

Genome-wide discovery and characterization of major RNAi gene families in Date palm (*Phoenix dactylifera*)

(Supplementary Figures)

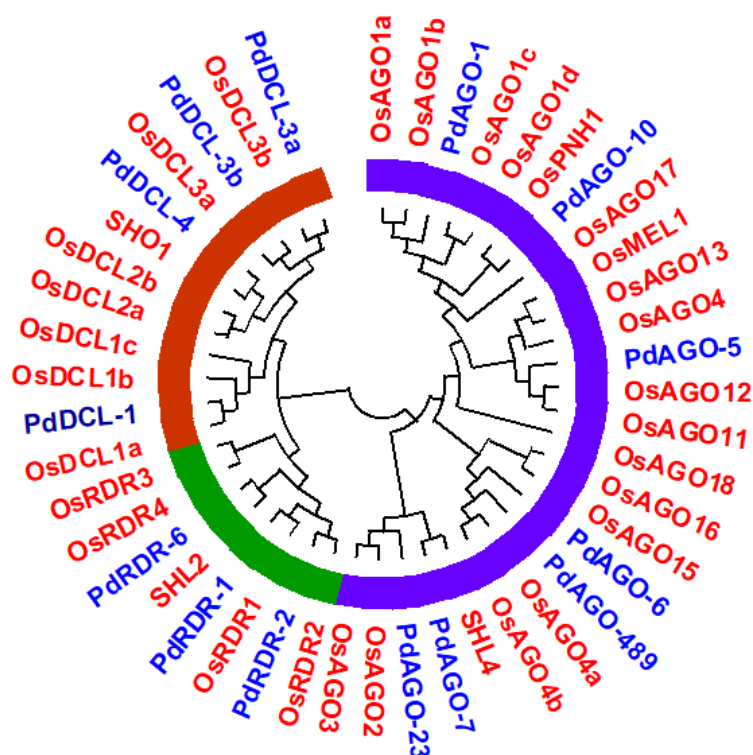


Figure 1. The combined phylogenetic tree. In this tree, the PdRNAi (PdDCLs, PdAGOs, PdRDRs) and OsRNAi (OsDCLs, OsAGOs, OsRDRs) genes were represented by green and red, respectively. Here AGOs, DCLs and RDRs families were represented by purple, orange and green circles, respectively.

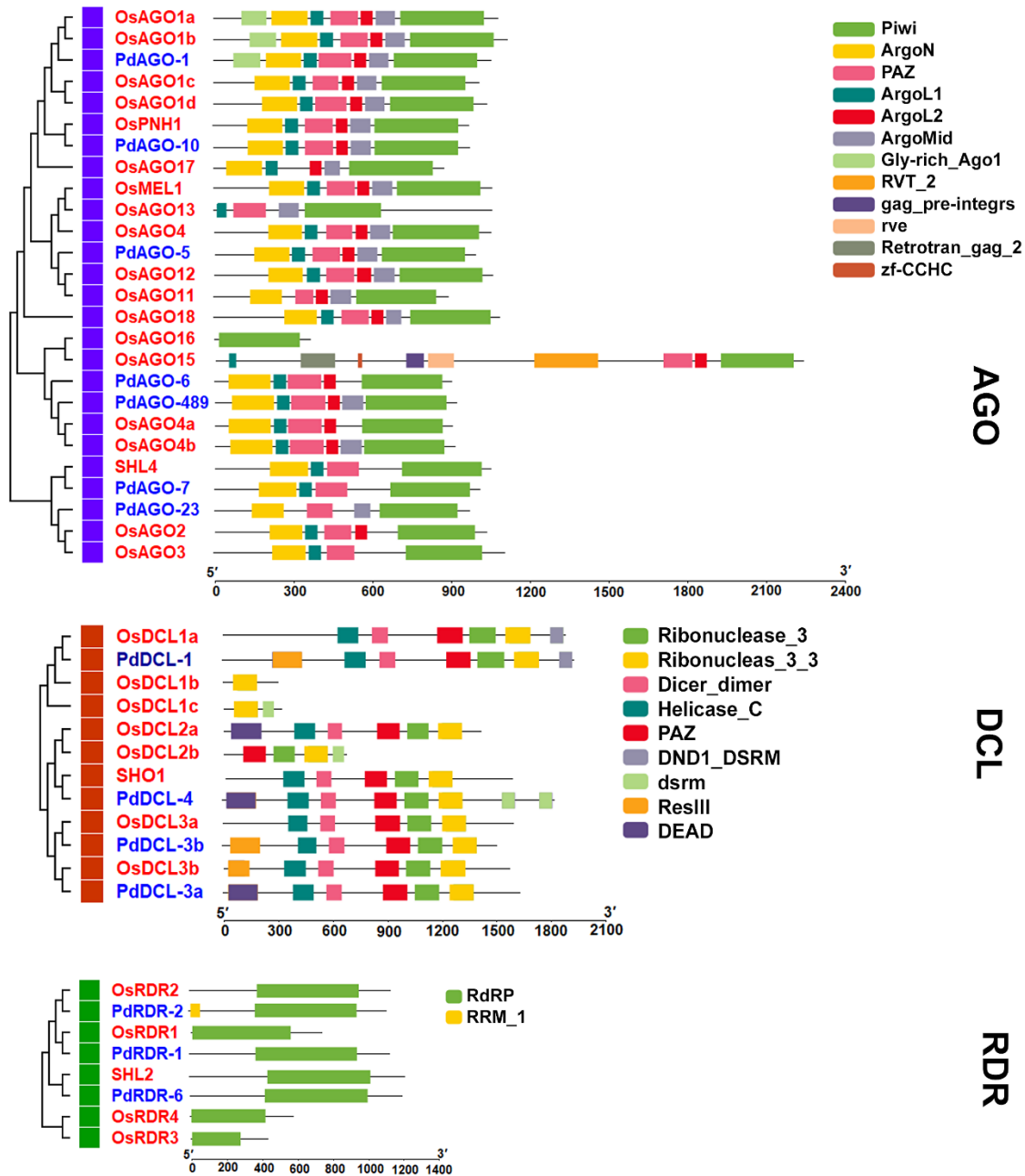


Figure 2. The conserved domains of OsRNAi and the PdRNAi proteins. Different color represents different conserved domains. Here Piwi indicates Piwi domain, ArgoN indicates N-terminal domain, PAZ indicates PAZ domain, ArgoL2 indicates Argonaute linker 2 domain, ArgoL1 indicates Argonaute linker 1 domain, ArgoMid indicates Mid domain of argonaute, Gly-rich_Ago1 indicates Glycine-rich region of Argonaut, RNase III indicates Ribonuclease III domain, Dicer_dimer indicates Dicer dimerization domain, Helicase_C indicates Helicase conserved C-terminal domain, dsrm indicates Double-stranded RNA binding motif, DEAD indicates DEAD/DEAH box helicase domain, RdRP indicates RNA dependent RNA polymerase, RRM_1 RNA recognition motif 1.

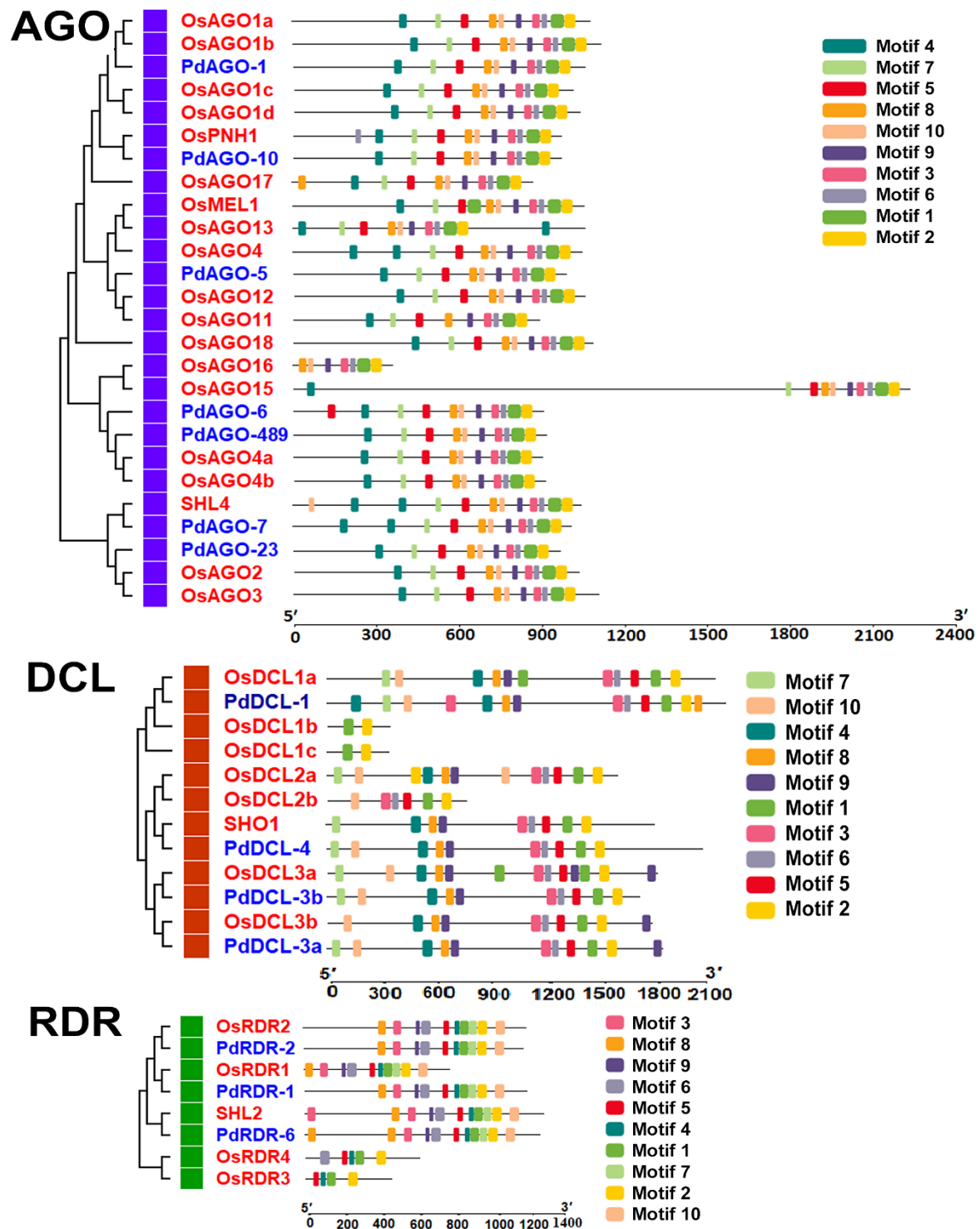


Figure 3. Motifs of OsRNAi and the PdRNAi proteins. Different color represents different motifs.

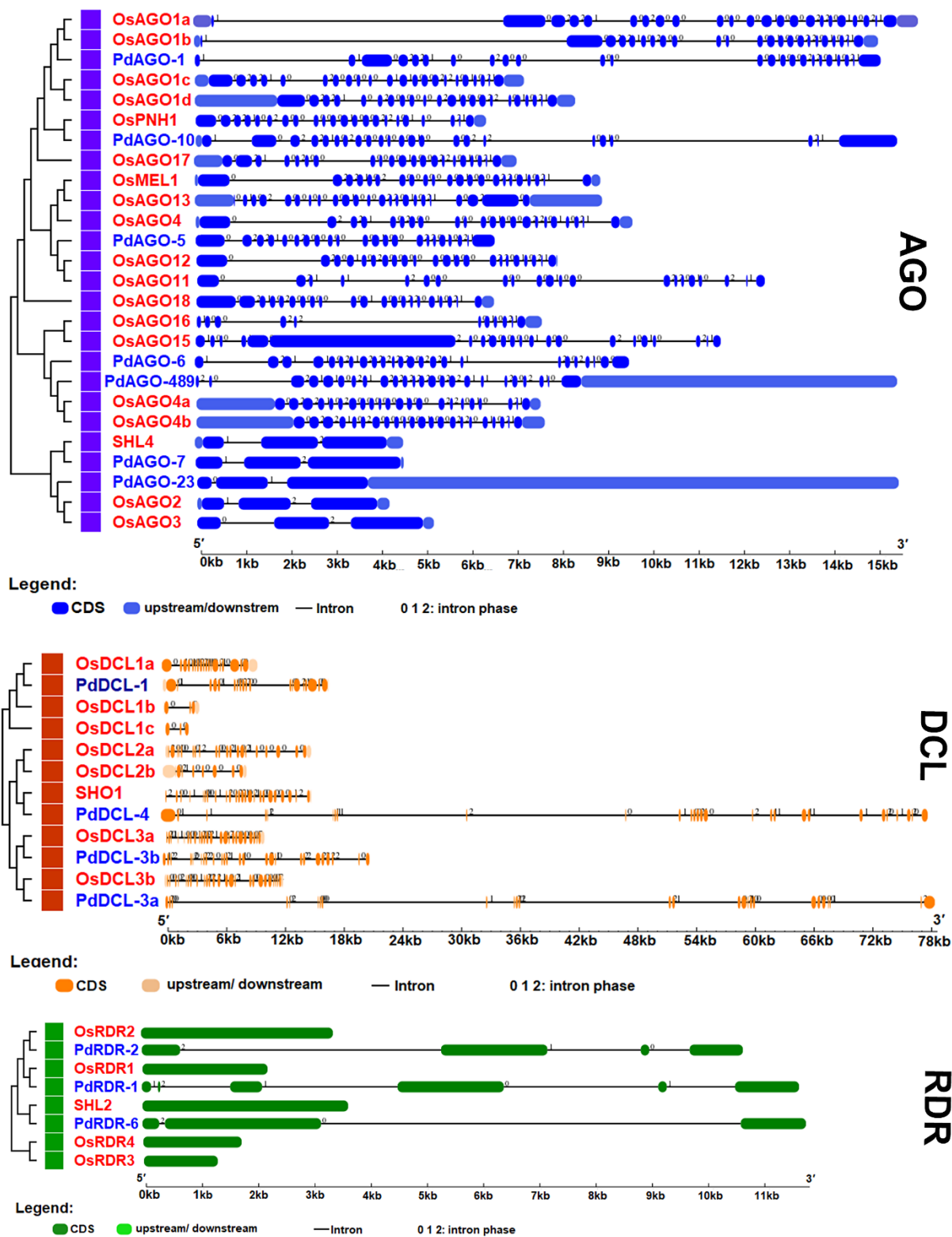


Figure 4. Structure of osRNAi and the predicted PdRNAi genes.

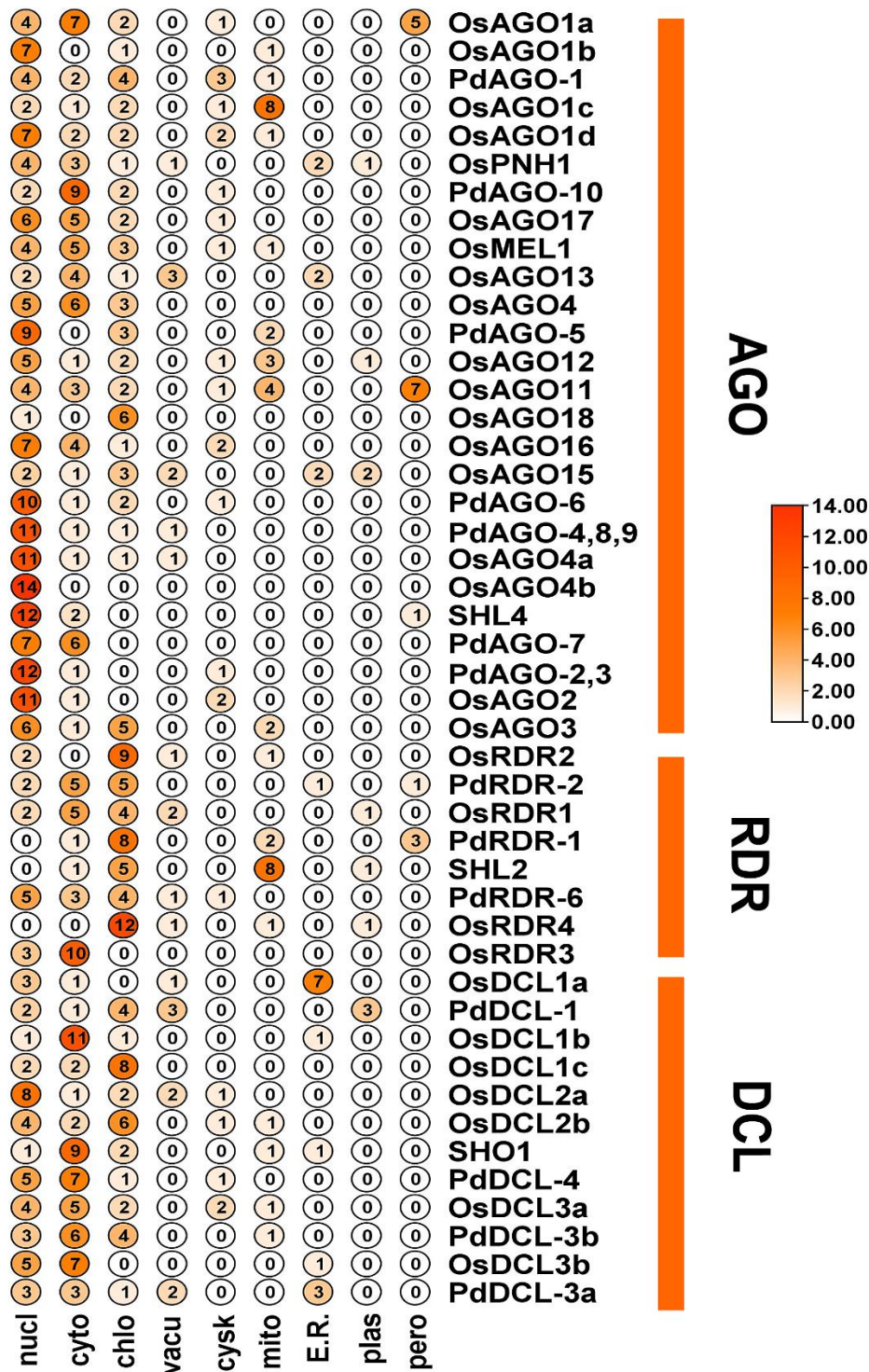


Figure 5. Sub-cellular localization analysis of OsRNAi and PdRNAi proteins. Protein percentages are found in several biological components. In this analysis, nucl – nucleus, cyto – cytosol, chlo – chloroplast, vacu – vacuole, cysk – Cytoskeletal, mito – mitochondria, E.R. – Endoplasmic Reticulum, plas – plastid, pero – peroxisome.

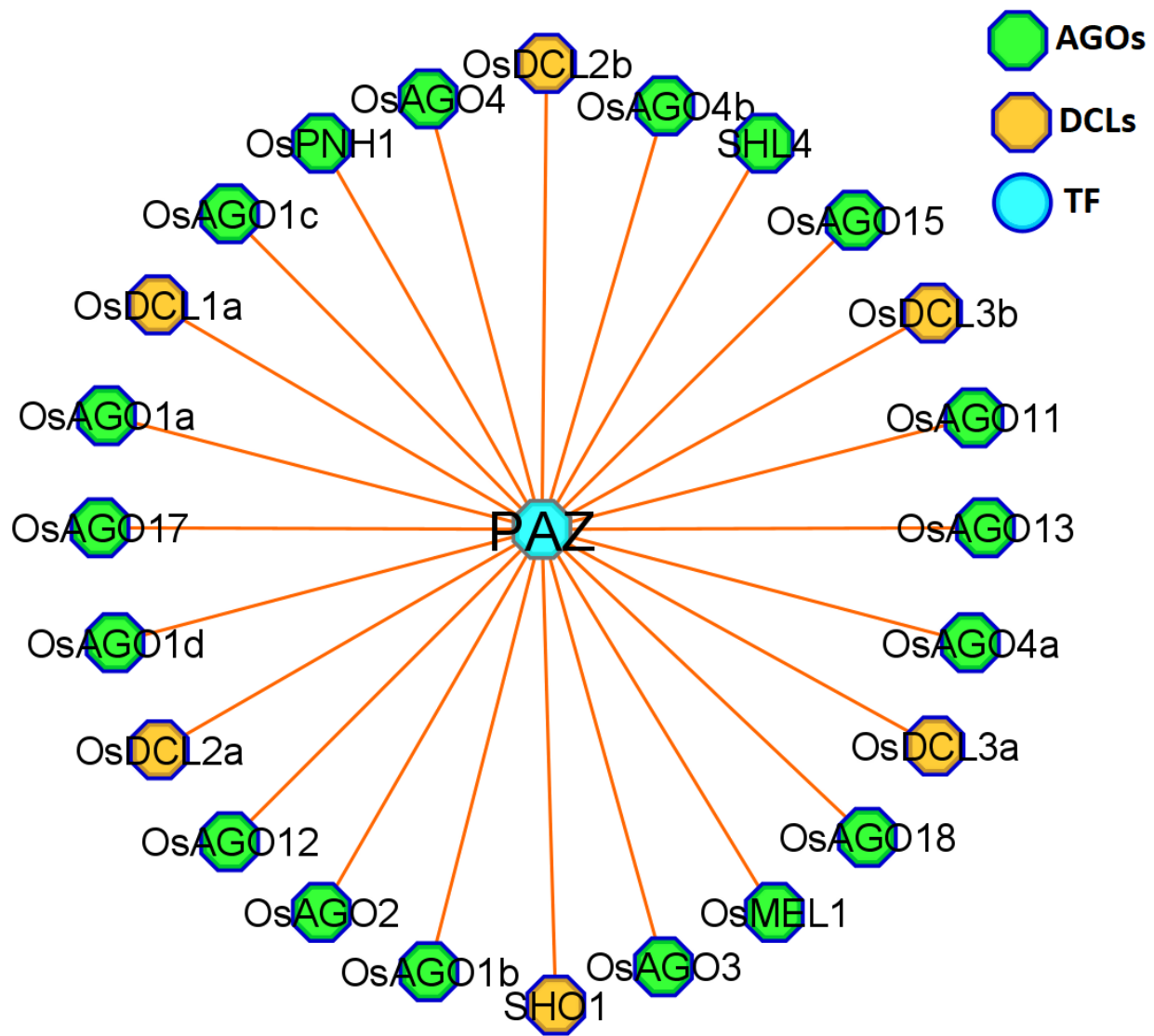


Figure 7. The regulatory network among the TFs and OsRNAi proteins. The nodes of the network were colored based on RNAi proteins (AGOs green, DCLs orange) and TFs (blue).

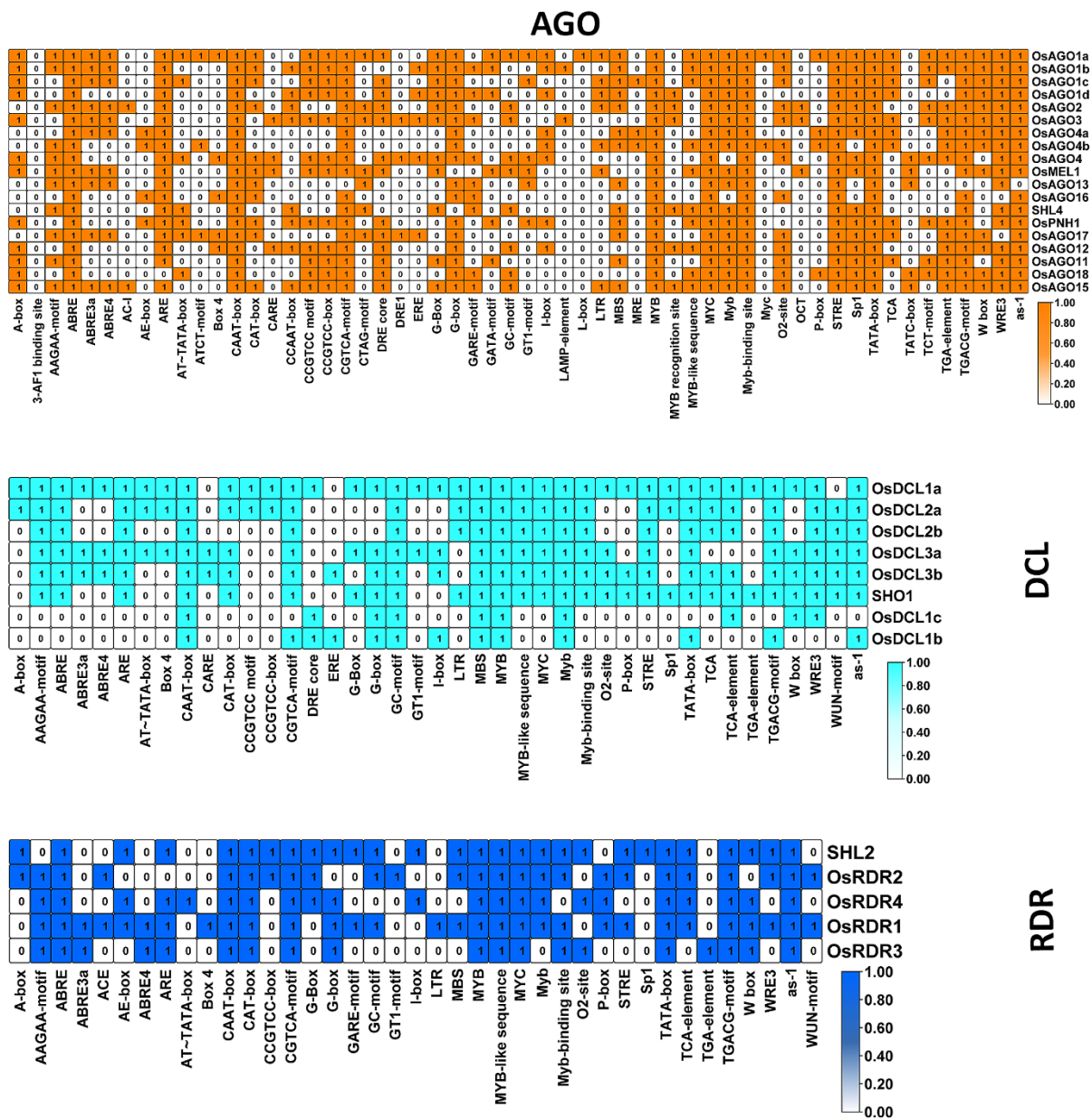


Figure 8. The cis-acting regulatory elements in the upstream promoter region of predicted OsDCL, OsAGO and OsRDR genes, respectively. The deep to light color represents the presence of that element with the corresponding genes.

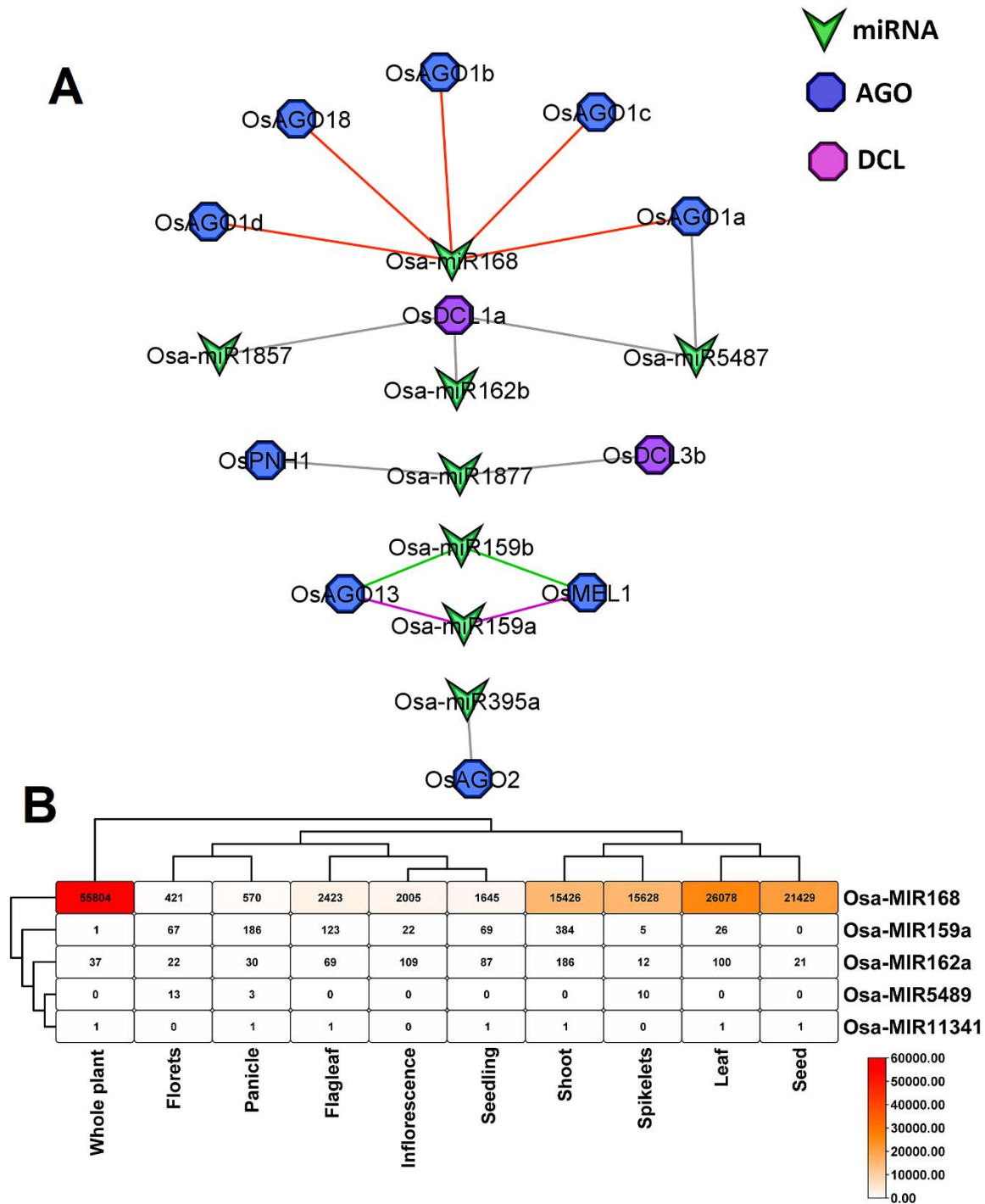


Figure 9. A: The regulatory network among the miRNA and Pd RNAi genes. B: miRNA expression level in different plant organs of Pd RNAi genes. DCL, AGO and RDR genes were represented by orange, purple and pest color, respectively and miRNAs were presented light green color.