Supplemental Figures

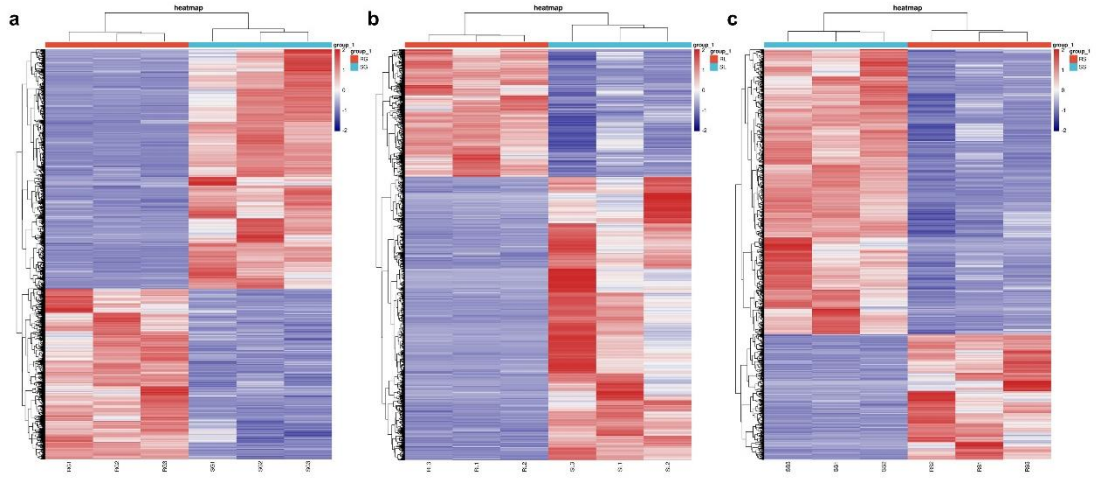

Fig.S1 Hierarchical clustering heatmaps of differentially expressed genes (DEGs) in different tissues of ZS54 and ZS57. (a) Resistant (left) and susceptible (right) glume; (b) Resistant (left) and susceptible (right) leaf; (c) Susceptible (left) and resistant (right) leaf sheath. Each panel shows three biological replicates.

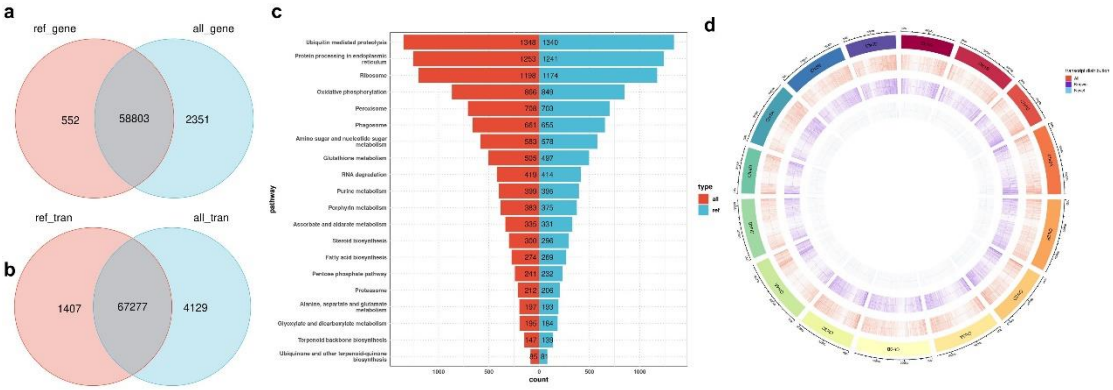

Fig.S2 Comparison of Identification Results: All Transcripts vs. Reference in ZS54 and ZS57. (a,b) Venn of genes/transcripts: ref vs all. (c) Differences in pathway annotation: ref vs. all. (d) Density distribution map of the transcriptome. Note: Outermost to innermost-chromosome, all transcripts, known transcripts, novel transcripts, strand-specific.

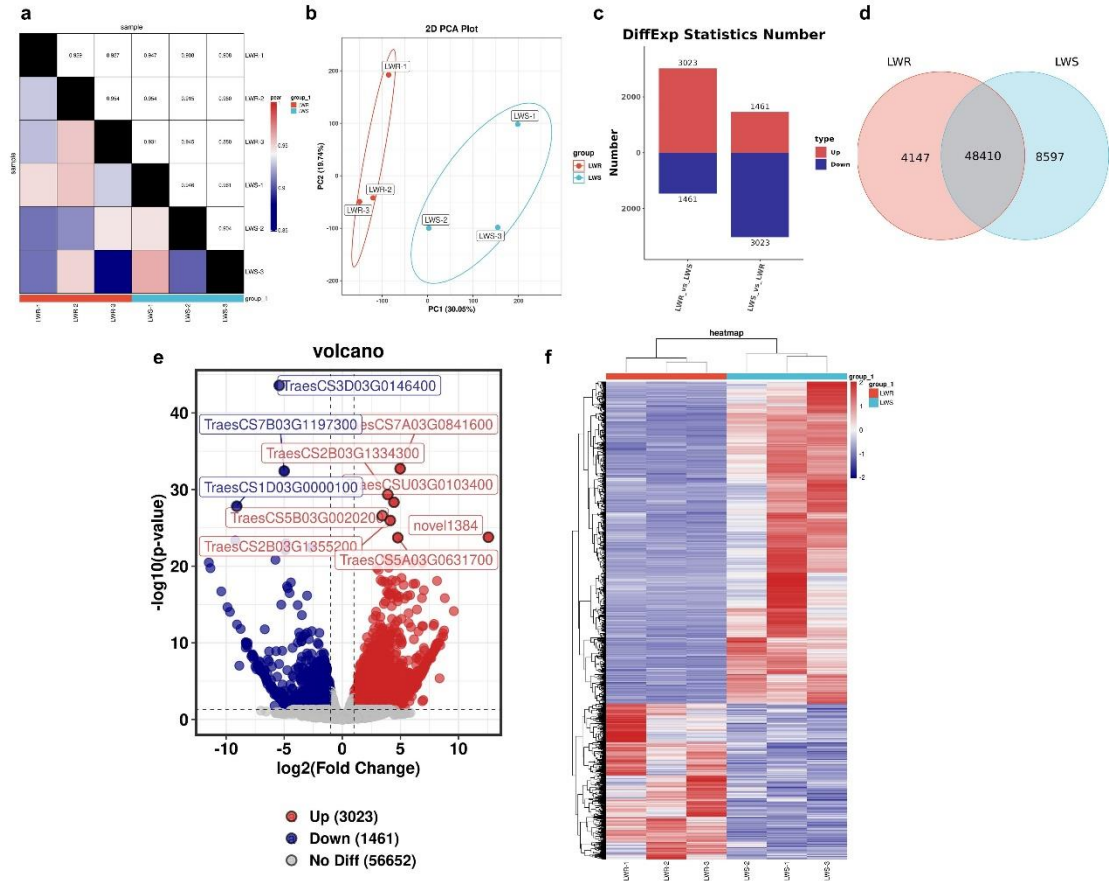

Fig.S3 RNA-seq performed on resistant and susceptible plants at different developmental stages in ZS54 and ZS57. (a) Sample correlation of all samples. (b) Principal component analysis (PCA) among groups. (c) Differentially expressed genes between the various comparison groups. Red means upregulation, and blue means downregulation. Note: NBF represents non-bagged fruits; BF represents bagged fruits. (d) Venn diagram of the DEGs. These genes were obtained from ZS31 VS ZS3 comparisons. Volcano plots of differentially expressed genes with up- or down-regulated DEGs in ZS31 VS ZS3 (e). Hierarchical clustering heatmaps of differentially expressed genes (DEGs) in different tissues of ZS31 and ZS3. (e) Resistant (left) and susceptible (right) leaves. Each panel shows three biological replicates.

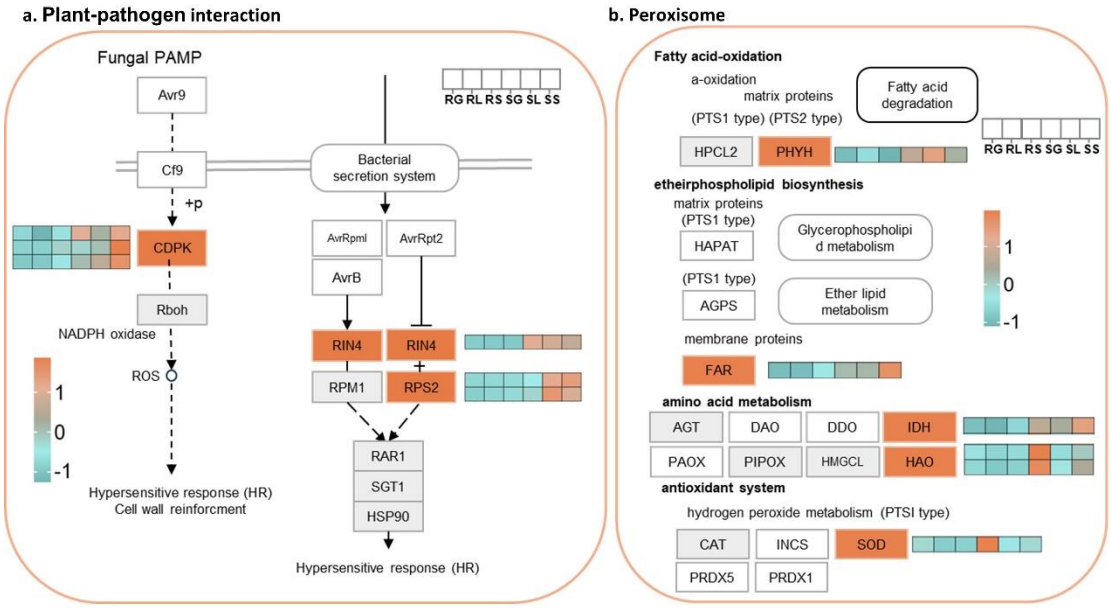

Fig.S4 Transcriptional profiles and pathway mapping for the plant-pathogen interaction (ko04626) and peroxisome (ko04146). Orange and blue denote up- and down-regulation in the susceptible genotype, respectively.

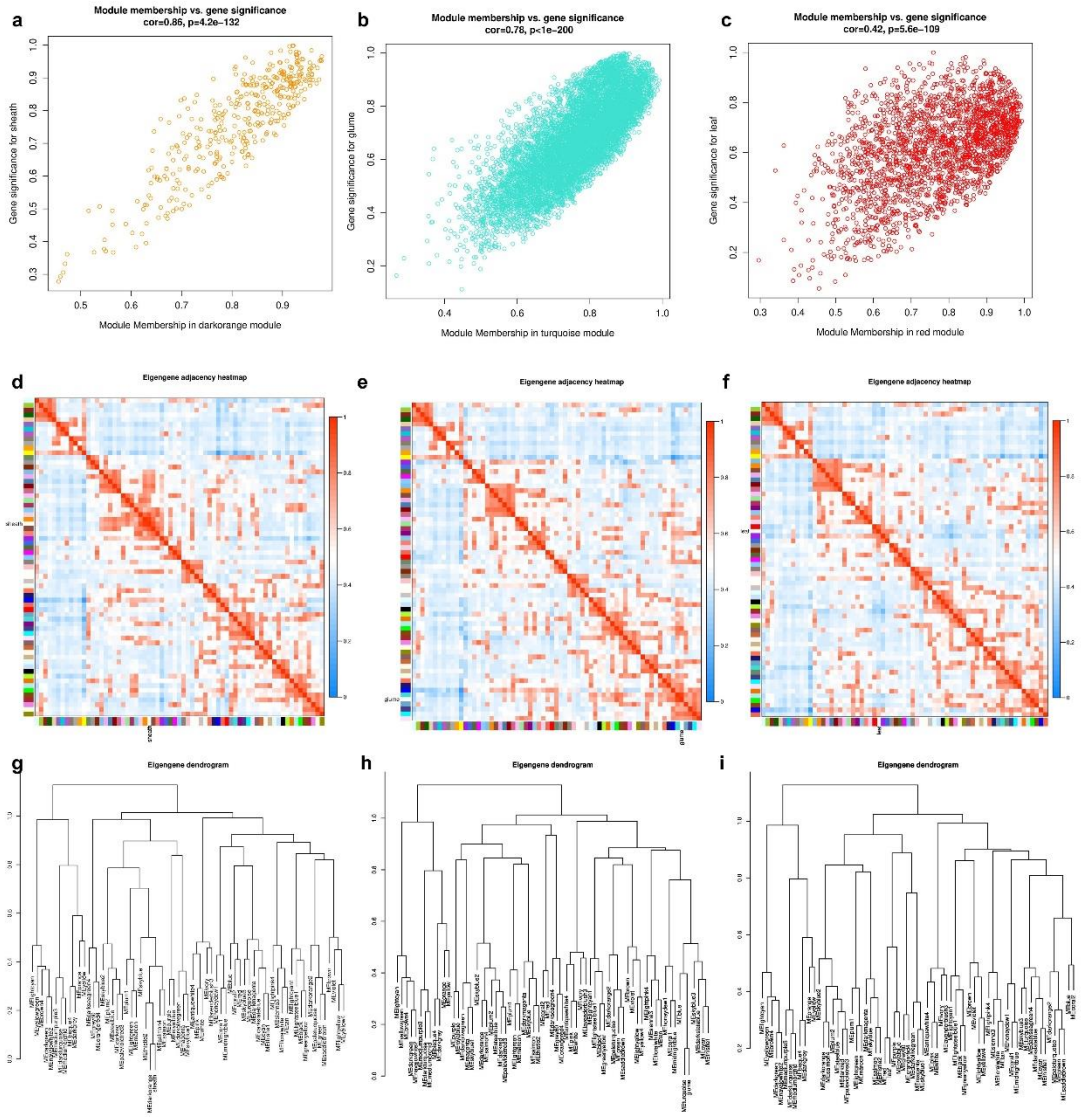

Fig.S5 Association of weighted gene co-expression network analysis (WGCNA) modules with disease-susceptibility traits across leaf sheath, glume, and leaf tissues. (a-c) Diagram of the relationship between genes and phenotypes within the module: darkorange (a), turquoise (b), red (c). Heatmap showing the correlation between sheath phenotypic traits and the darkorange module (d), glume phenotypic traits and the turquoise module (e), and leaf phenotypic traits and the red module (f); Clustering dendrogram illustrating the relationships between sheath phenotypic traits and the darkorange module (g), glume phenotypic traits and the turquoise module (h), and leaf phenotypic traits and the red module (i).

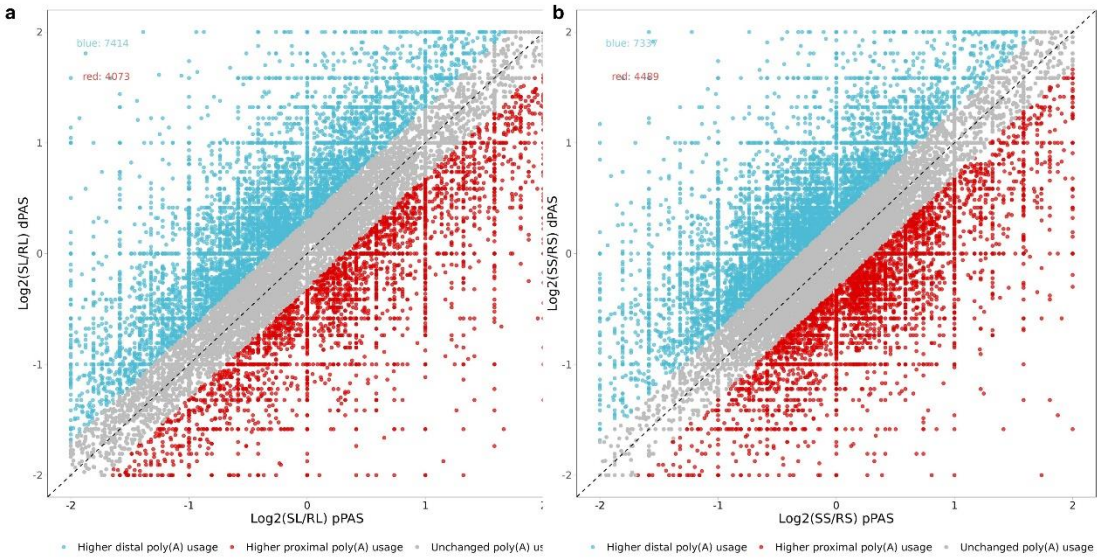

Fig.S6 Preference for poly(A) sites of SL vs RL (a) and SS VS RS (b).