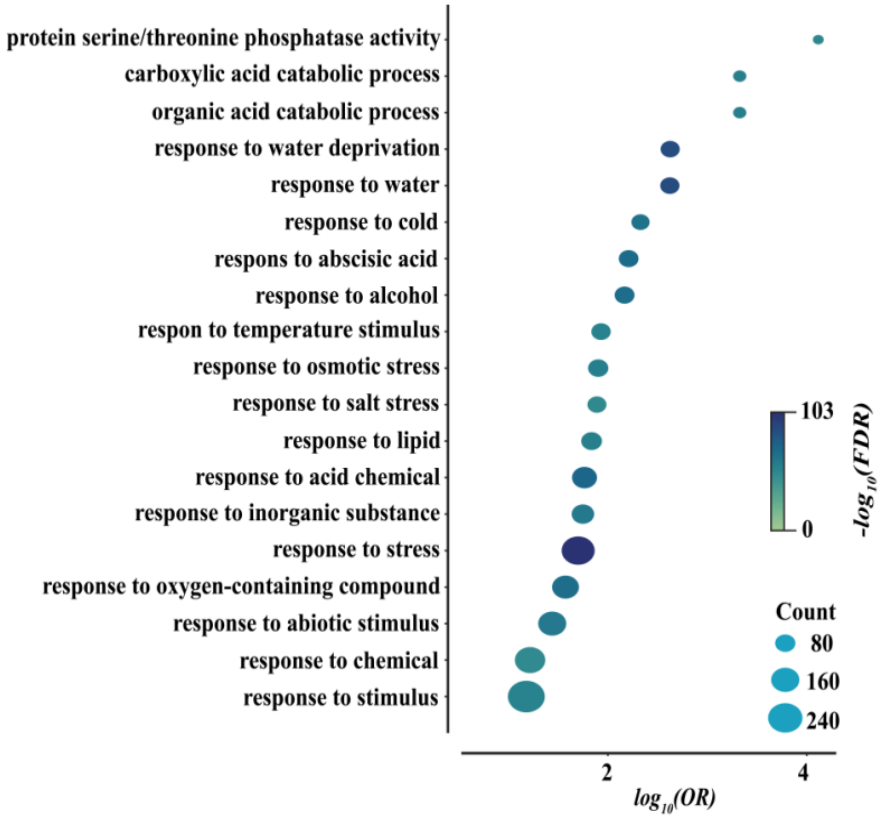
Changes in Cutin Content and Composition under Varying Degrees of Drought Stress in *B. napus*

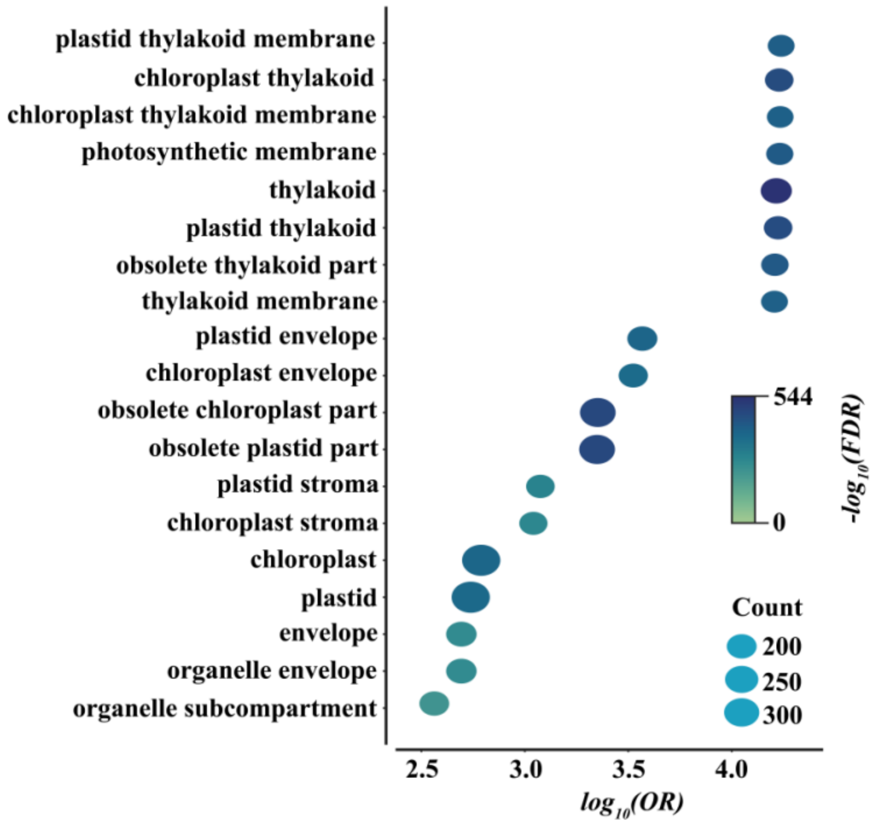


- Severe drought (SD) stress caused a significant increase in the total cutin loads.
- A total of six types of substances were identified in the cutin composition and most of their content significant increased under SD conditions.

Transcriptome Analysis Revealed Gene Expression Alternation under Severe Drought Stress-GO analysis

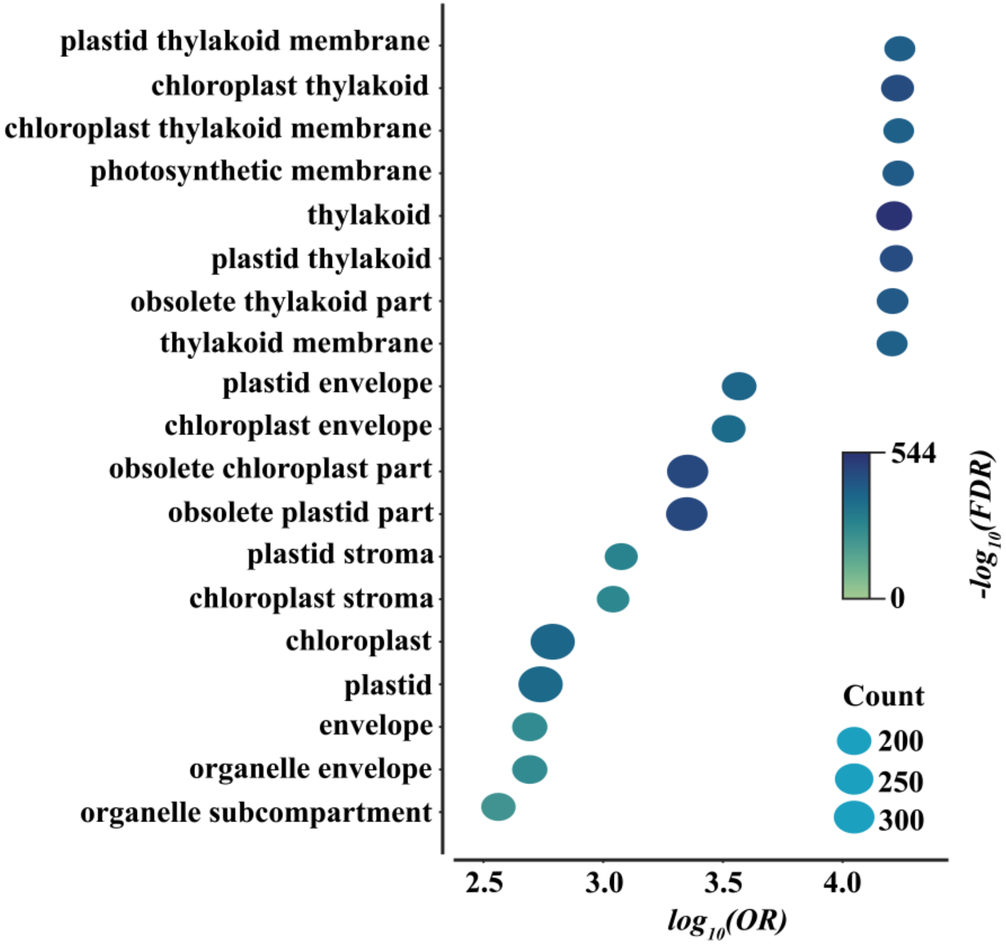




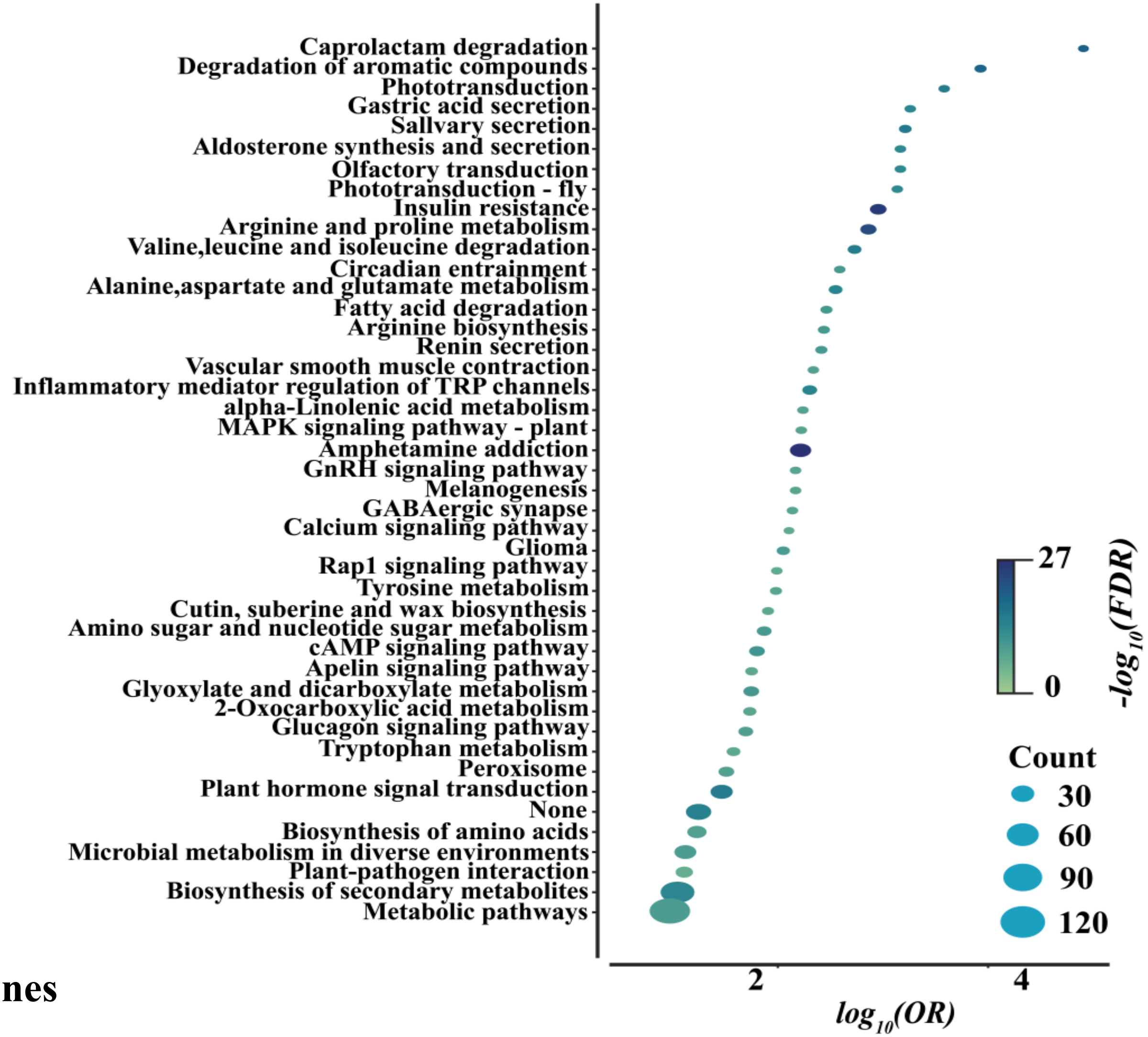


795 up-regulated and 1050 down-regulated differentially expressed genes were identified.

Transcriptome Analysis Revealed Gene Expression Alternation under Severe Drought Stress-KEGG analysis



KEGG enrichment of down-regulated differentially expressed genes

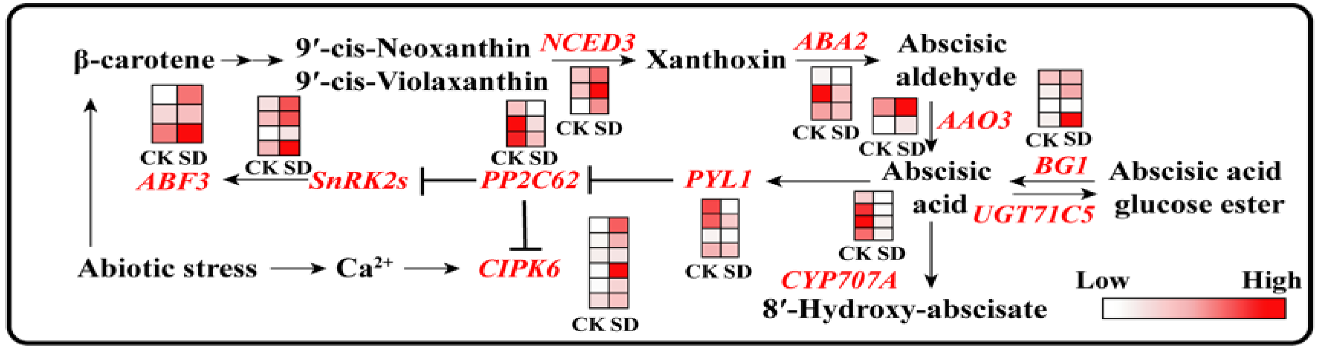


KEGG enrichment of up-regulated differentially expressed genes

Transcriptome Analysis Revealed Gene Expression Alternation under Severe Drought Stress

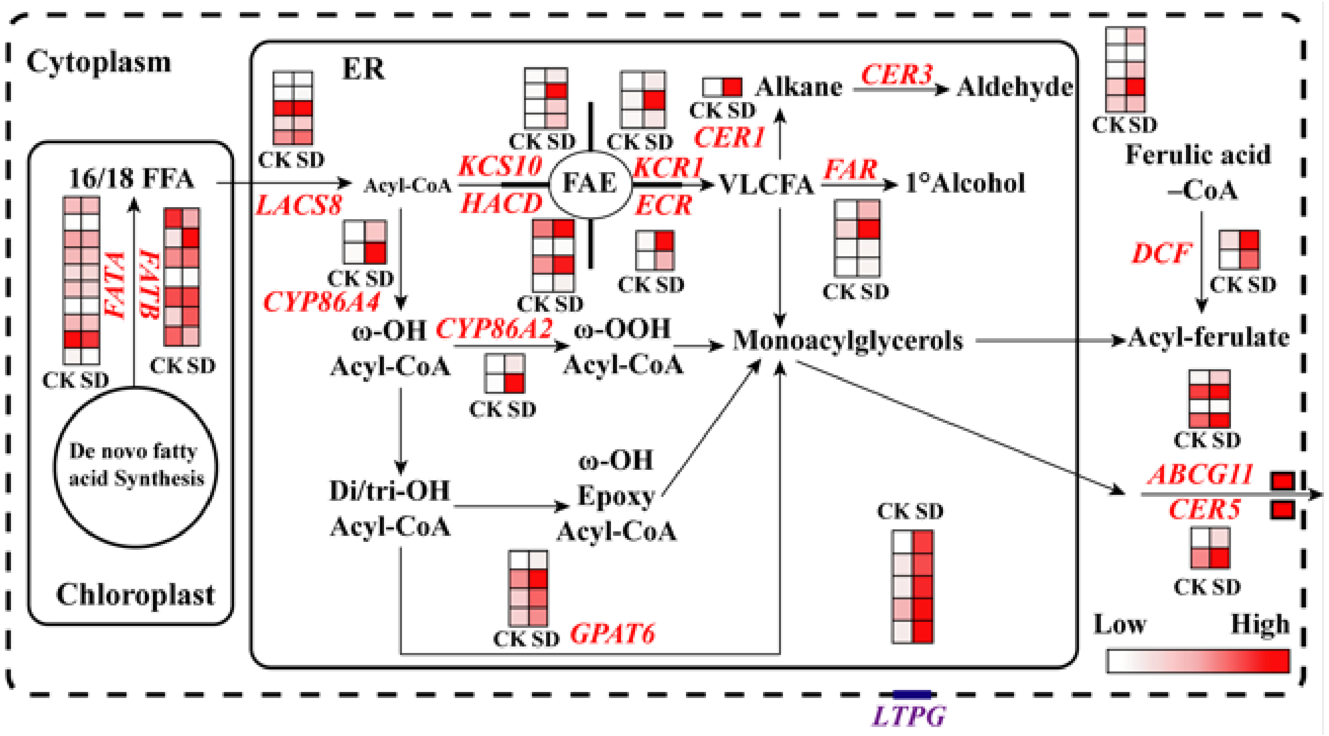
ABA biosynthesis and signaling transduction pathway

A

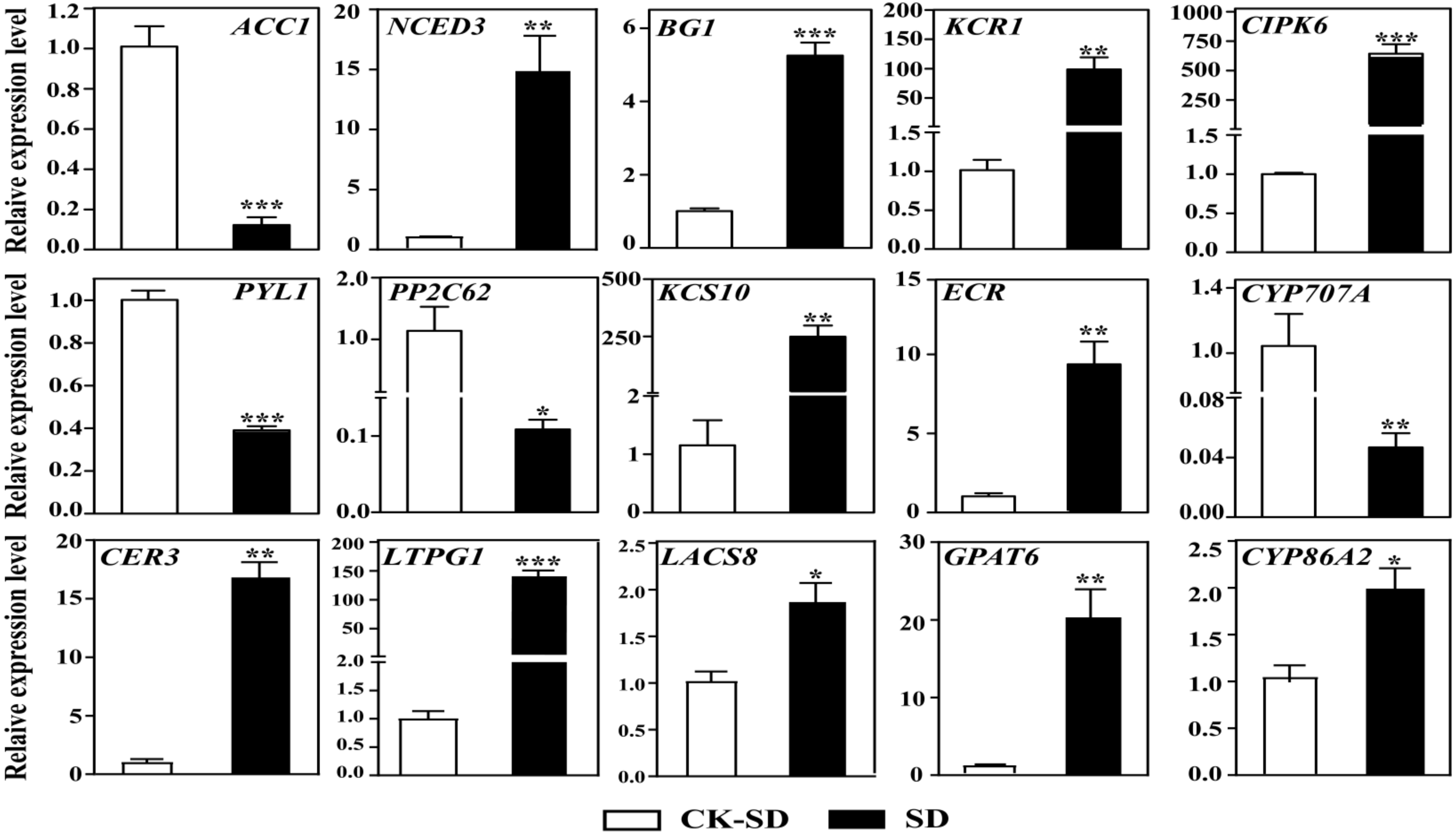


Wax and cutin biosynthesis and signaling transduction pathway

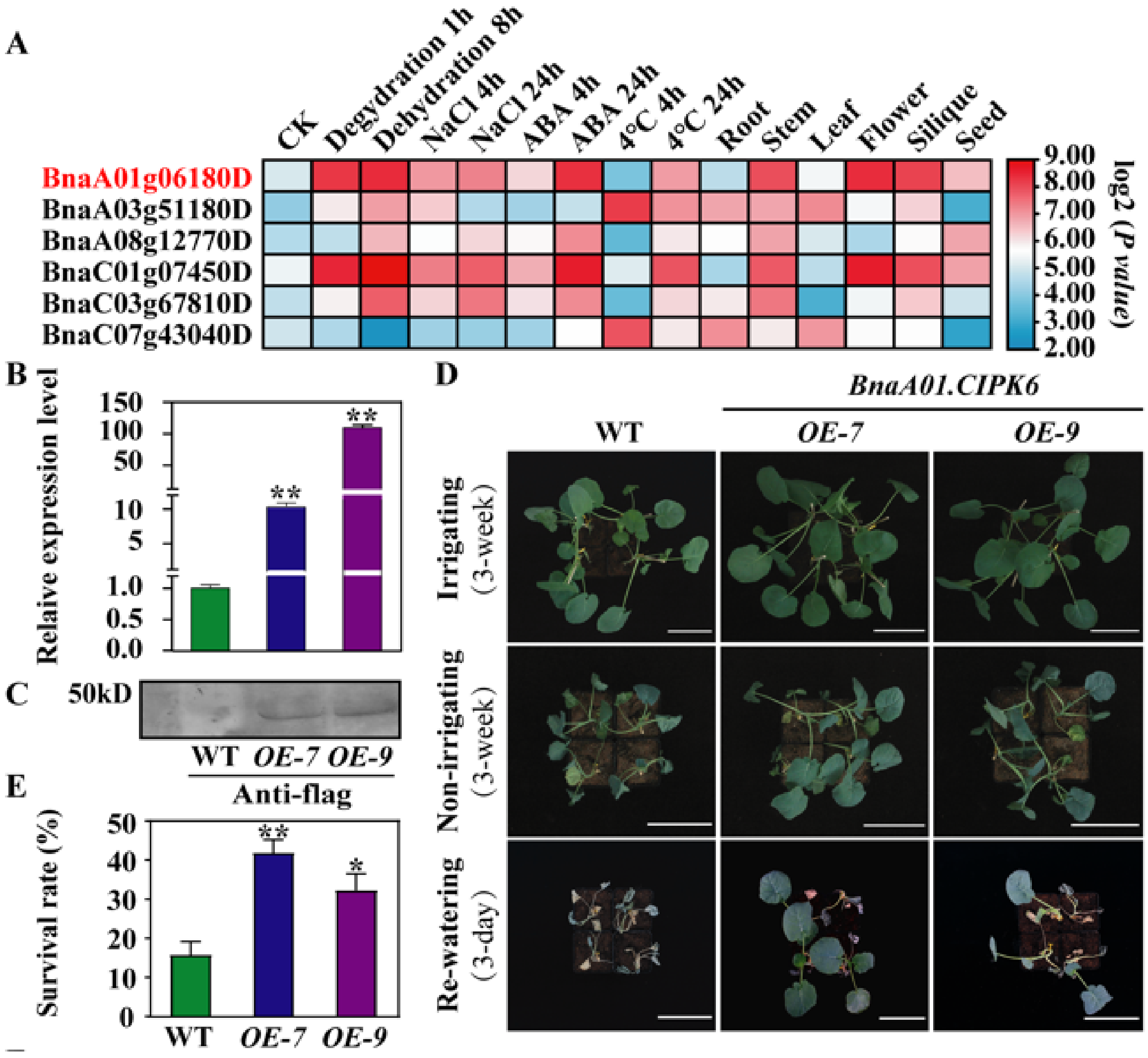
B

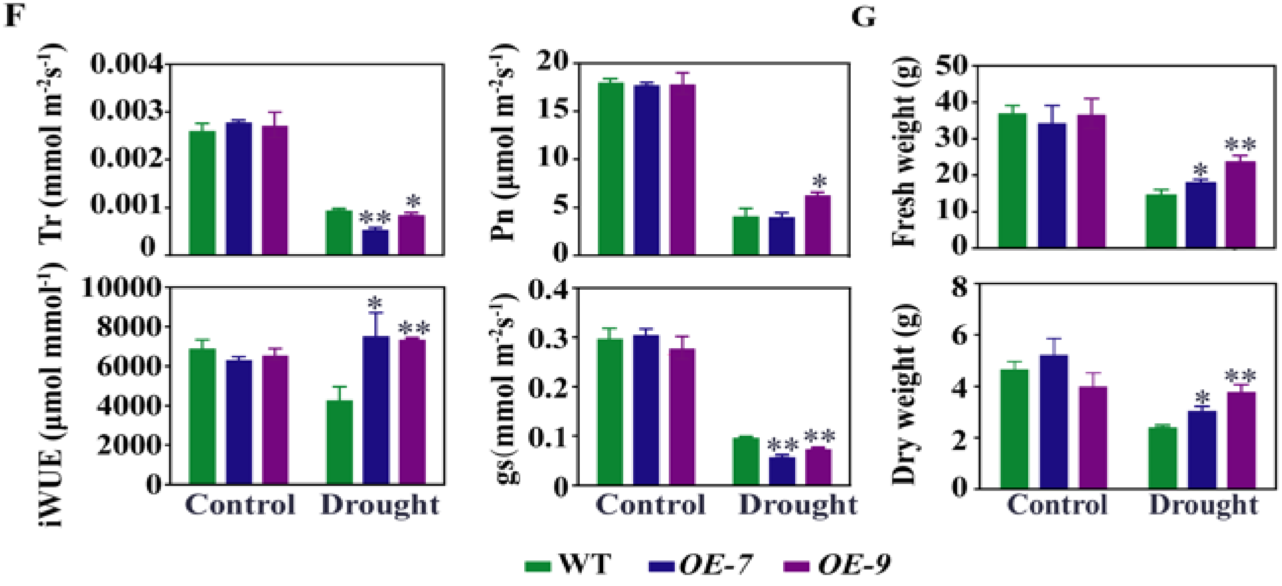


Transcriptome results were verified by qPCR



Over-expression of BnaA01.CIPK6 Confers Drought Tolerance in *B. napus*



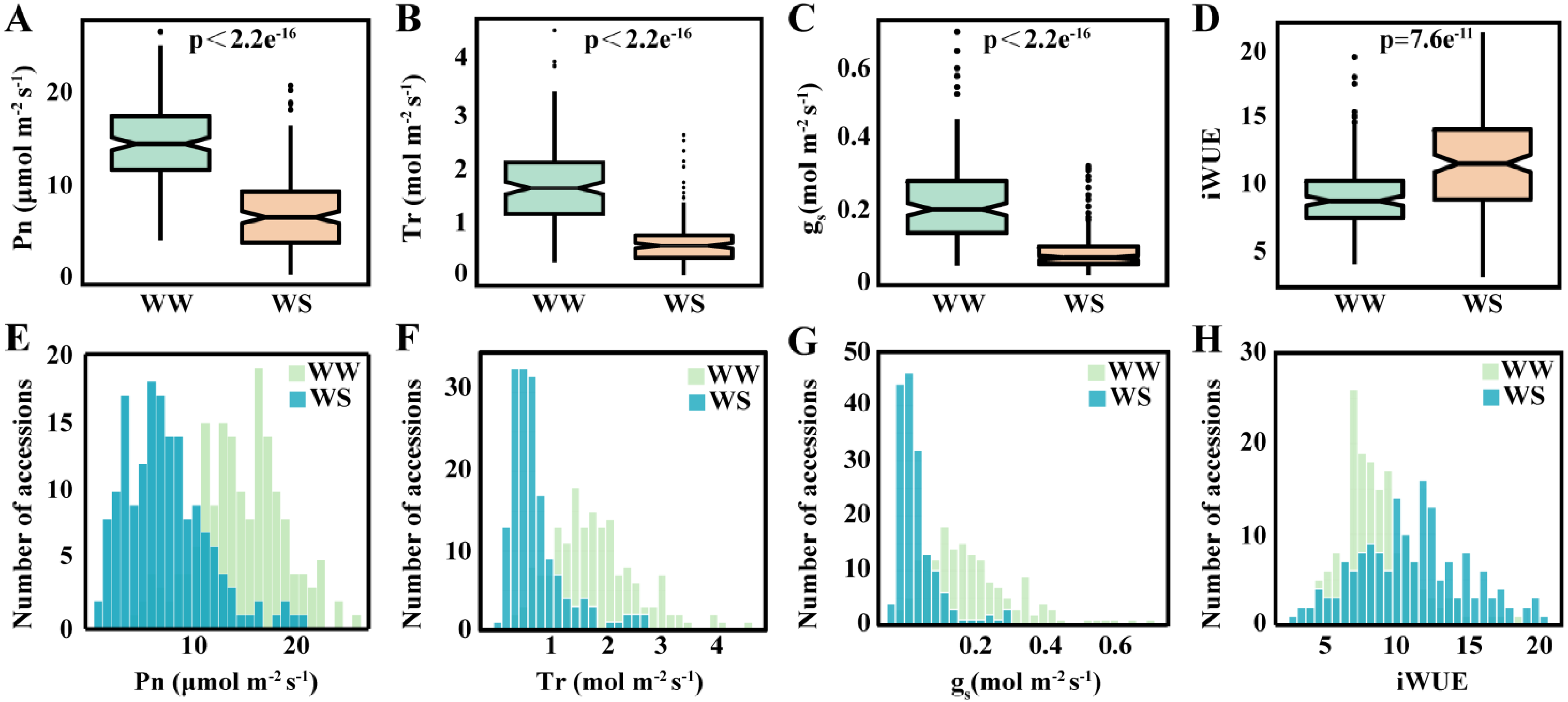


- The differentially expressed gene ***BnaA01.CIPK6*** was induced by various abiotic stresses
- ***BnaA01.CIPK6*** positively regulated drought resistance in *B.napus*

① combining physio-biochemical characterization and transcriptome analysis reveal the Responses to Varying Degrees of Drought Stress in *B.napus*

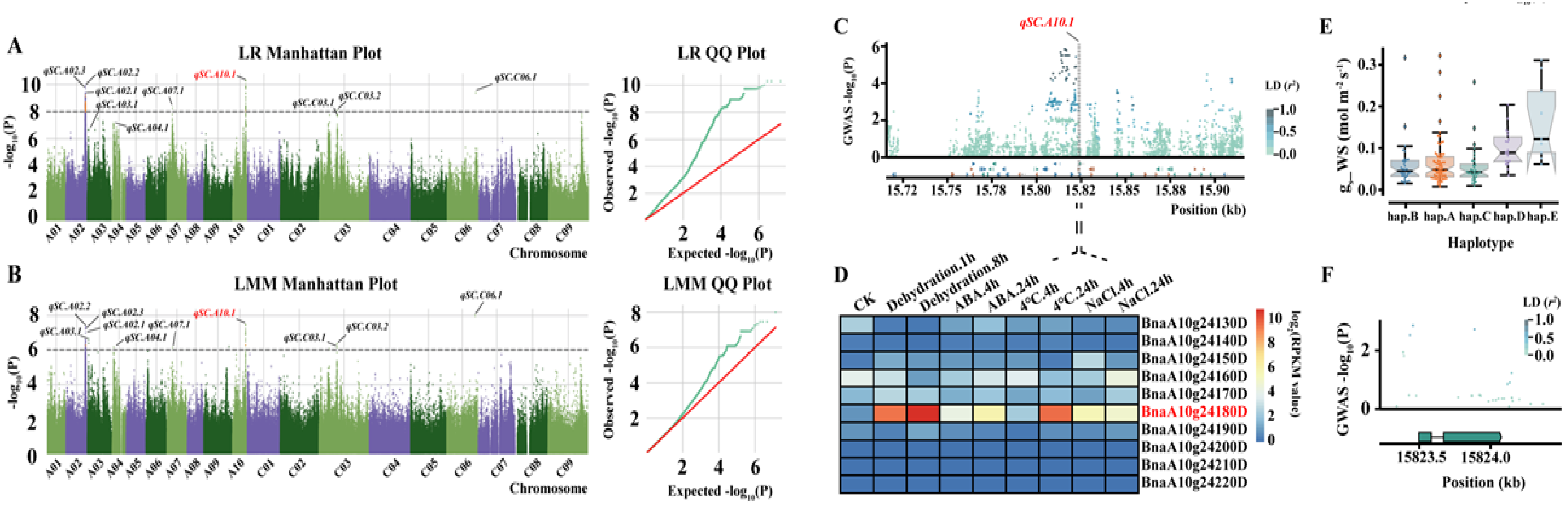
② **Genome-wide association studies of stomatal conductance under mild drought stress**

Frequency distribution of photosynthesis-related traits under mild drought stress and normal conditions



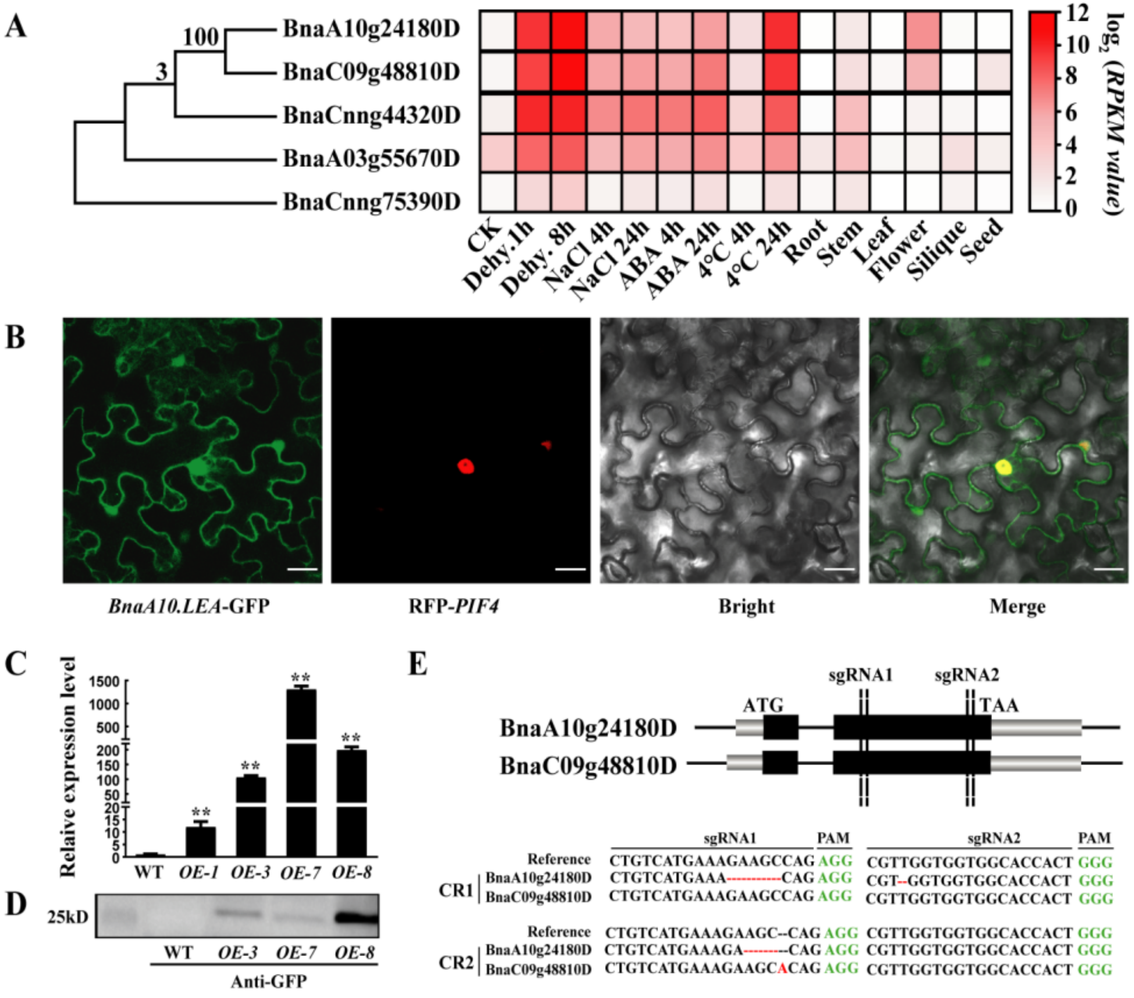
Unpulished data

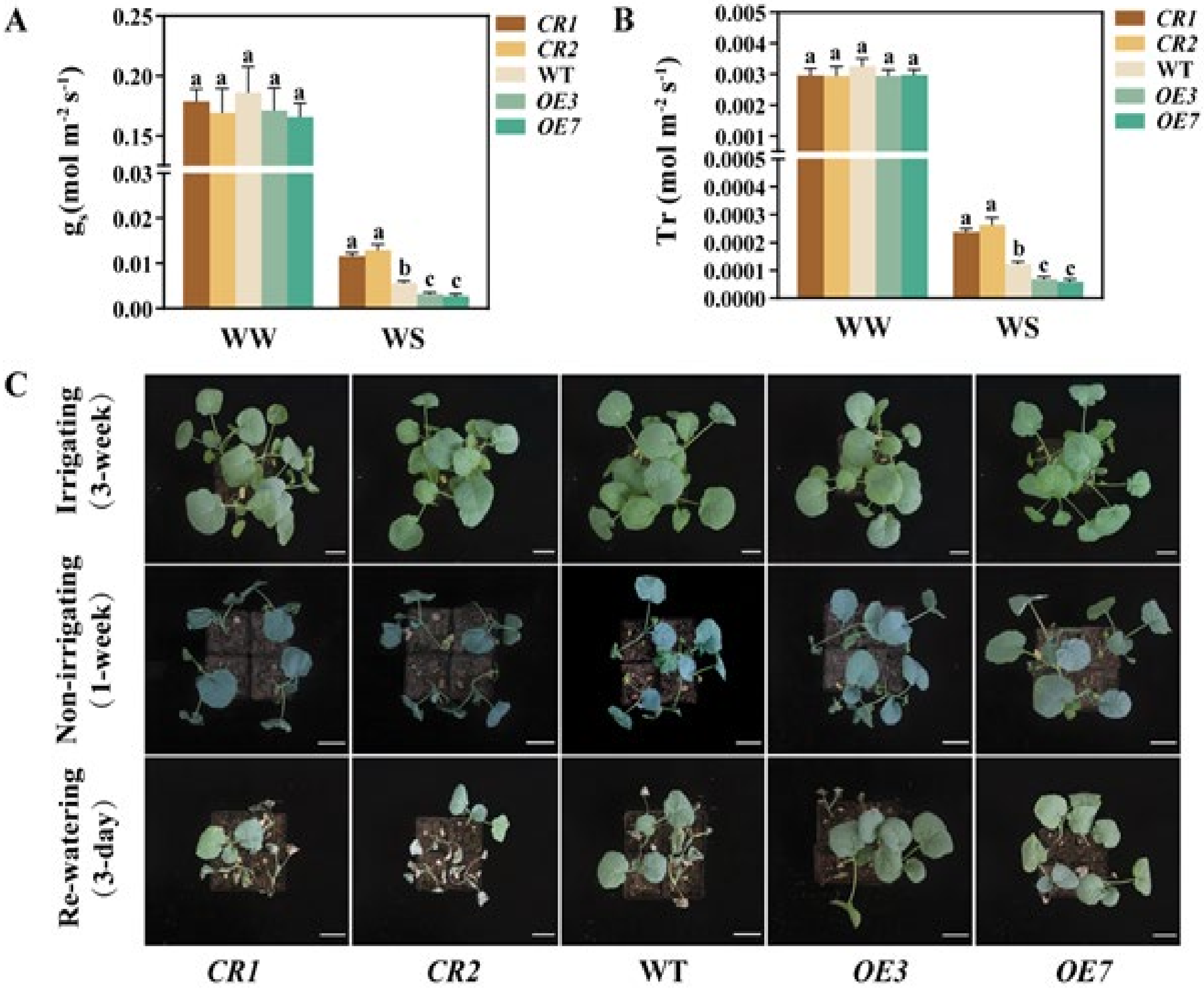
Genome-wide association studies were used to locate QTLs and candidate genes related to stomatal conductance under mild drought stress.



Unpulished data

Expression pattern analysis and gene function identification of *BnaLEA4-5*





Unpulished data

Summary

- **Stomatal transpiration is the main way of water loss in rape under LD and MD stress conditions while cuticle transpiration plays an important role in the SD stress conditions.**

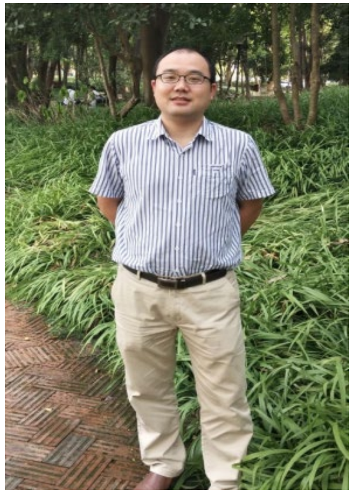
- **A total of 1845 DEGs were identified under severe drought stress and most of them involved in the stress responses. And we also proved *BnaA01.CIPK6* positively regulated drought resistance in rapeseed.**

- ***14* QTLs have been identified through stomatal conductance under mild drought and *BnaLEA* may positively affect drought resistance of rapeseed.**

Acknowledgement

Prof. Liang Guo

Prof. Xuan Yao



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Thank you ！