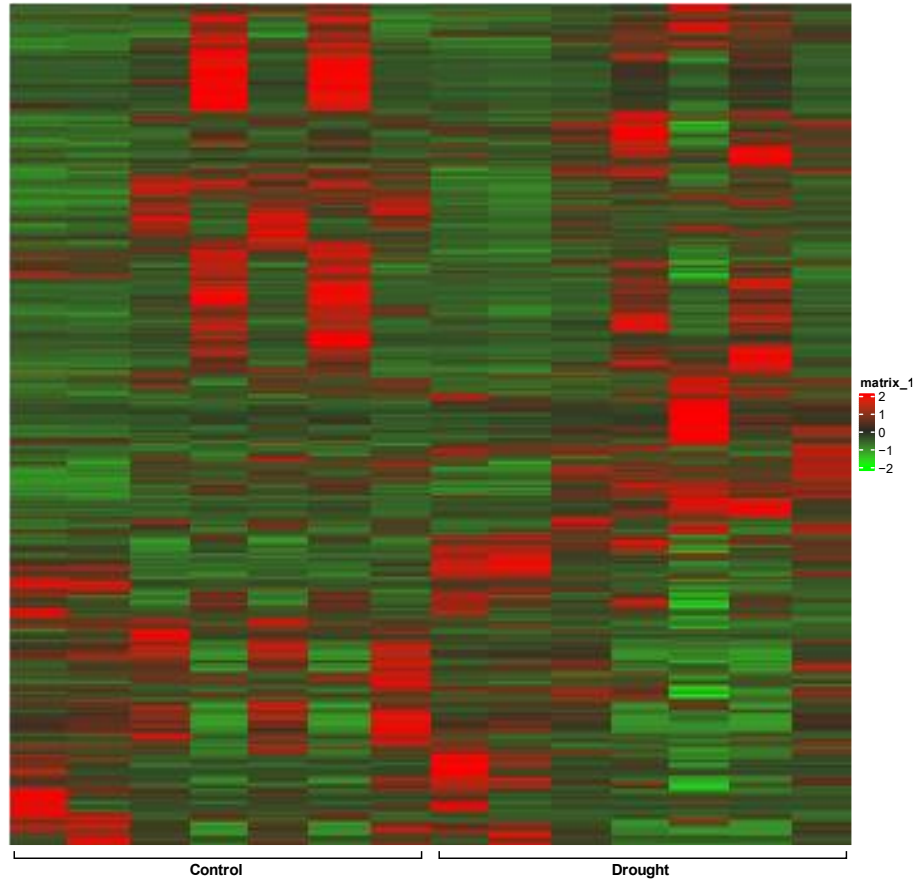
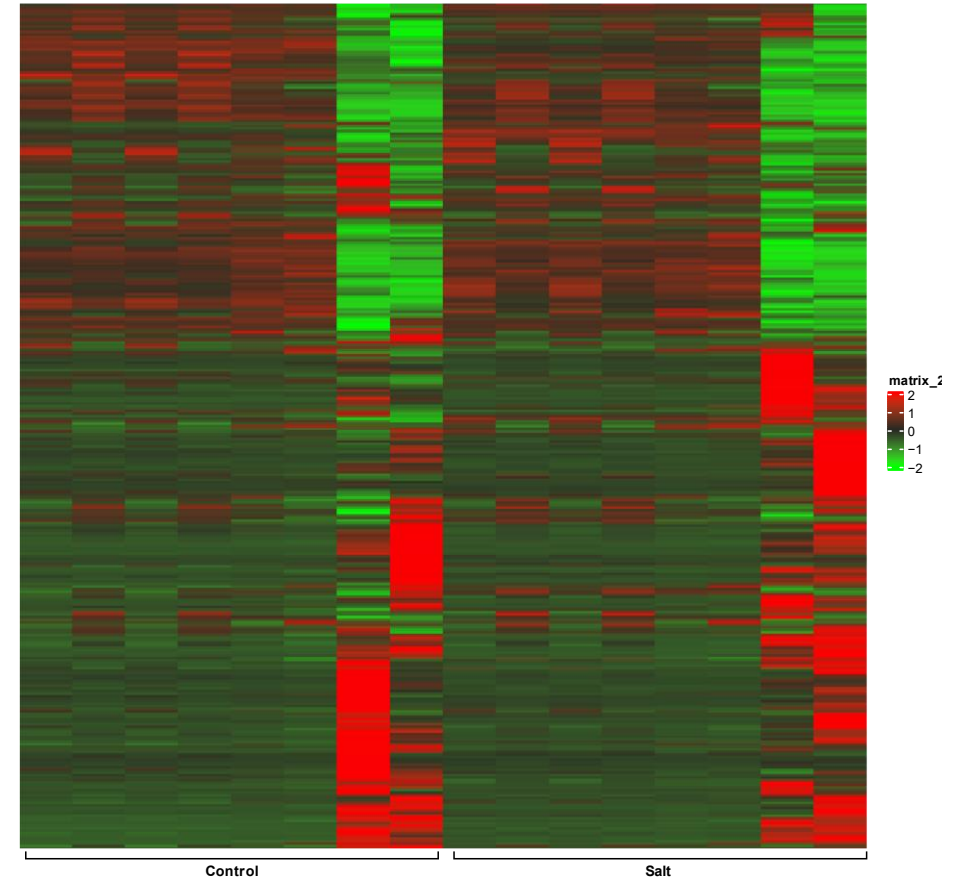
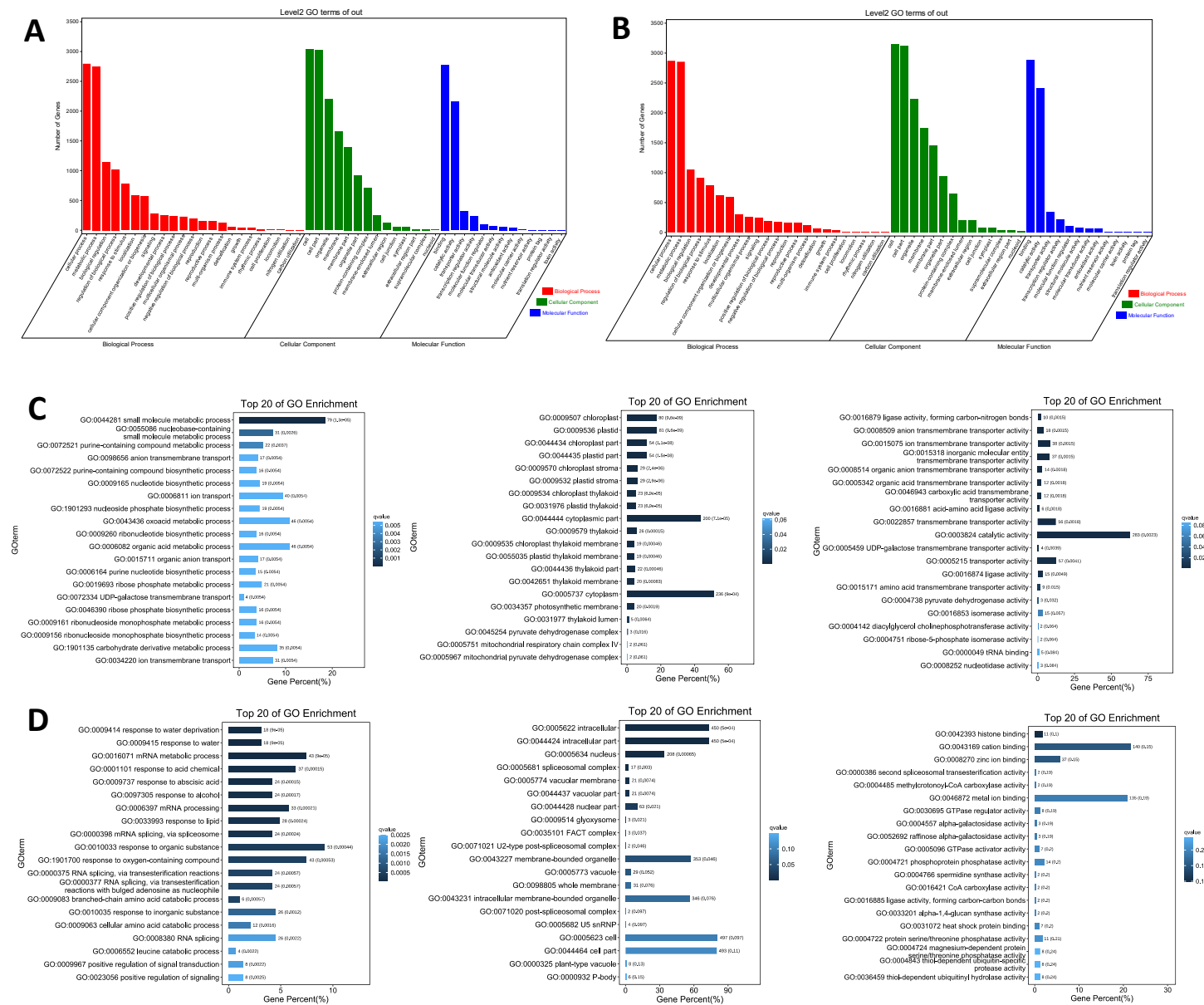
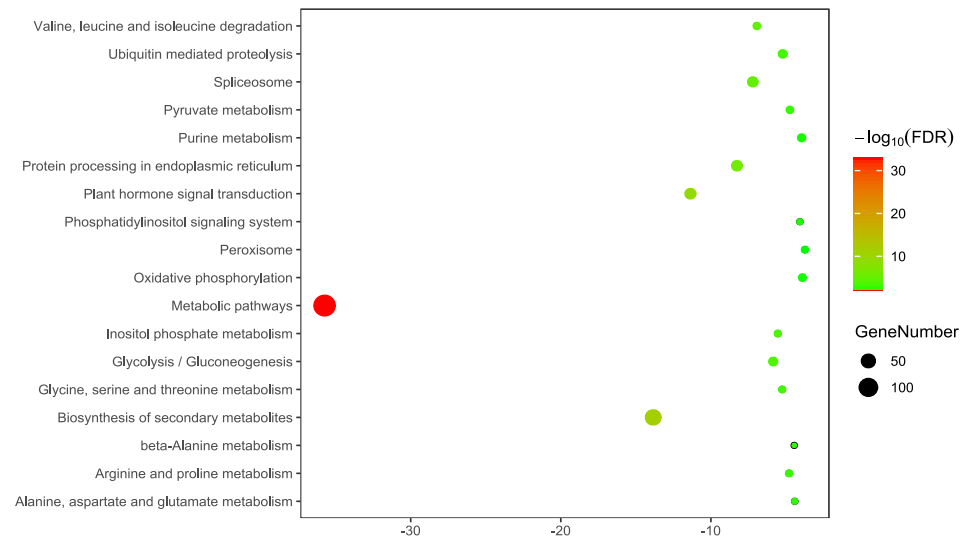


**A****B**

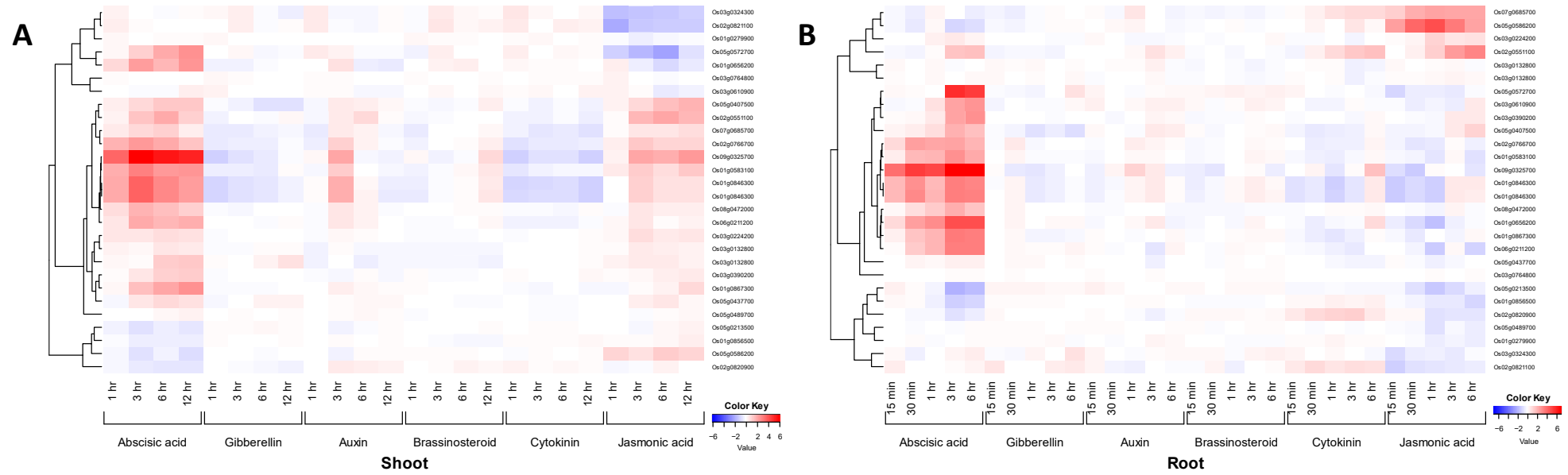
Supplementary Figure S1. Cluster analysis of all DEGs in different tissues under drought (**A**) and salt (**B**) treatments.



Supplementary Figure S2. (A) Gene ontology (GO) classification of drought-related genes. (B) GO classification of salt-related genes. (C) Significantly GO enrichment of up-regulated drought and salt co-response genes in biological process (BP), cellular process (CC) and molecular function (MF) terms. (D) Significantly GO enrichment of down-regulated drought and salt co-response genes in BP, CC, MF terms.

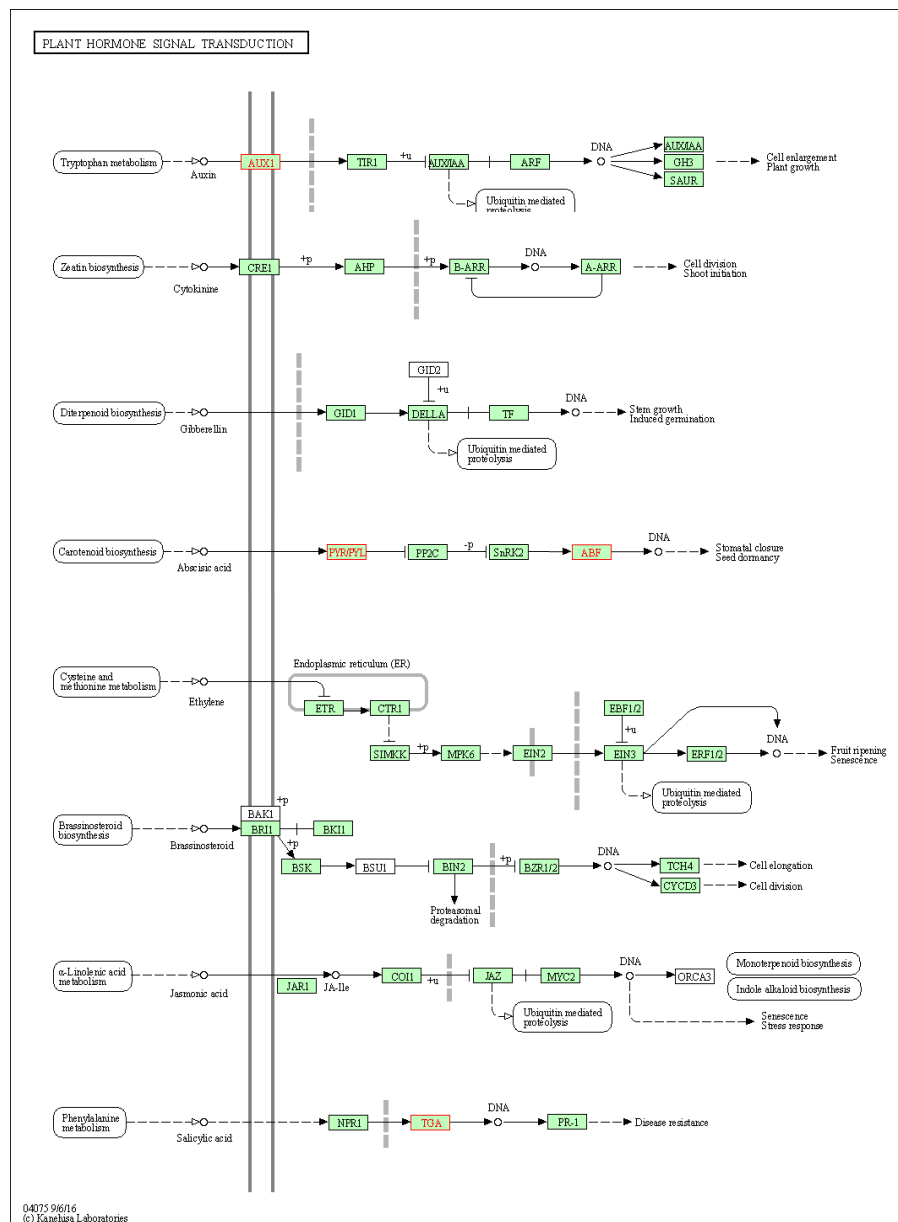


Supplementary Figure S3. KEGG analysis of drought and salt co-response genes.

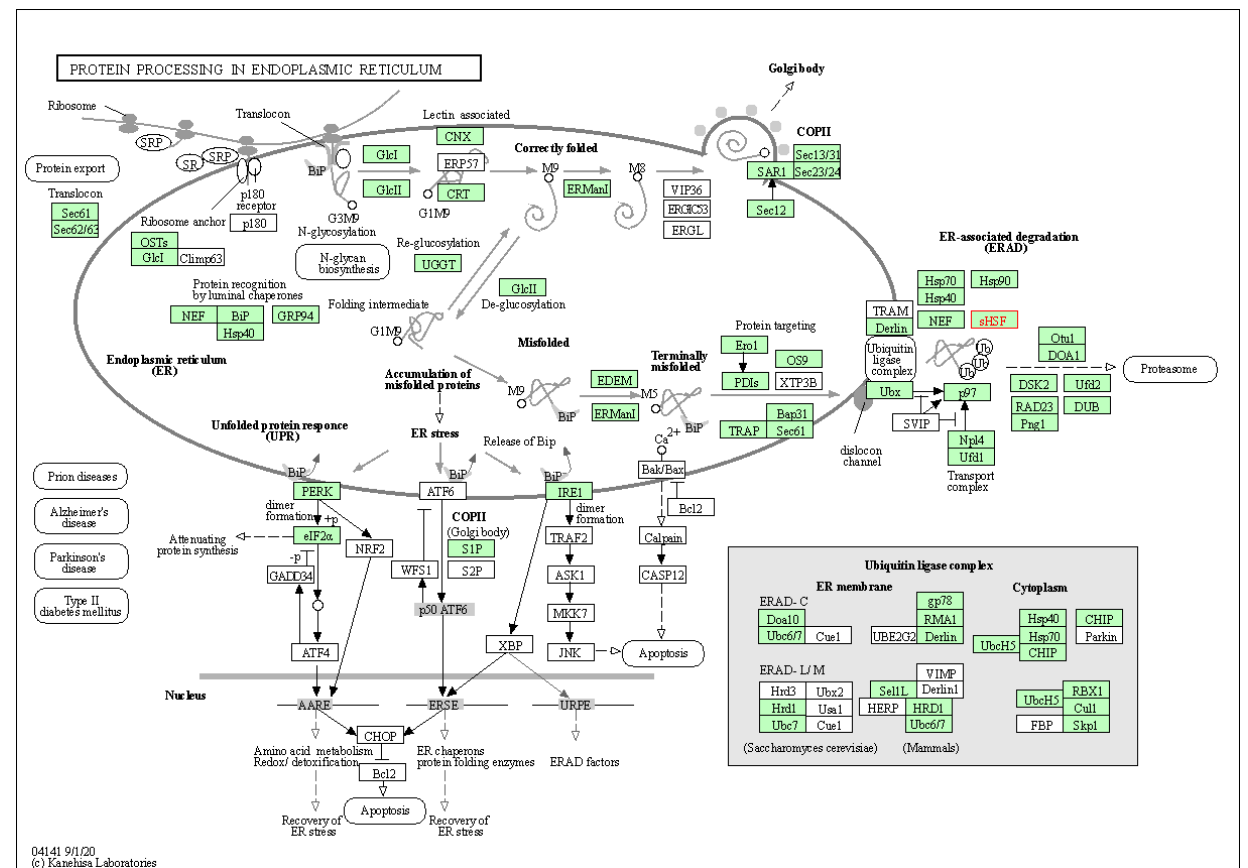


Supplementary Figure S4. The heatmap of 24 candidate genes expression under hormone treatments between **(A)** shoot and **(B)** root.

A

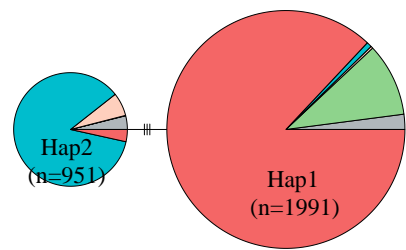


B

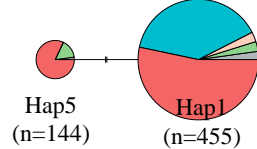


Supplementary Figure S5. KEGG pathway analysis of (A) osa04075 (plant hormone signal transduction) and (B) osa04141 (protein processing in endoplasmic reticulum).

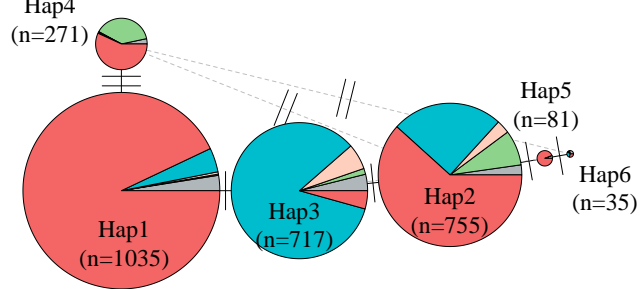
*OsAUX1*  
*Os01g0856500*



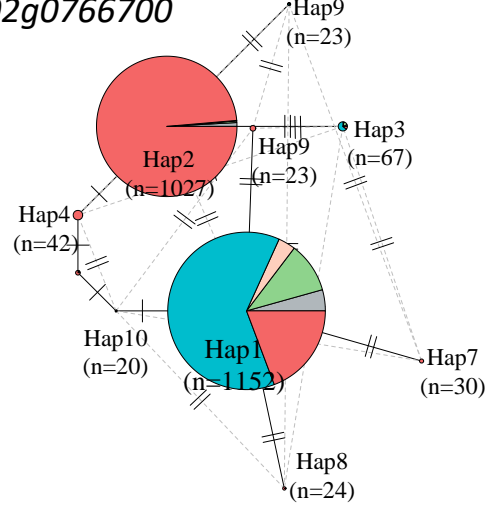
*OsPYL5*  
*Os05g0213500*



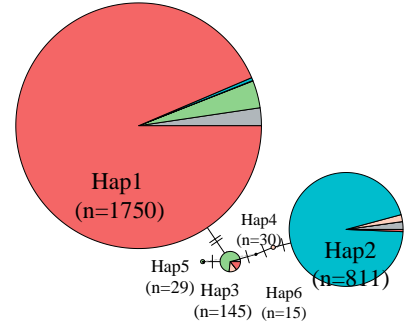
*OsHSP17.0*  
*Os01g0136200*



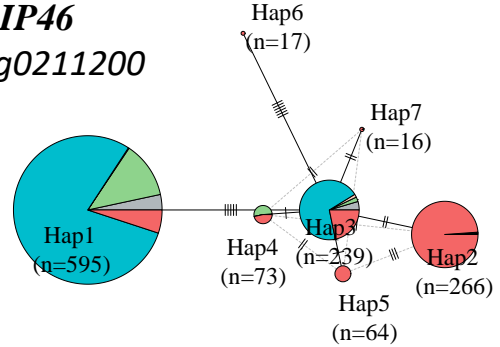
*OsZIP23*  
*Os02g0766700*



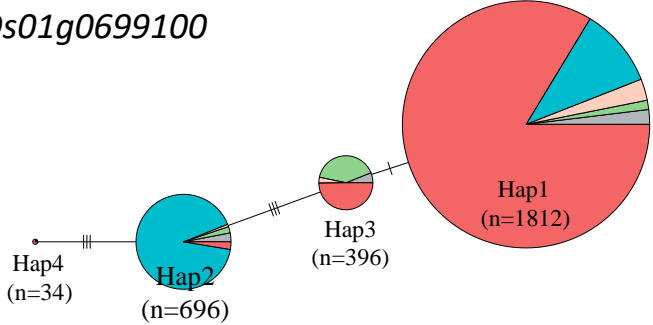
*OsZIP42*  
*Os05g0489700*



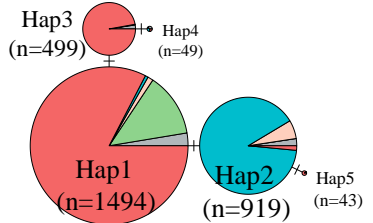
*OsZIP46*  
*Os06g0211200*



*OsMPKKK63*  
*Os01g0699100*



*OsMPK3*  
*Os03g0285800*



Supplementary Figure S6. Haplotype networks of seven DT and ST co-response genes in 3KRG.