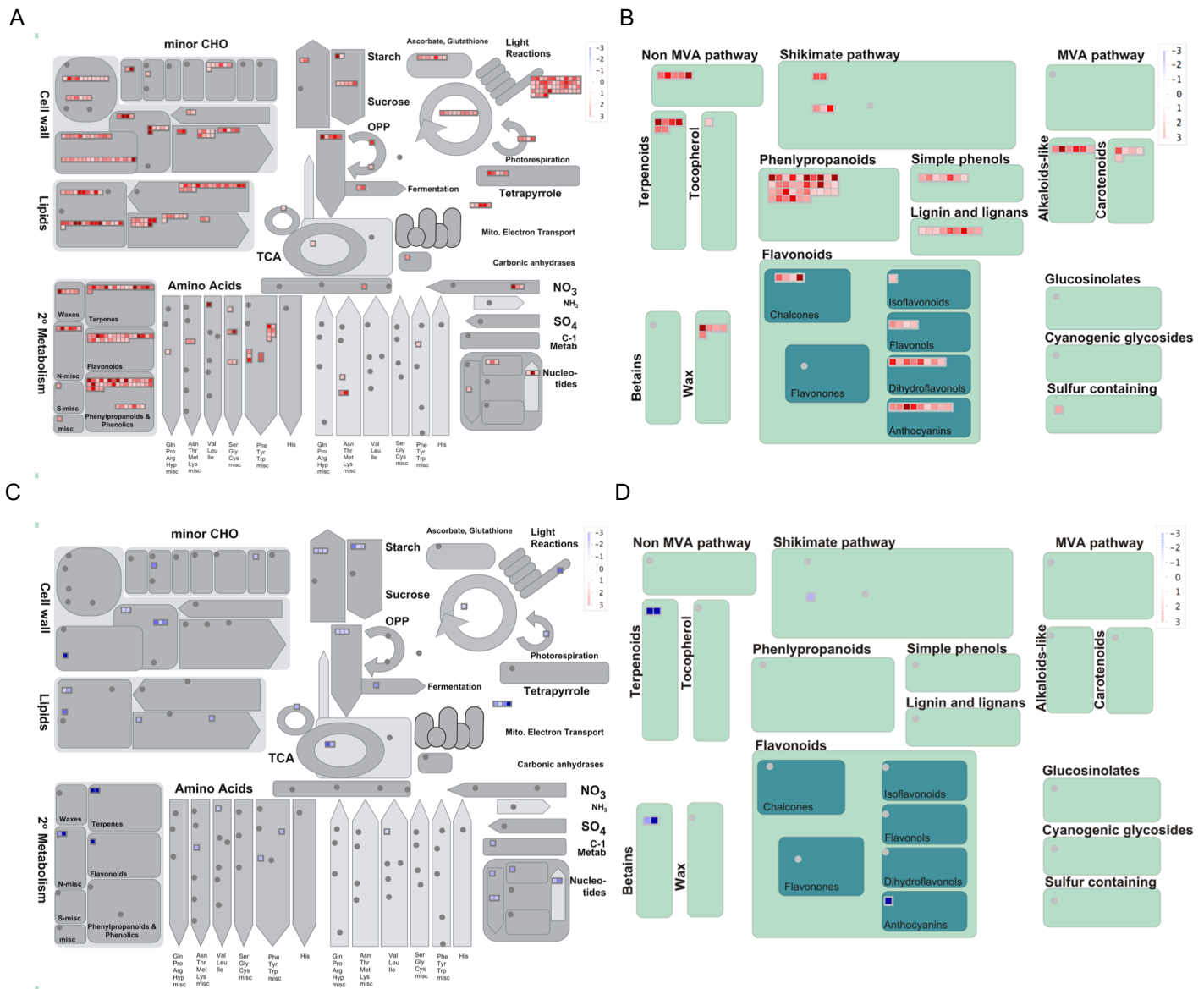
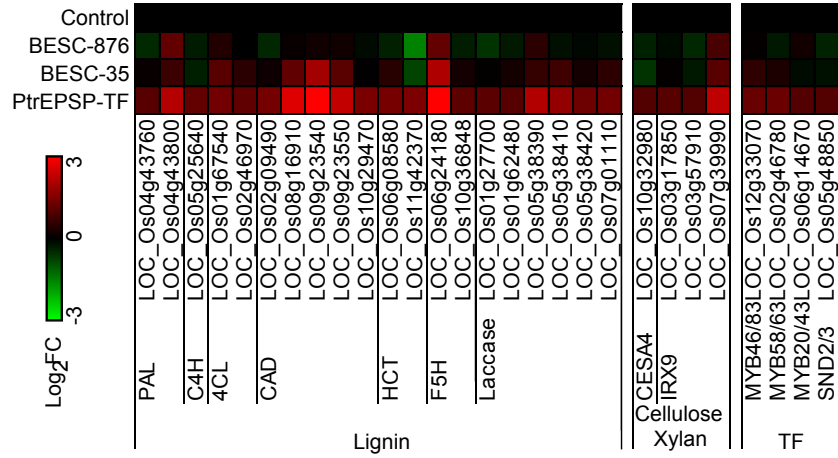


**Figure S1.** Venn diagrams of DEGs from BESC-35 (blue), BESC-876 (red), and PtrEPSP-TF (green). Left panel: up-regulated genes. Right panel: down-regulated genes.



**Figure S2.** Genes associated with cell wall, secondary metabolism, and phenylpropanoid/lignin metabolism are enriched among genes up-regulated in *PtrEPSP-TF* expression rice. (A) MapMan metabolism overview maps of up-regulated genes in *PtrEPSP-TF* expression rice. (B) MapMan secondary metabolism overview maps of up-regulated genes in *PtrEPSP-TF* expression rice. (C) MapMan metabolism overview maps of down-regulated genes in *PtrEPSP-TF* expression rice. (D) MapMan secondary metabolism overview maps of down-regulated genes in *PtrEPSP-TF* expression rice.



**Figure S3.** Heat map showing expression patterns of genes related with secondary cell wall biosynthesis in rice plants expressing the archetypic *PtrEPSP-TF*, *BESC-35 PtrEPSP-TF*, and *BESC-876 PtrEPSP-TF*, respectively. Color scales represent the value of  $\text{Log}_2\text{FC}$ .  $\text{Log}_2\text{FC}$  of mean expression levels of the four independent replicates of each transgenic lines was used to generate the heat map.  $\text{Log}_2\text{FC}$  of mean expression levels of empty vector control was set as 0.

LOC\_Os11g08210 (NAC081)



1,952 out of 3,423 genes  
(57.03%%)

LOC\_Os03g42630 (NAC058)



984 out of 3,423 genes  
(28.75%)

LOC\_Os05g35500 (MYB4)  
LOC\_Os08g43550 (MYB4)  
LOC\_Os12g07640 (MYB4)



963 out of 3,423 genes  
(28.13%)

**Figure S4.** The enrichment of cis-elements recognized by LOC\_Os11g08210 (NAC081), LOC\_Os03g42630 (NAC058), LOC\_Os05g35500 (MYB4), LOC\_Os08g43550 (MYB4), and LOC\_Os12g07640 (MYB4).