

Supplementary Material 1

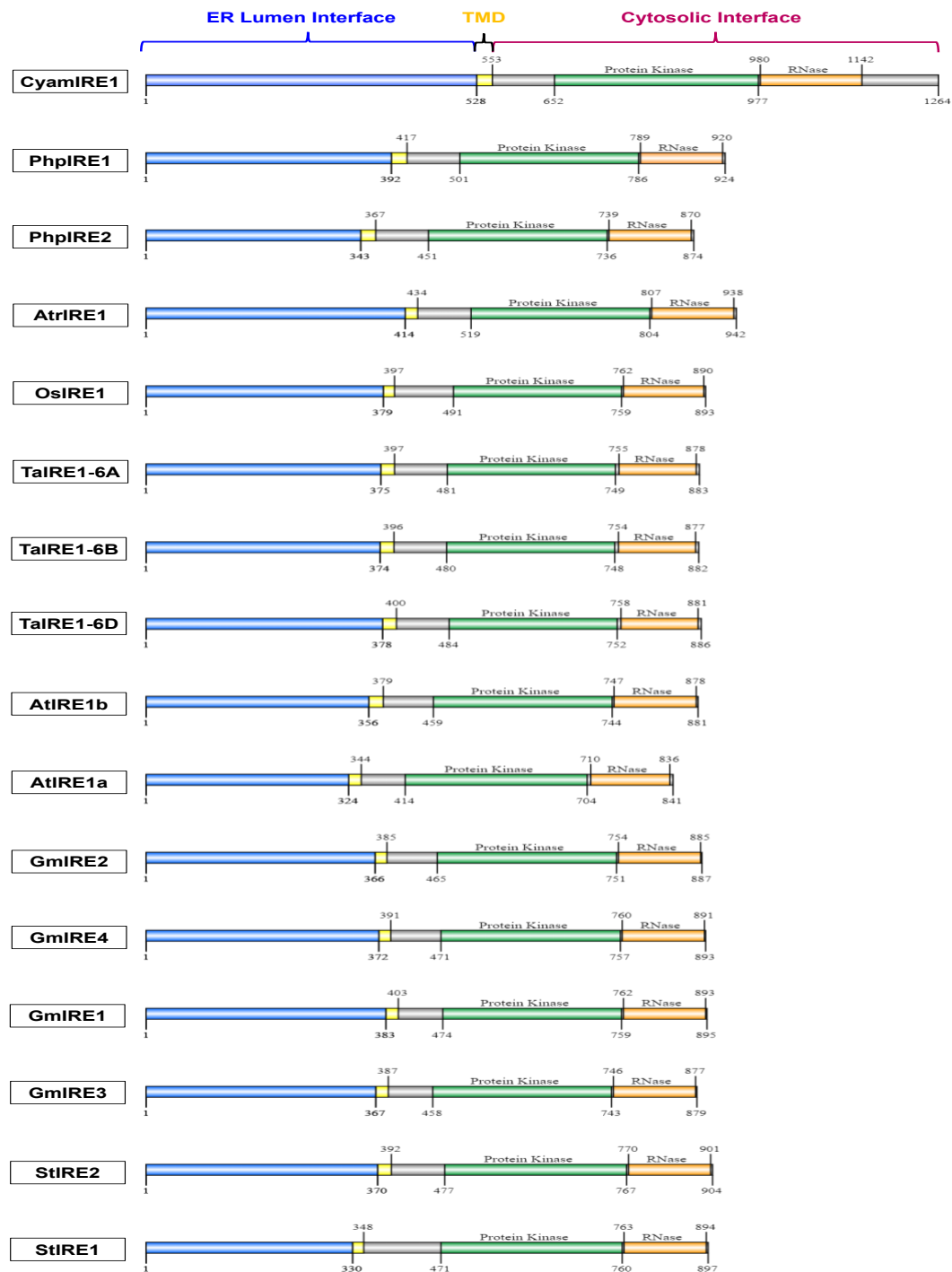
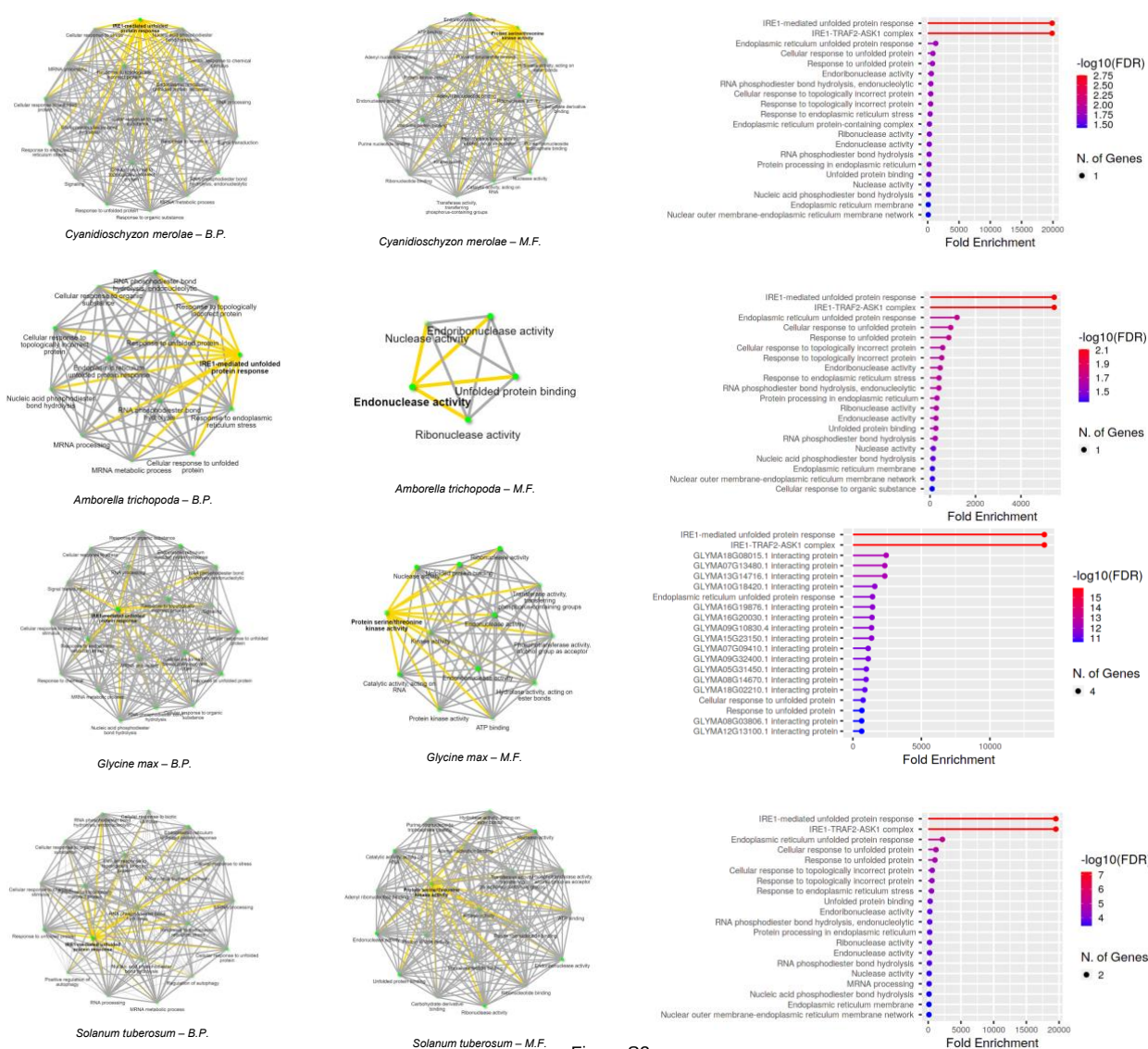
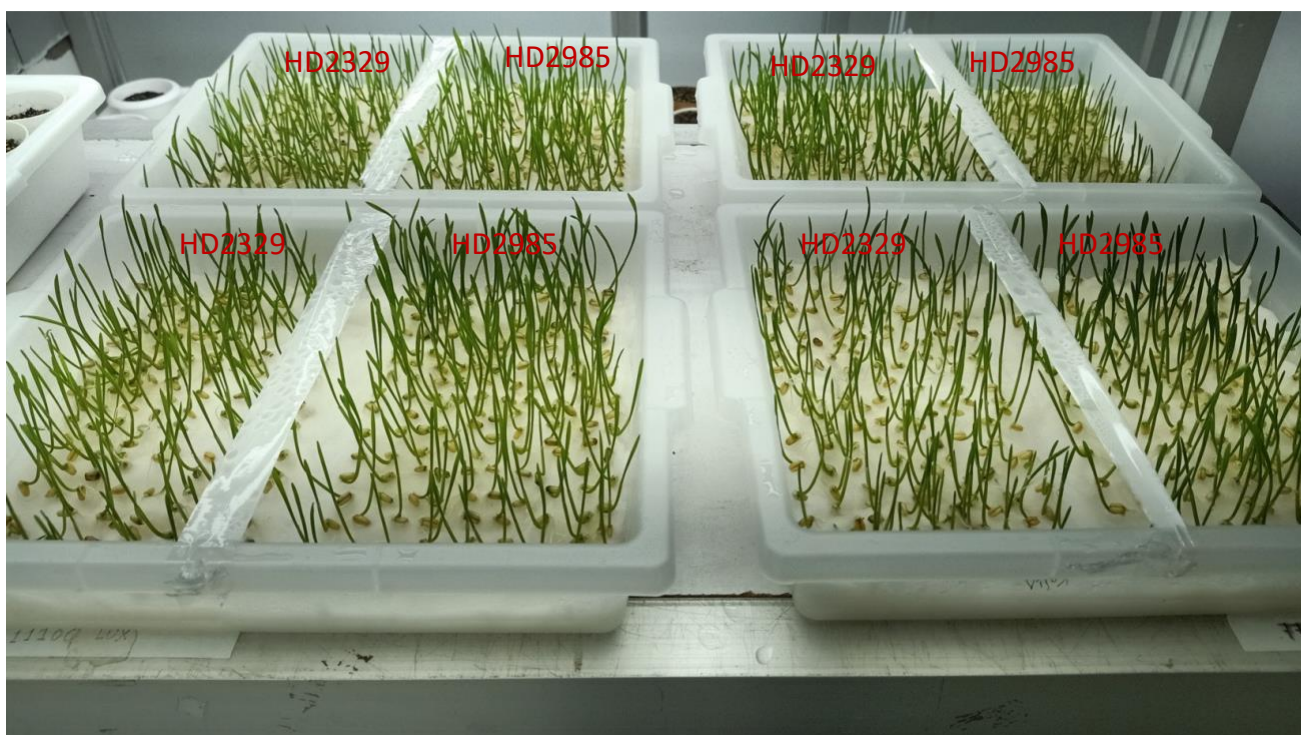


Figure S1

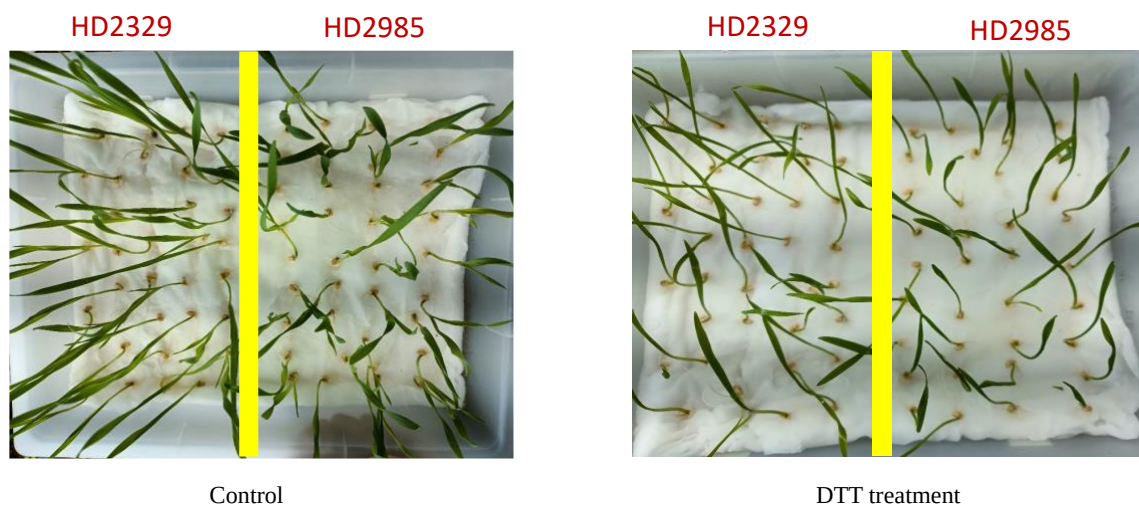
Supplementary Figure S1. Conserved domain composition of *IRE1* genes in different species. Three conserved domains i.e. ER Lumen Interface, Transmembrane domain (TM) and cytosolic interface domains represented in different colors were depicted in the protein structure of different species.



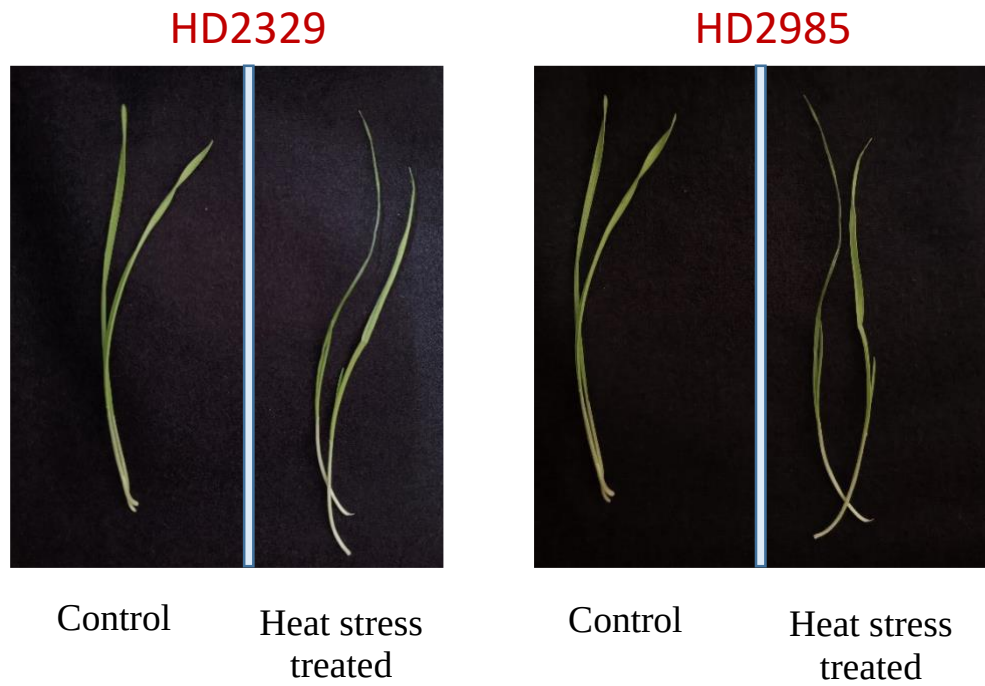
Supplementary Figure S2. Gene Ontology (GO) analysis using ShinyGO identified enriched biological processes of *IRE1* family genes of *Cyanidioschyzon merolae*, *Amborella trichopoda*, *Glycine max*, *Solanum tuberosum*. The green dots represent the nodes for each GO biological process; while the lines (yellow and grey) represent the interaction between the nodes (minimum of 20% genes common between two connected) GO processes.



Supplementary Figure S3. Pictorial view of one-week-old seedlings of two wheat genotypes (HD2329 and HD2985) grown in a plant culture room at 22°C, used in various experiments.



Supplementary Figure S4. One-week-old seedlings of two wheat genotypes (HD2329 and HD2985) under control conditions and following treatment with DTT.



Supplementary Figure S5. One-week-old seedlings of two wheat genotypes (HD2329 and HD2985) under control conditions and following treatment with heat stress (42°C for 6h).