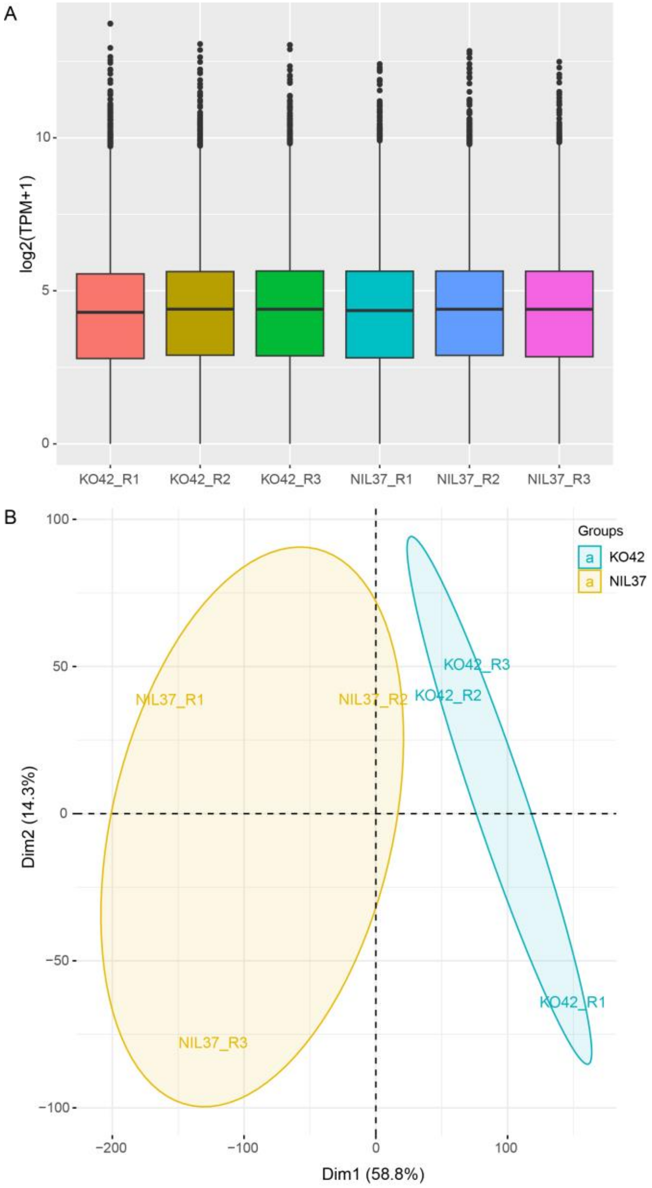

Figure S1. TPM distribution and principal component analysis (PCA) of KO42 and NIL37 samples. **(A)** Boxplot showing TPM distribution across samples. **(B)** PCA of grouped KO42 and NIL37 samples.

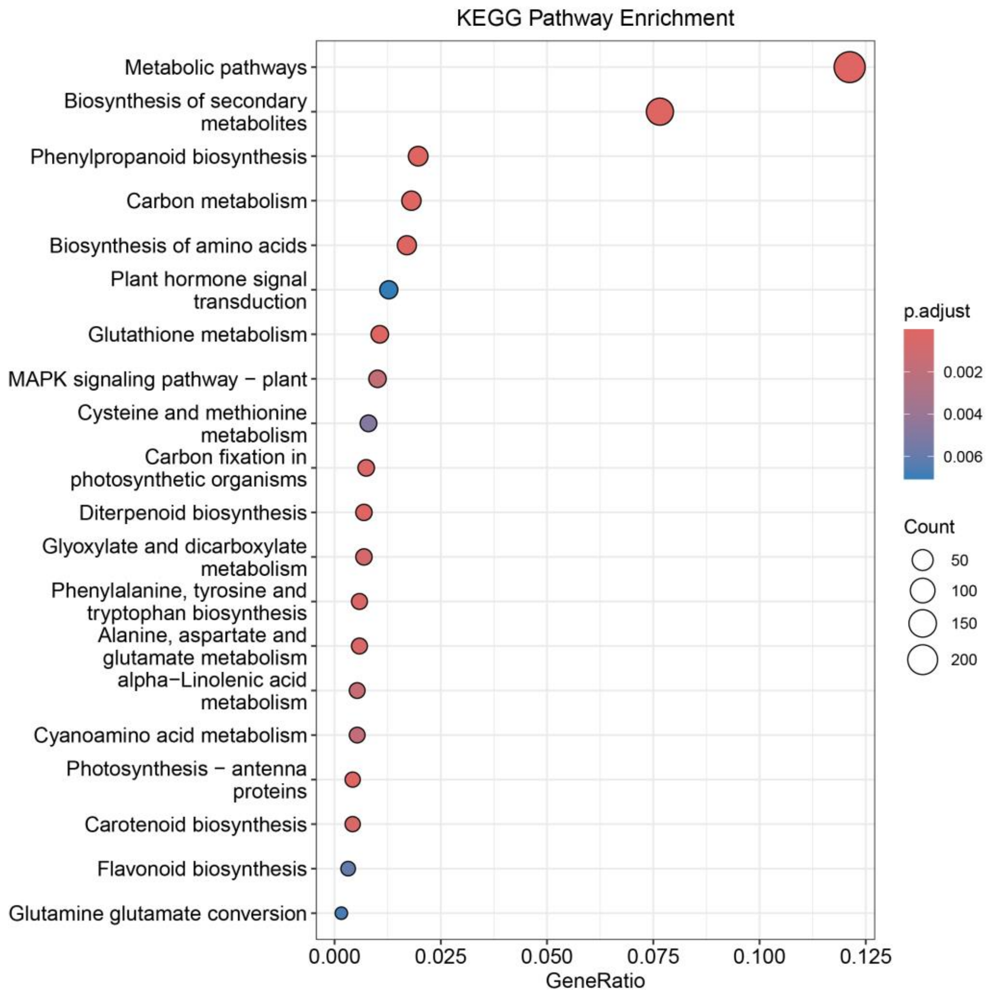

Figure S2. KEGG pathway enrichment analysis of differentially expressed genes (DEGs) in the *OsPRR37* knockout line. Enriched pathways were visualized as a dot plot generated using clusterProfiler (v4.0). Dot size represents the number of genes per pathway, and color intensity corresponds to the adjusted *p*-value.

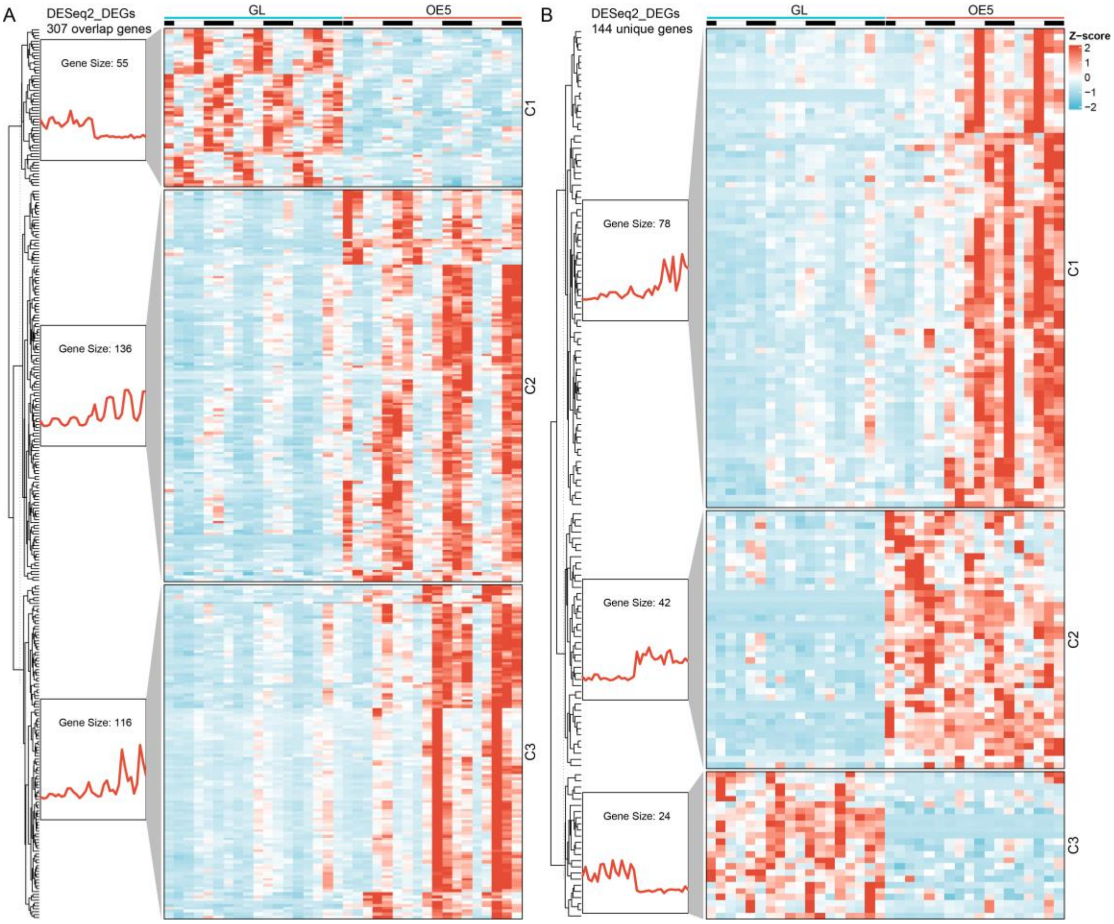

Figure S3. Analysis of DEGs in *OsPRR37* overexpression lines. (A) Clustering heatmap of 307 overlapping genes identified by DESeq2 and DiffCircaPipeline. **(B)** Clustering heatmap of 144 unique genes identified by DESeq2.

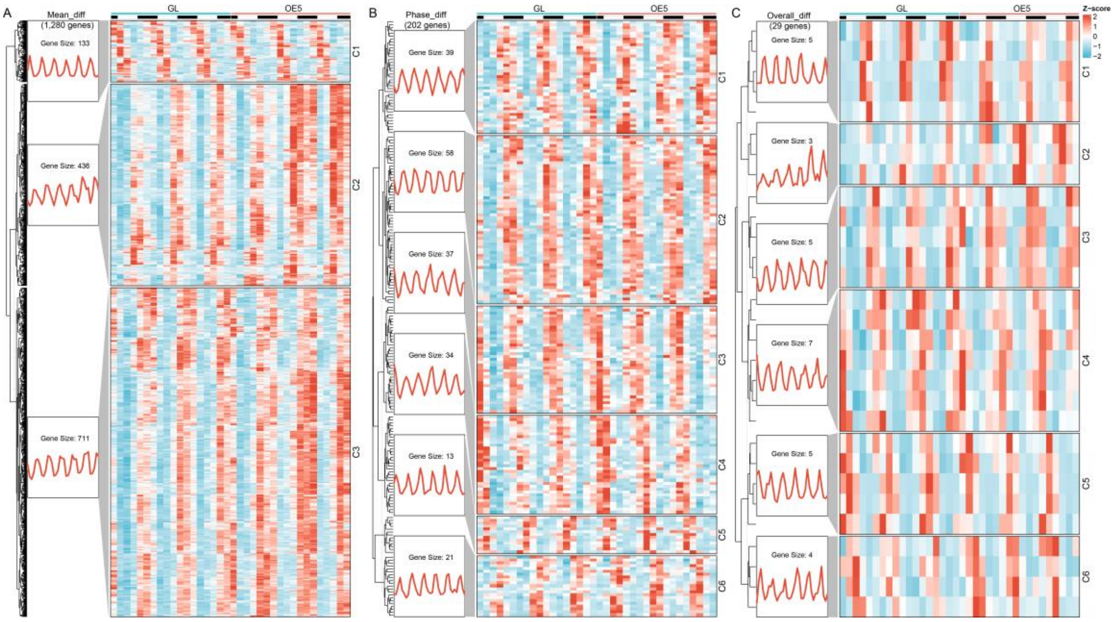

Figure S4. Analysis of rhythmically expressed genes (DRGs) in *OsPRR37* overexpression lines. (A) Clustering heatmap of 1,283 genes unique to the Mean_diff category. **(B)** Clustering heatmap of 202 genes unique to the Phase_diff category. **(C)** Clustering heatmap of 29 genes unique to the Overall_diff category.

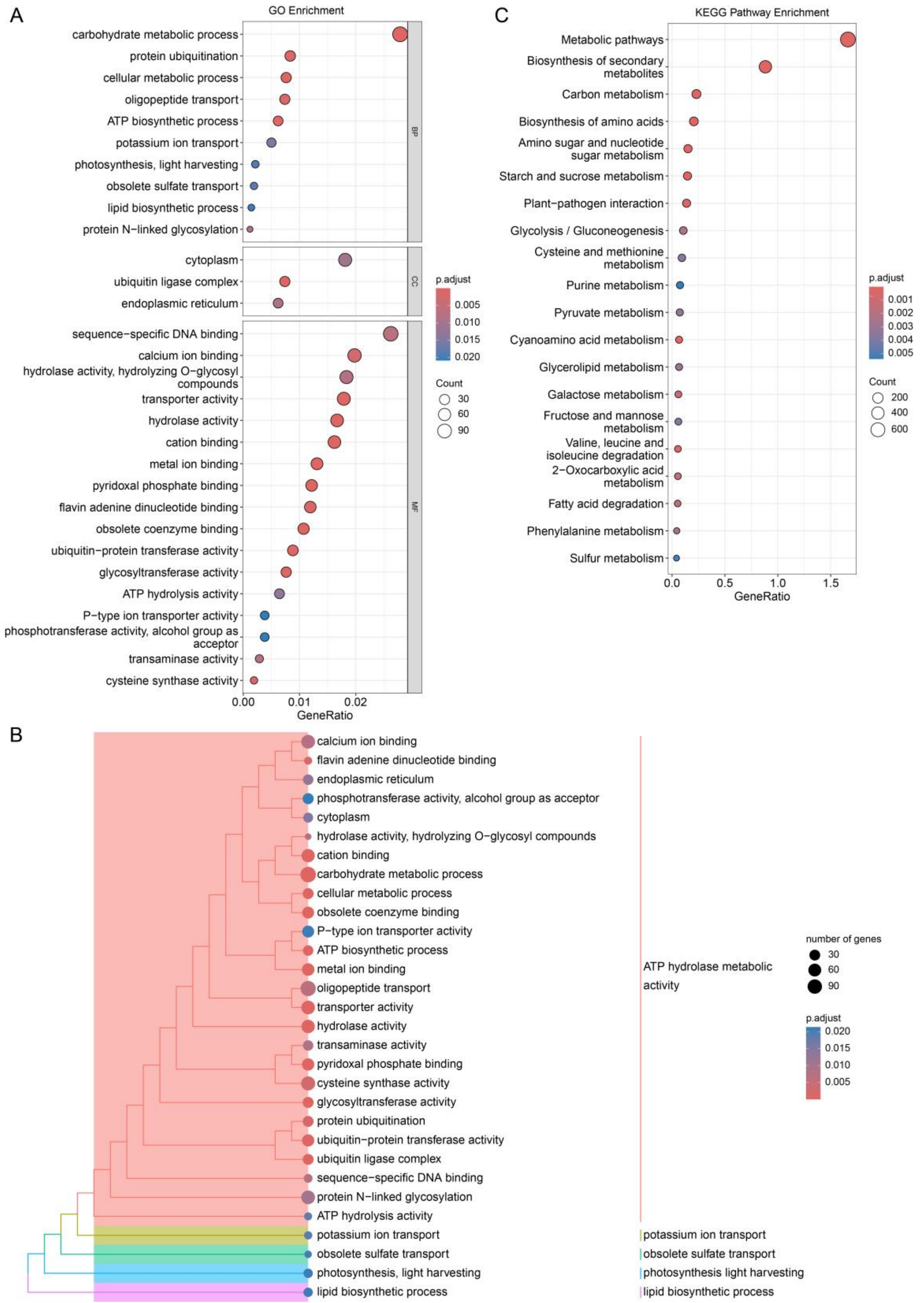

Figure S5. Enrichment analysis of differentially and rhythmically expressed genes (6,882 DRGs) in *OsPRR37* overexpression lines. (A) Dot plot of GO enrichment analysis. **(B)** Hierarchical clustering of enriched GO terms. Redundant GO terms (pairwise similarity > 0.7) were removed, retaining the most significant term (lowest adjusted p-value). The resulting tree plot shows hierarchical clustering (average linkage, five clusters) with terms colored by adjusted p-value. **(C)** Dot plot of KEGG pathway enrichment analysis.

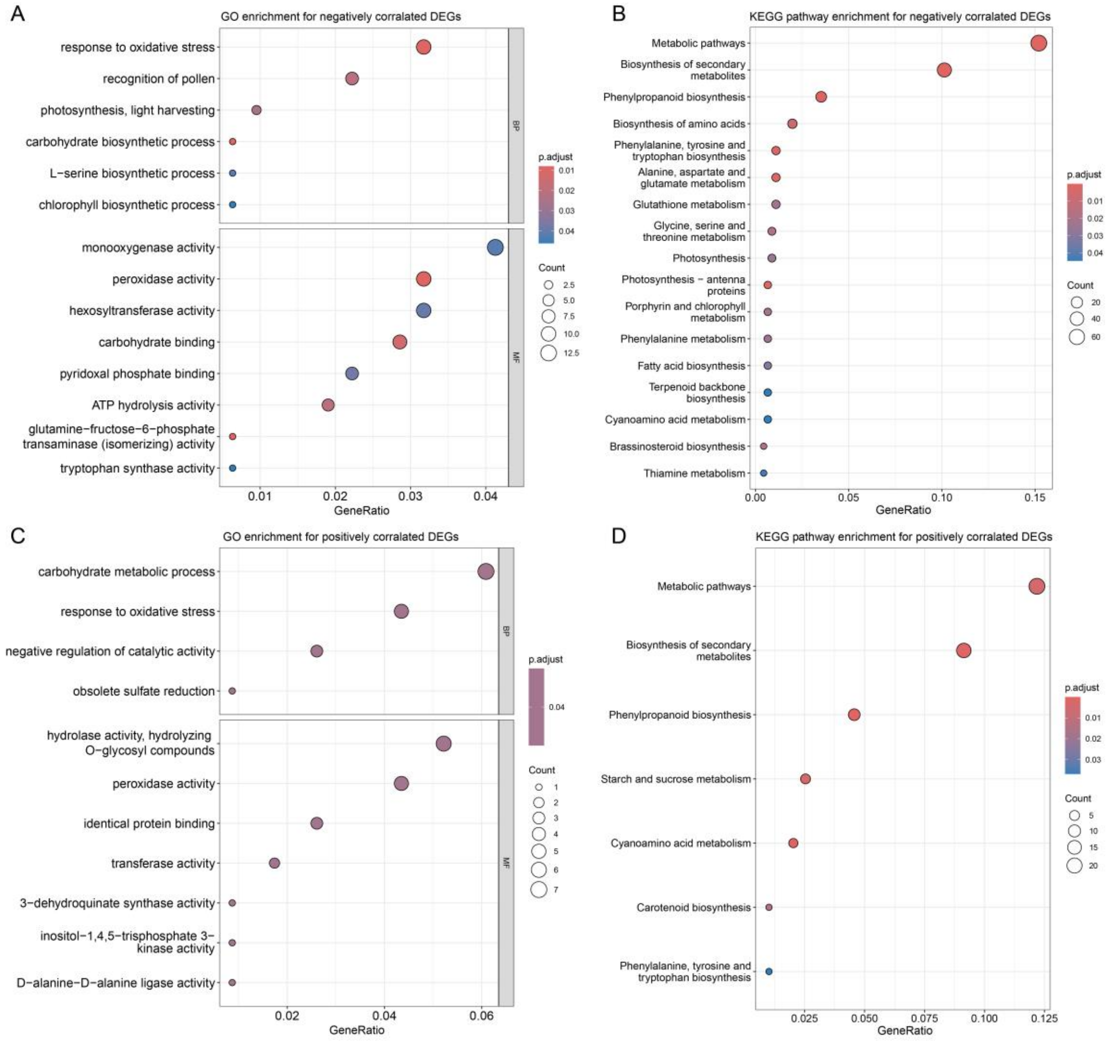

Figure S6. Enrichment analysis of negatively and positively correlated DEGs upon *OsPRR37* knockout and overexpression. (A) GO enrichment analysis of negatively correlated DEGs. **(B)** KEGG pathway enrichment analysis of negatively correlated DEGs. **(C)** GO enrichment analysis of positively correlated DEGs. **(D)** KEGG pathway enrichment analysis of positively correlated DEGs.

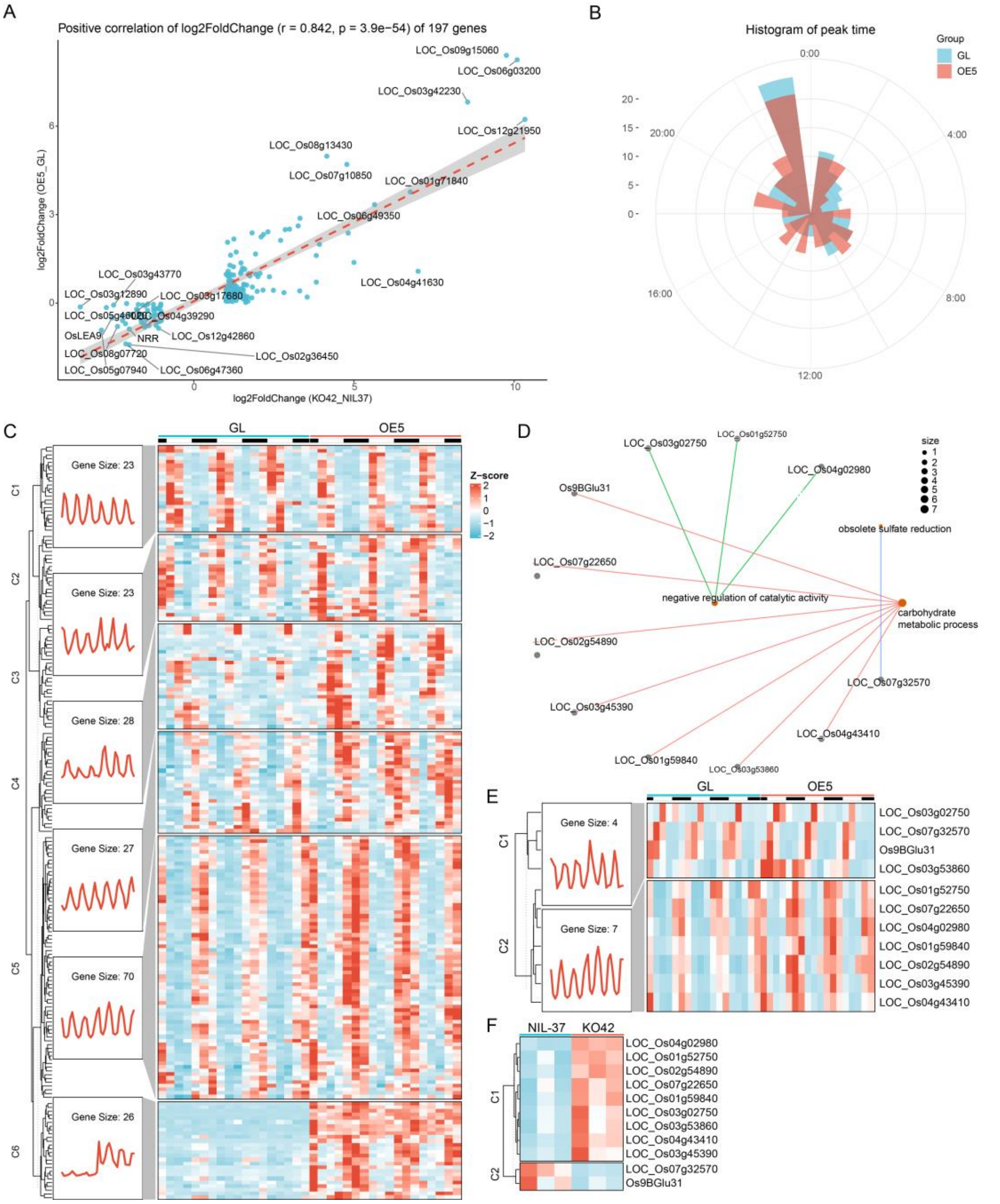

Figure S7. Characterization of positively correlated DEGs following *OsPRR37* knockout and overexpression. **(A)** Positively correlation analysis of the coherently regulated genes. **(B)** Phase distribution of the positively correlated genes. **(C)** Clustering heatmap of the positively correlated genes. **(D)** Network analysis between BP terms and their corresponding genes of the positively correlated genes. Redundant GO terms were removed based on semantic similarity using the pairwise_termsim() function with a threshold of 0.7 and then visualized using cnetplot() to display the network of representative GO categories and their associated genes. Clustering heatmap of the genes in the network analysis in OE5 vs GL **(E)** and KO42 vs NIL37 **(F).**