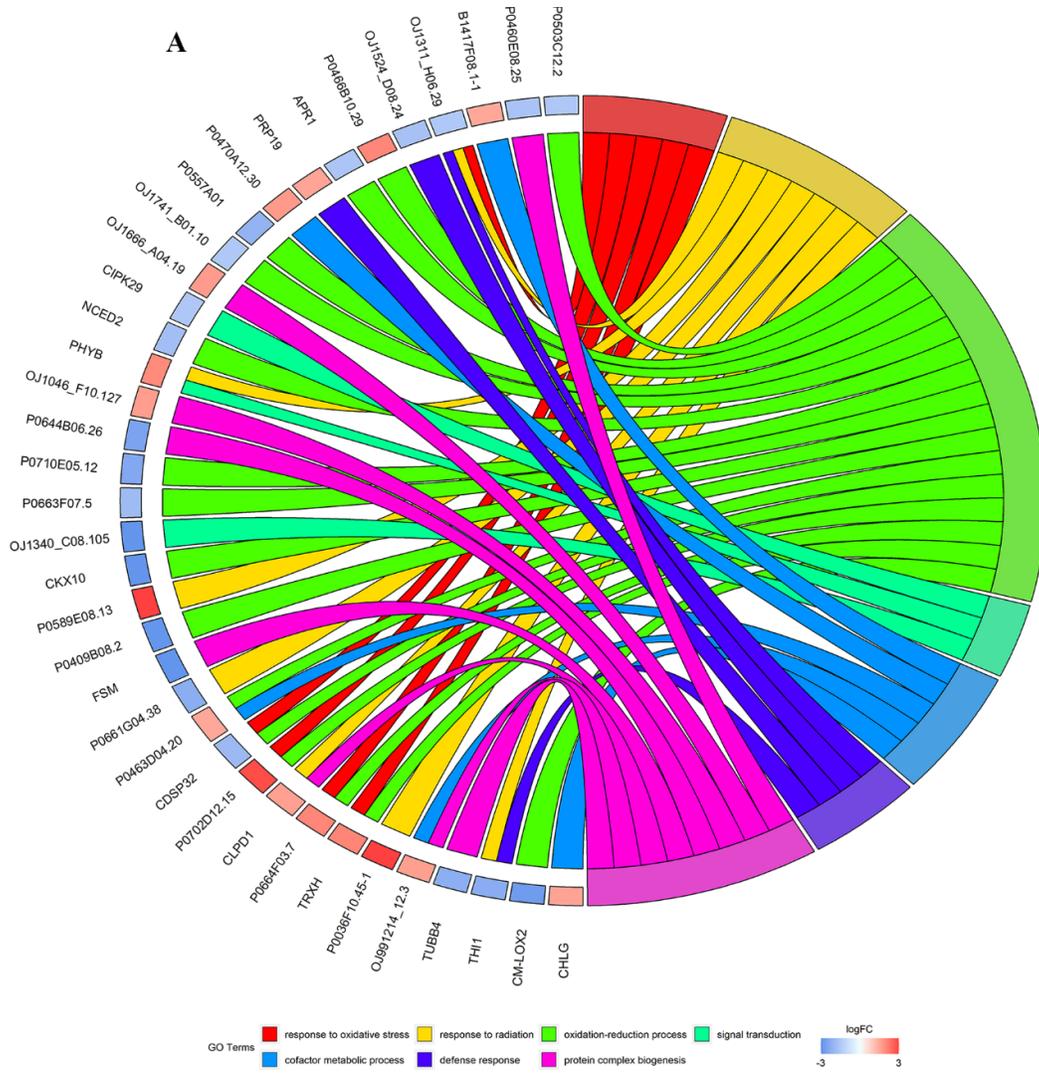




Figure S1. Photographs of progeny rice plants in TS.



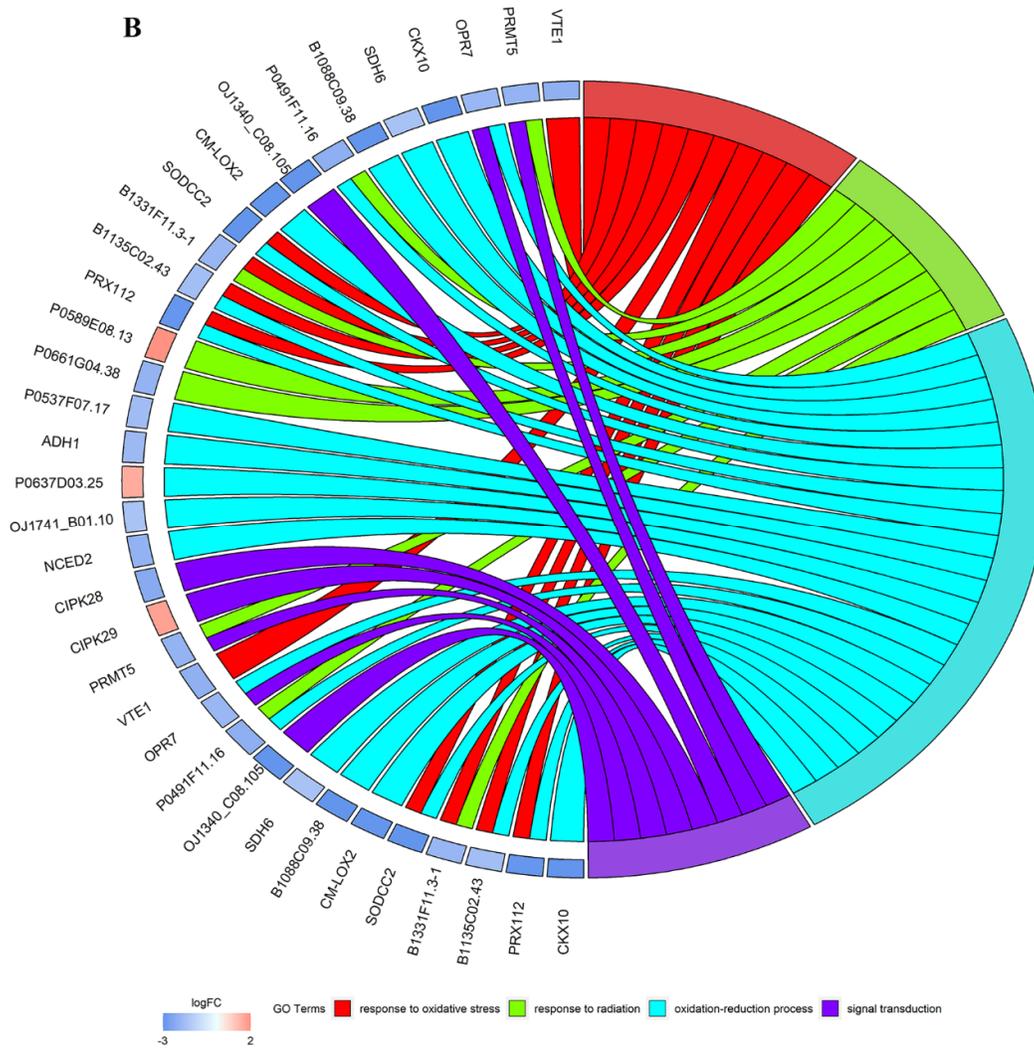
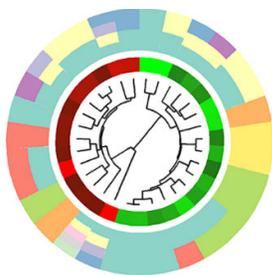
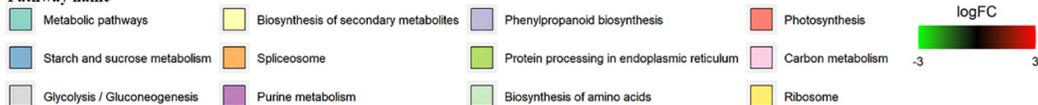


Figure S2. Chord diagram analyzes the interactions between BPs. A represents the different metabolites at the TLS; B represents the different metabolites at the TS; TLS and TS stand for three-leaf stage and tillering stage, respectively.

A



Pathway name



B



Pathway name

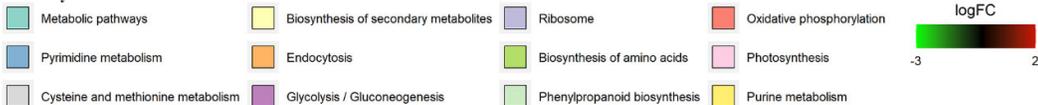


Figure S3. KEGG pathway enrichment analysis of proteins with differential abundance; TOP 12 of pathway enrichment; (A) three-leaf stage; (B) tillering stage.

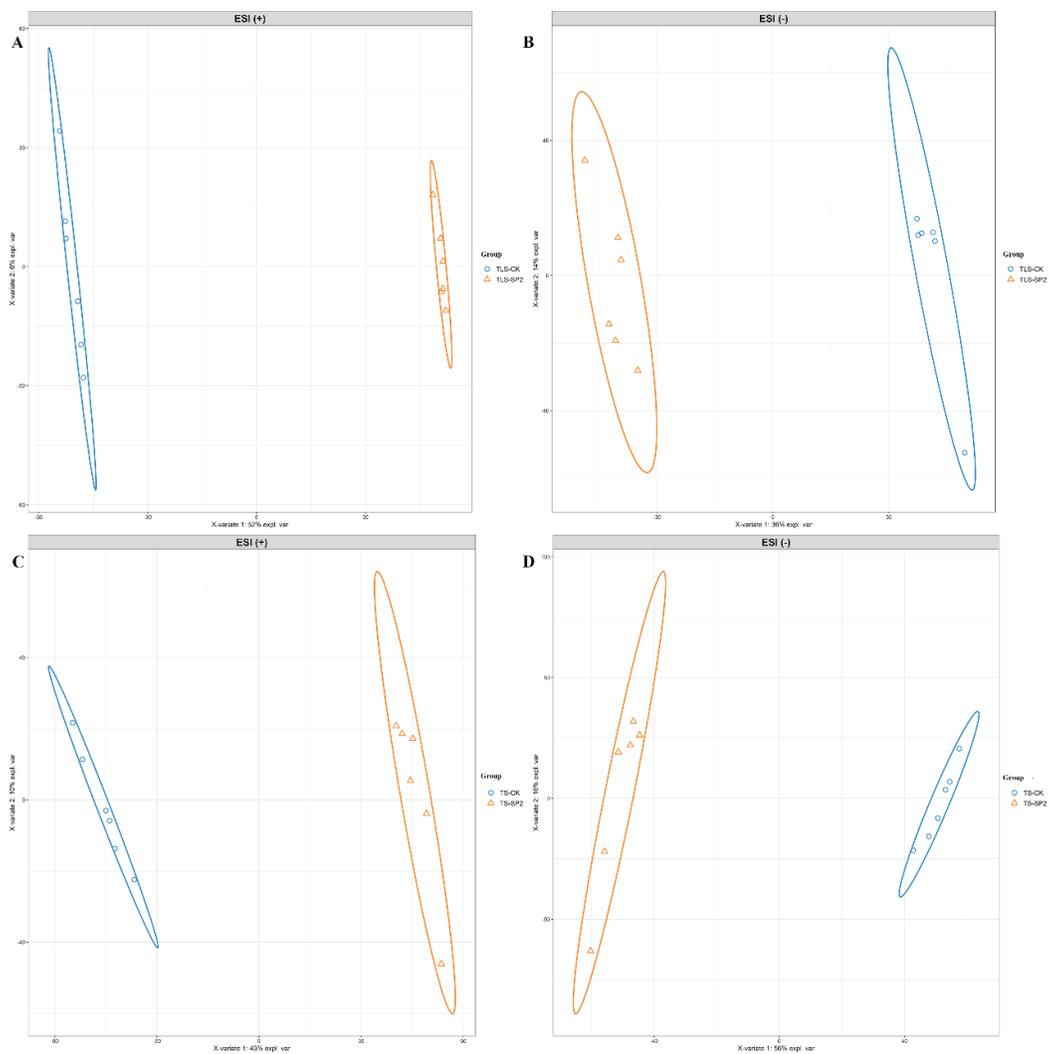
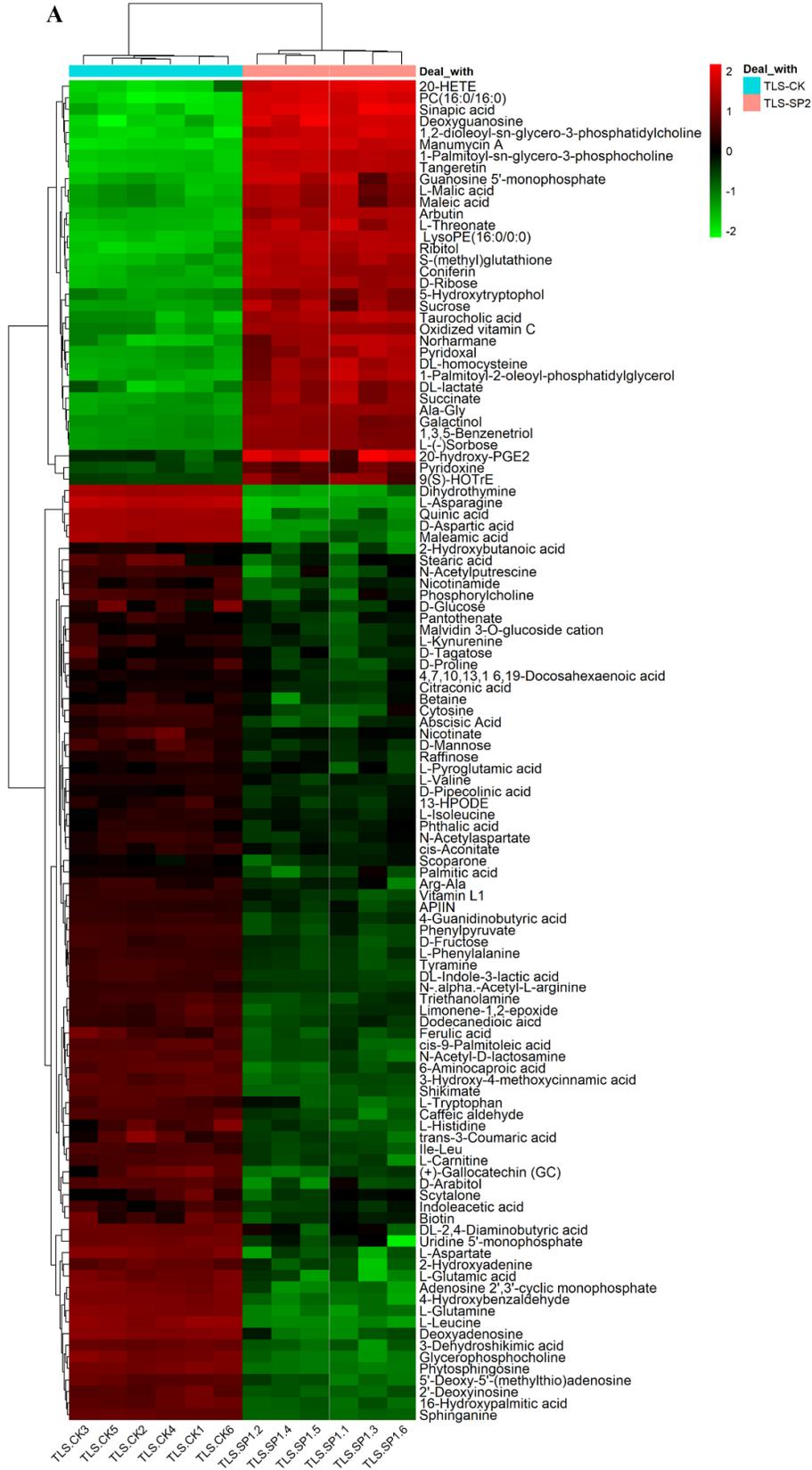


Figure S4. Partial least squares discriminant analysis (PLS-DA) score map of different rice sample groups based on UHPLC-QTOF/MS data (six biological replicates). (A) Positive ion mode of TLS, (B) Negative ion mode of TLS. (C) Positive ion mode of TS, (D) Negative ion mode of TS; TLS and TS represent three leaf period and tillering stage. CK represent control group. SP2 represent the offspring of rice after spaceflight.

A



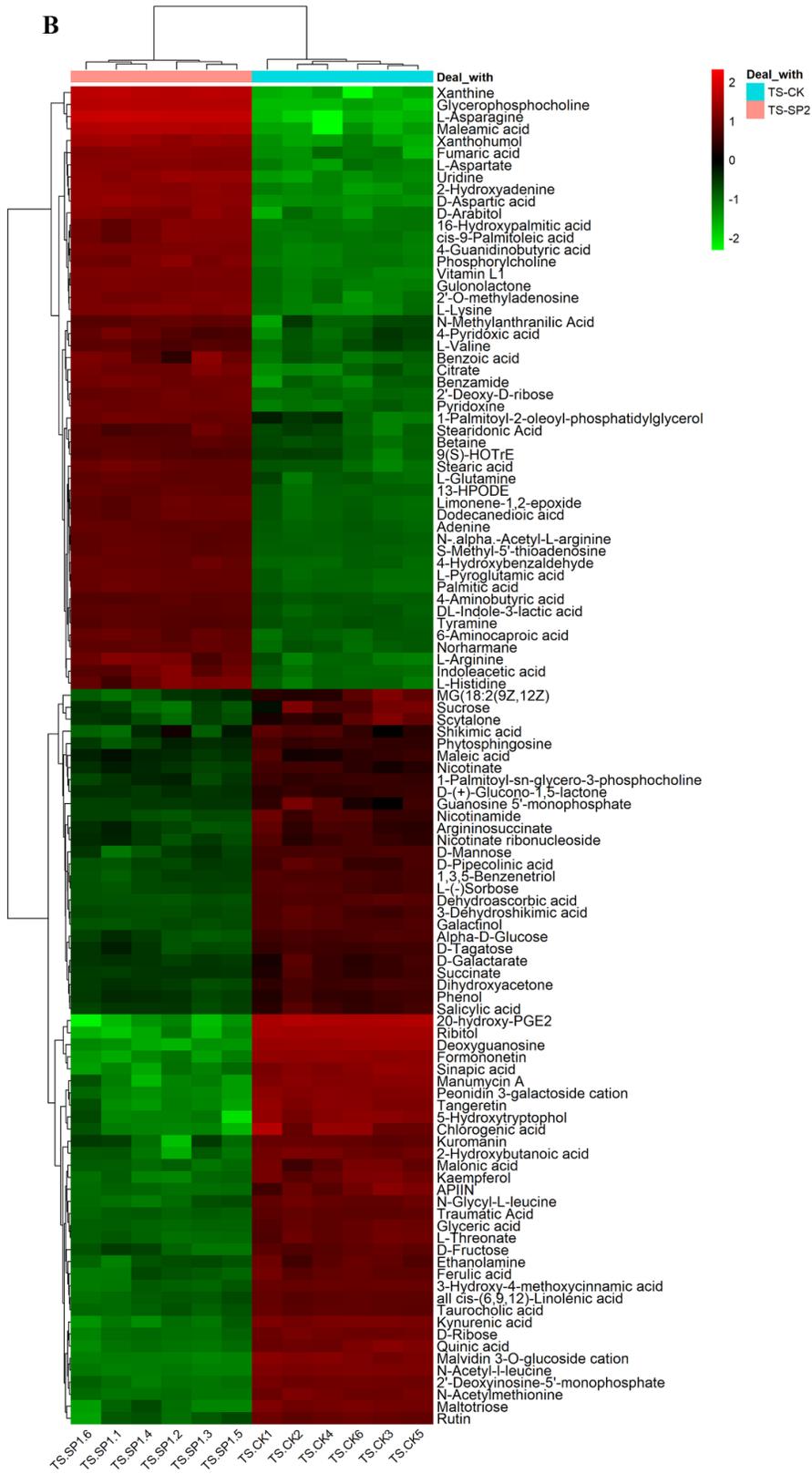


Figure S5. Results of hierarchical cluster analysis of changed metabolites pools. Hierarchical trees were drawn based on the detected changed metabolites in leaves of rice, (A) TLS, (B) TS. Columns correspond to the

repetition between different treatments, while rows represent different metabolites. Red and green colors indicate increased and decreased metabolite concentrations, respectively.

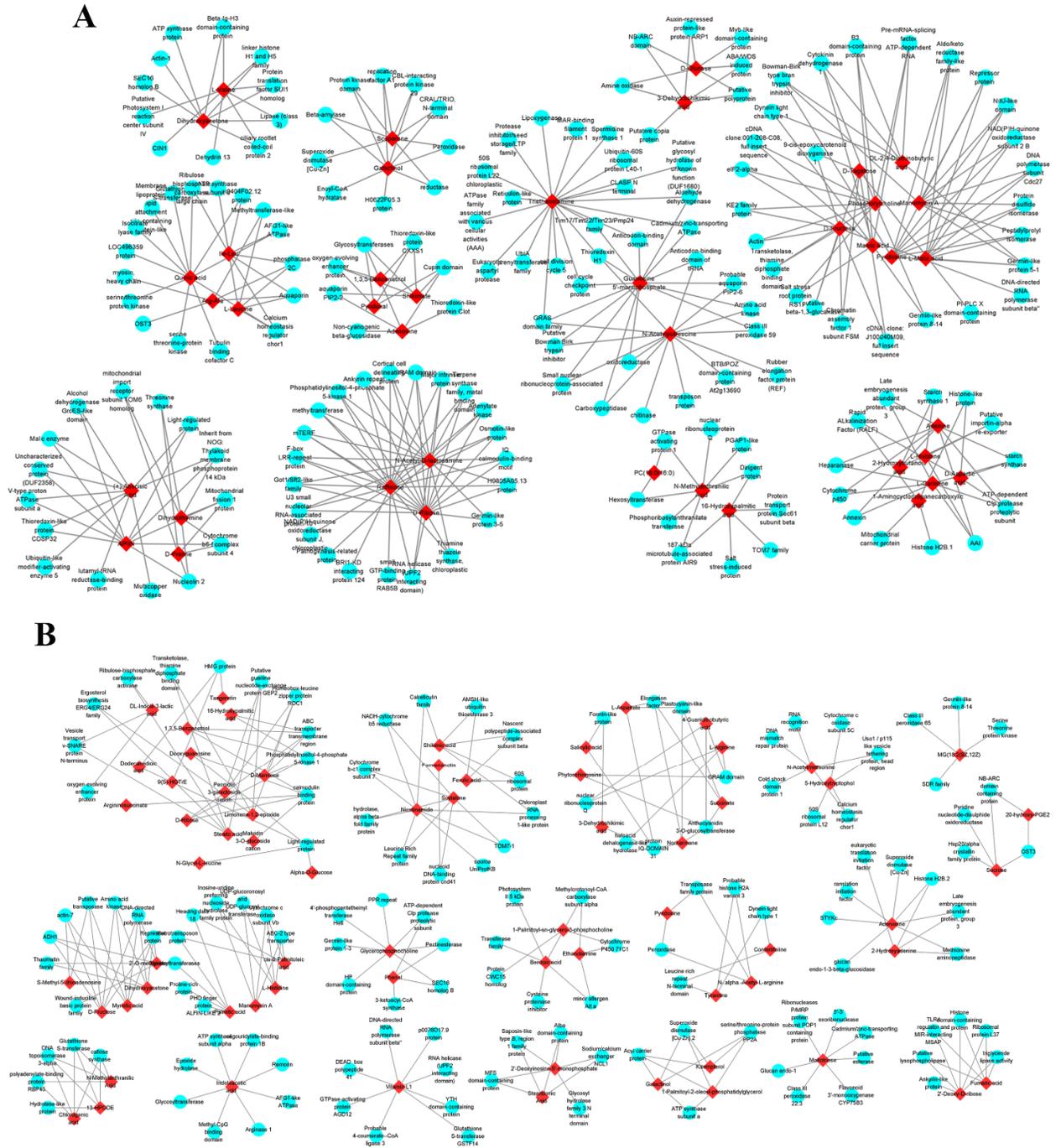


Figure S6. Analysis of the relationship between proteomics and metabolomics. The psych package of R software is used for analysis, and cytoscap was used for visualization. Red represents protein and blue represents metabolites.

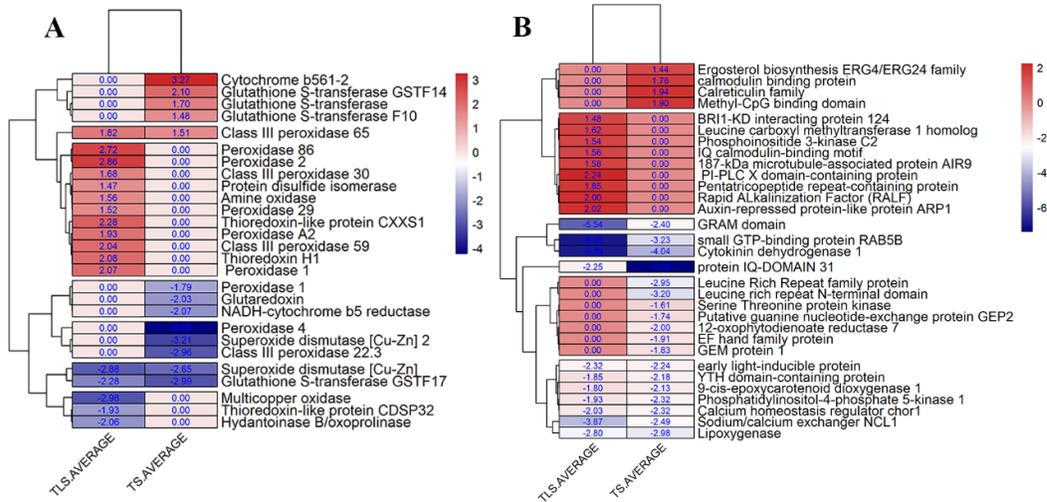


Figure S7. DAPs involved in redox reactions and signal transduction processes. A represents the DAPs involved in the redox reaction. B represents the DAPs involved in the signal transduction process. The number represents $\log_{1,2}(FC)$, a positive number represents an up-regulated protein, a negative number represents a down-regulated protein, and 0.00 represents a protein that is not significantly different.

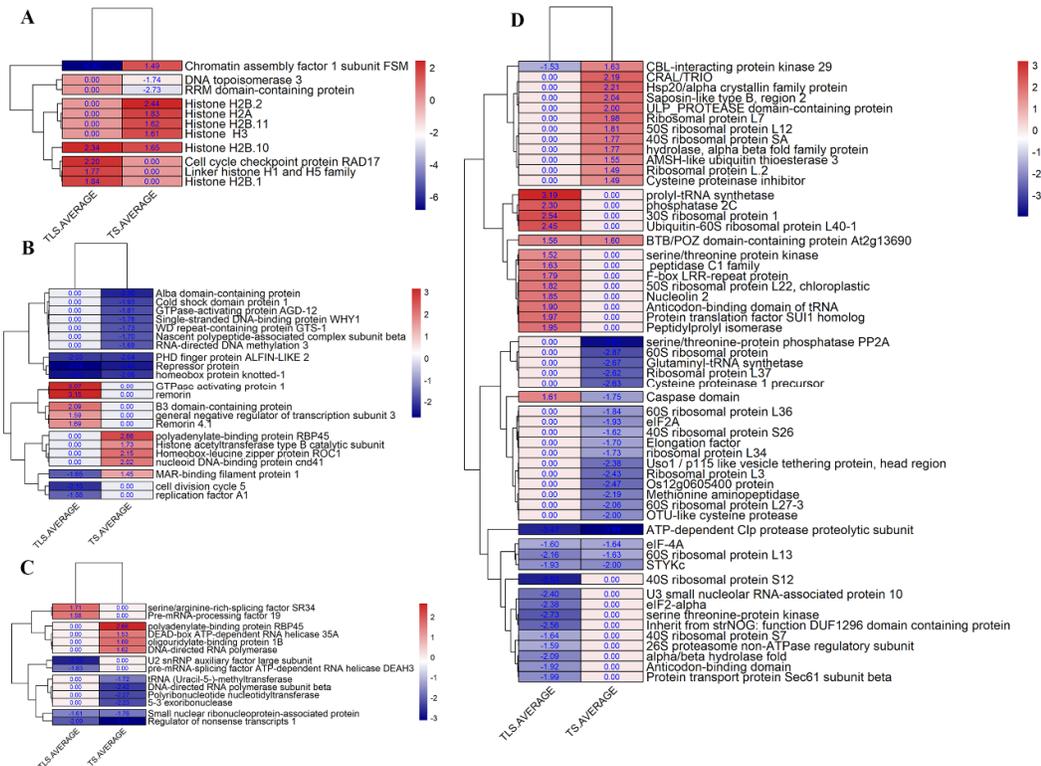


Figure S8. Genetic material metabolism and protein reorganization are the key processes of offspring rice coping with spaceflight. A represents the DAPs involved in the DNA. B represents the change of transcription factors. C represents DAPs involved in RNA processing. D represents DAPs in protein synthesis, processing and degradation. The number represents $\log_{1,2}(FC)$, a positive number represents an up-regulated protein, a negative number represents a down-regulated protein, and 0.00 represents a protein that is not significantly different.

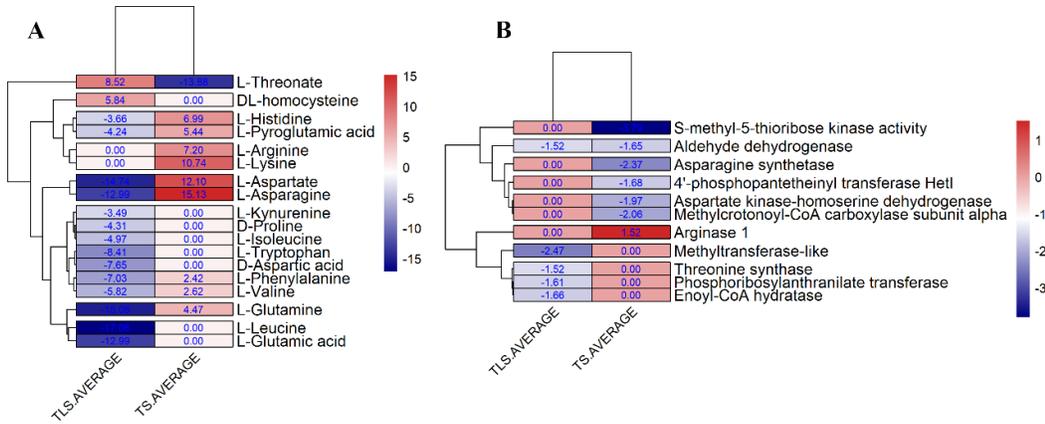


Figure S9. Spaceflight changed the amino acid metabolism profile of offspring rice. A represents the DAPs involved in amino acid metabolism. B represents DAPs involved in amino acid metabolism. The number represents $\log_{1.2}^{(FC)}$, a positive number represents an up-regulated protein, a negative number represents a down-regulated protein, and 0.00 represents a protein that is not significantly different.

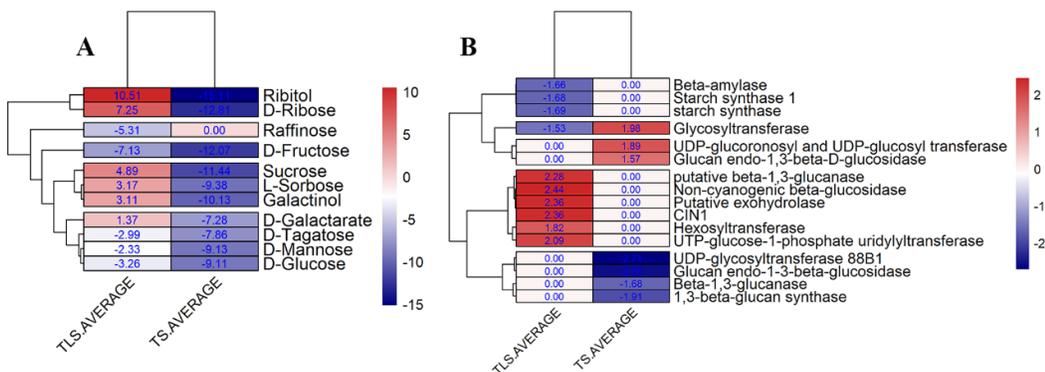


Figure S10. Spaceflight changed the carbohydrate metabolism profile of offspring rice. A represents the DAPs involved in carbohydrate metabolism. B represents DAPs involved in carbohydrate metabolism. The number represents $\log_{1.2}^{(FC)}$, a positive number represents an up-regulated protein, a negative number represents a down-regulated protein, and 0.00 represents a protein that is not significantly different.

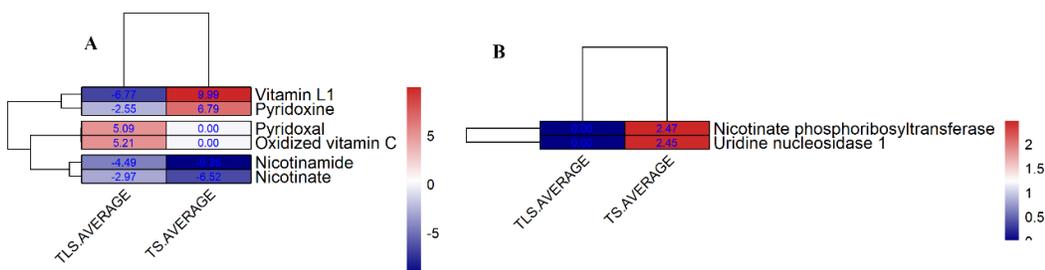


Figure S11. Spaceflight changed the vitamin and cofactor metabolism profile of offspring rice. A represents the DAPs involved in vitamin and cofactor metabolism. B represents DAPs involved in vitamin and cofactor metabolism. The number represents $\log_{1.2}^{(FC)}$, a positive number represents an up-regulated protein, a negative number represents a down-regulated protein, and 0.00 represents a protein that is not significantly different.