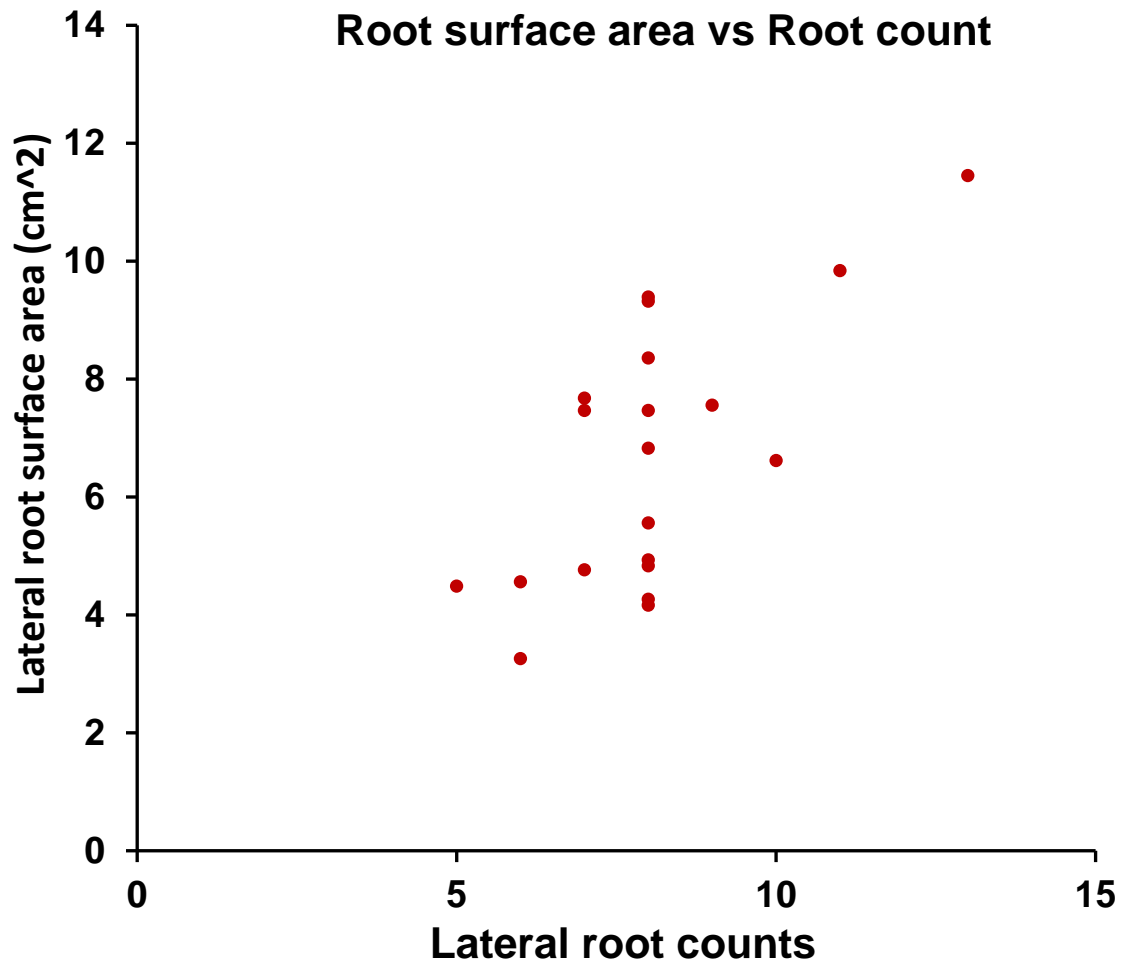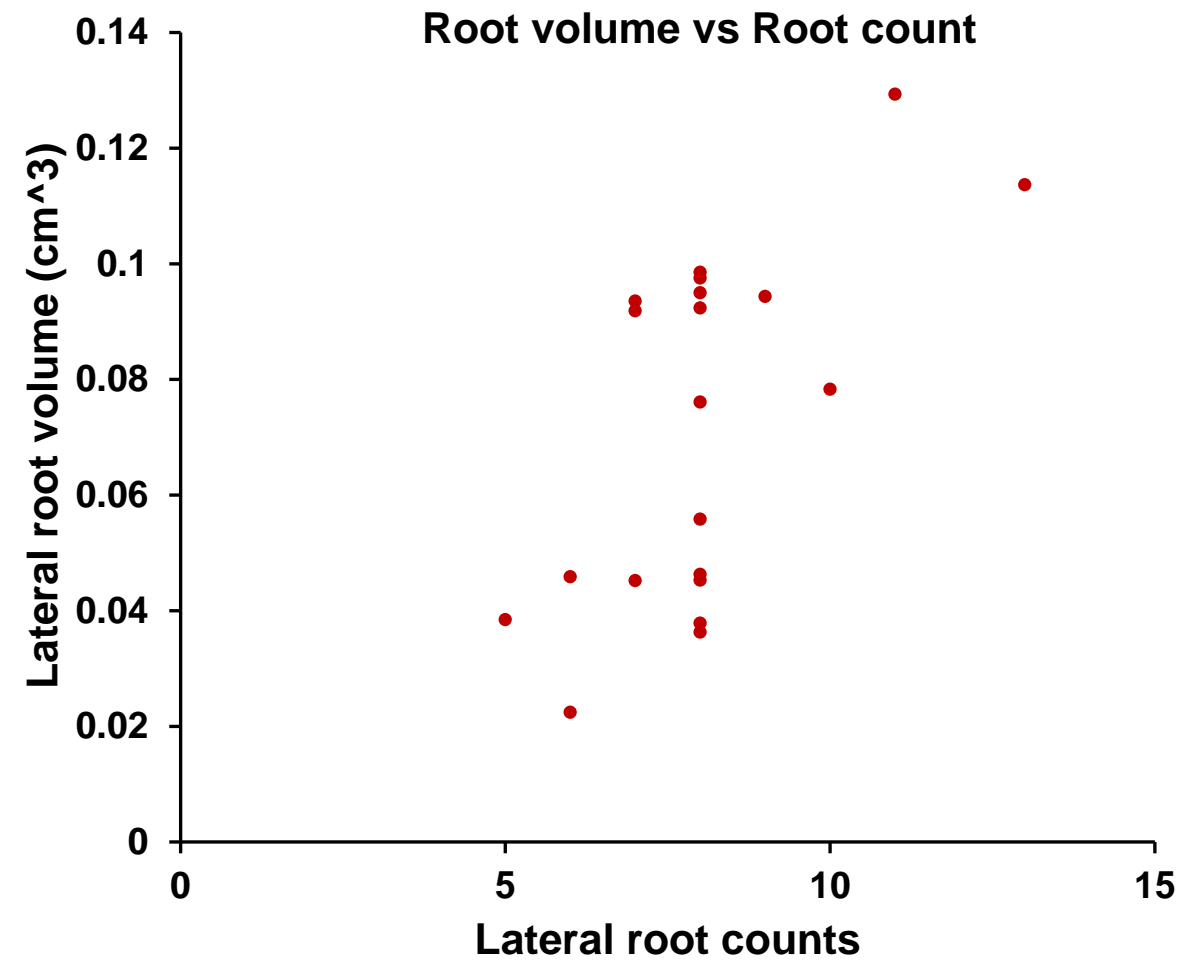**Figure S1**. Effect of chlorate uptake on plant height in eight rice genotypes (Cocodrie, Bengal, Cheniere, Cypress, PSRR-1, Dular, Nona Bokra, and Pokkali after 5-day treatment with 0.1% KClO $_3$. Scale bar is 3 mm.

Figure S2. Pearson correlations and p-value of lateral root surface area and volume versus lateral root count.
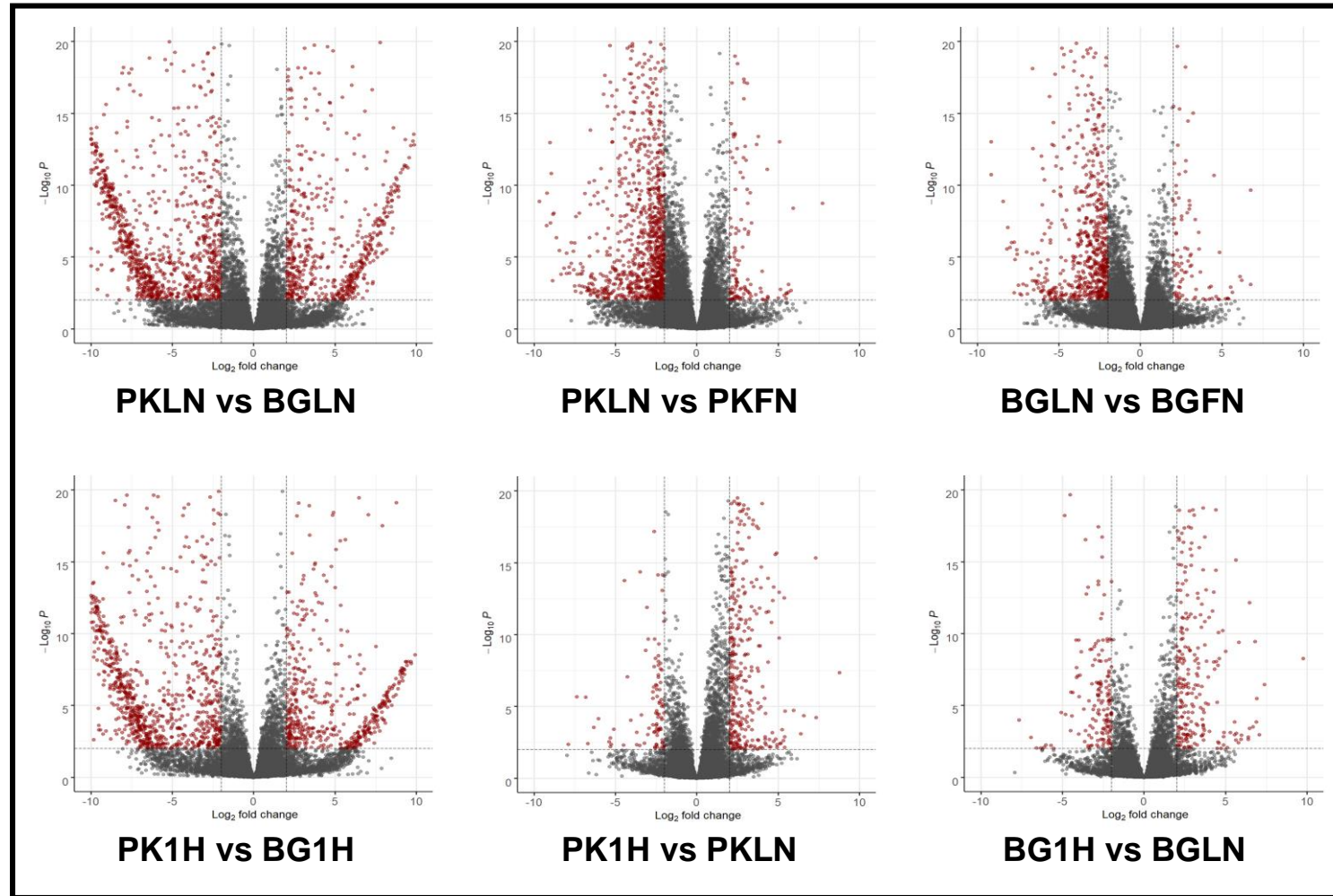
Figure S3. Volcano plot of multiple pairwise comparison between Pokkali and Bengal at low nitrogen and 1h after full nitrogen. Differentially expressed genes are shown as red dots. Gray dots represent genes that did not pass the cut-off point of $|\log_2$ fold change$| \geq 2$ and *padj* < 0.01. Plot was visualized using Bioconductor (release 3.10) package *EnhancedVolcano*.
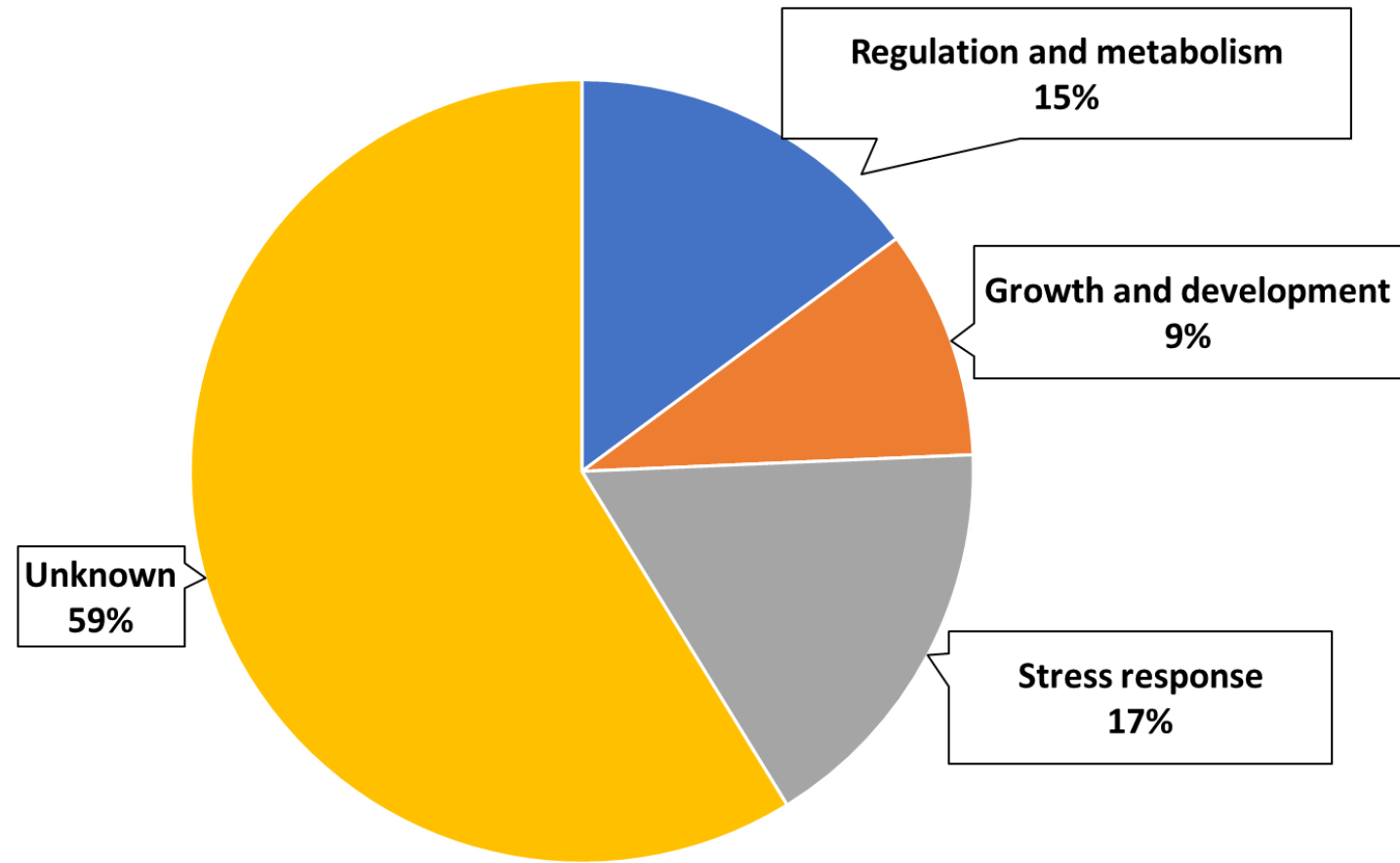
Figure S4. Gene ontology-based functional classification of root Pokkali-specific differentially expressed genes.
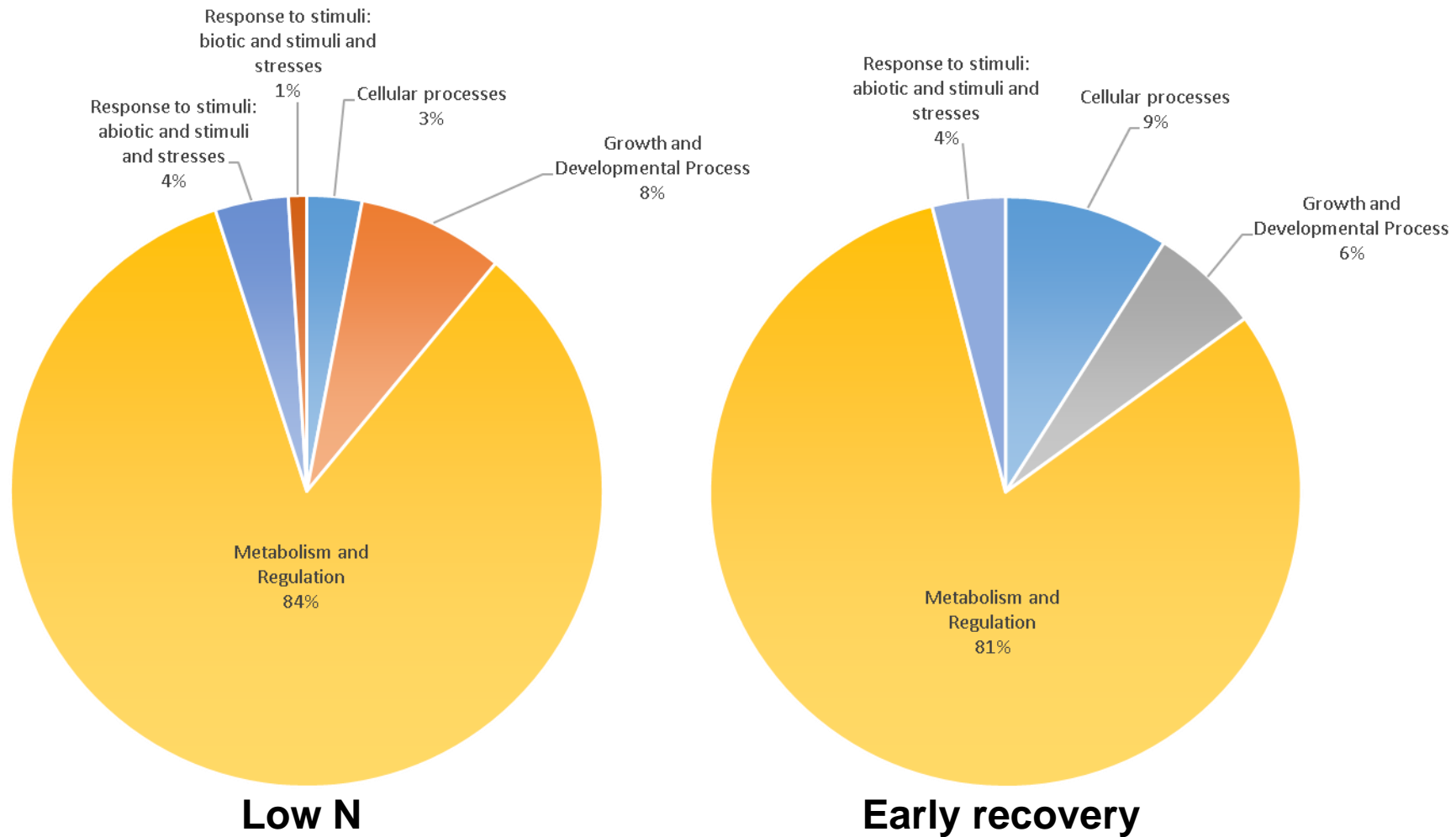
Figure S5. Distribution of DEGs based on the plant reactome pathway analysis. Differentially expressed genes obtained from combined data of low N (PKLN vs PKFN, PKLN vs BGLN, and BGLN vs BGFN) and 1-h recovery/early N response (PK1H vs PKLN, PK1H vs BG1H, and BG1H vs BGLN) were considered for this analysis.
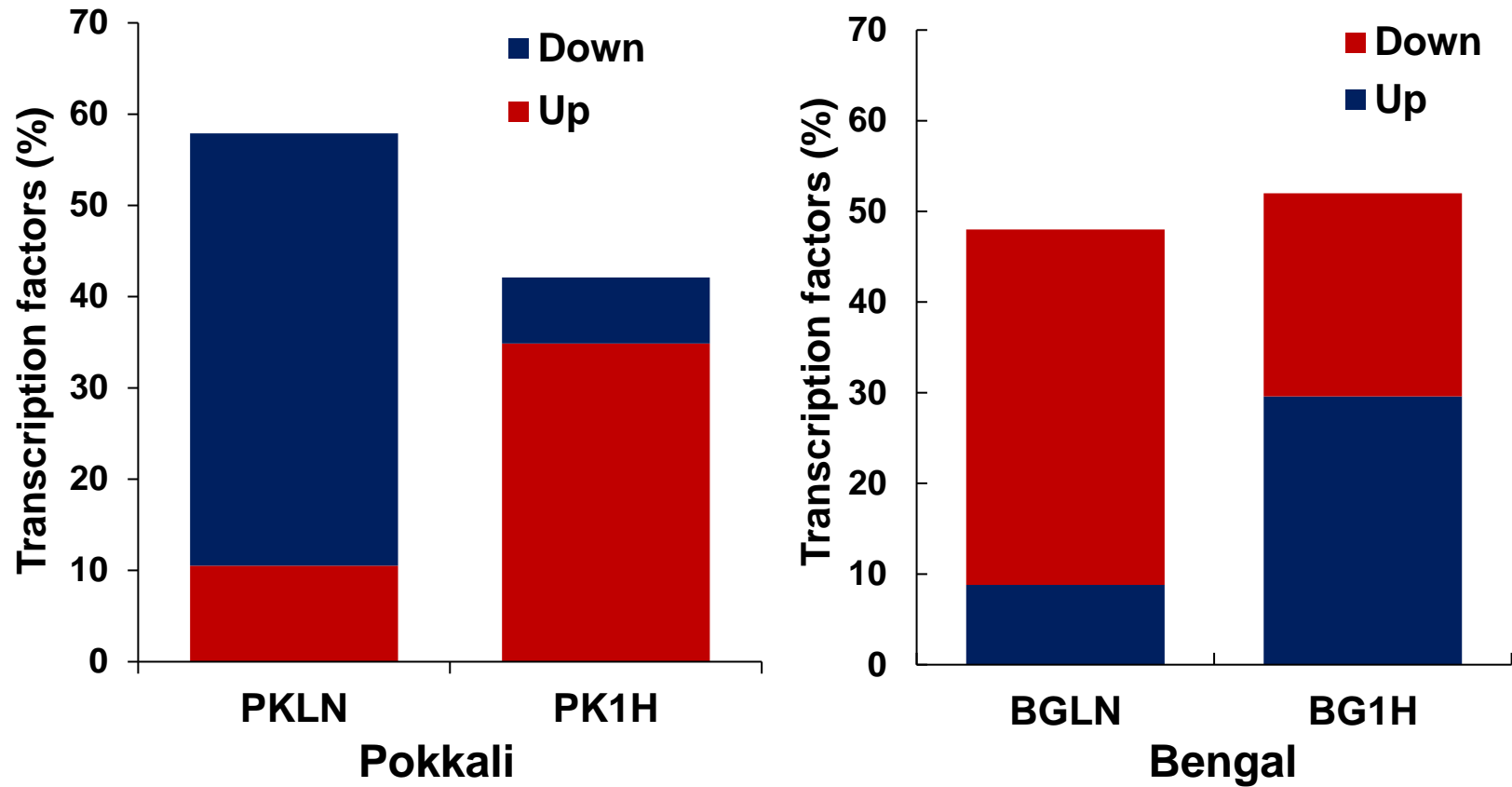
Figure S6. Regulation pattern of transcription factors in Pokkali (n=152) and Bengal (n=125) in different N conditions. Differentially expressed TF genes obtained from combined data of low N (PKLN vs PKFN, PKLN vs BGLN, and BGLN vs BGFN) and 1-h recovery/early N response (PK1H vs PKLN, PK1H vs BG1H, and BG1H vs BGLN. Red and blue bars indicate up-regulated and down-regulated transcription factors, respectively.
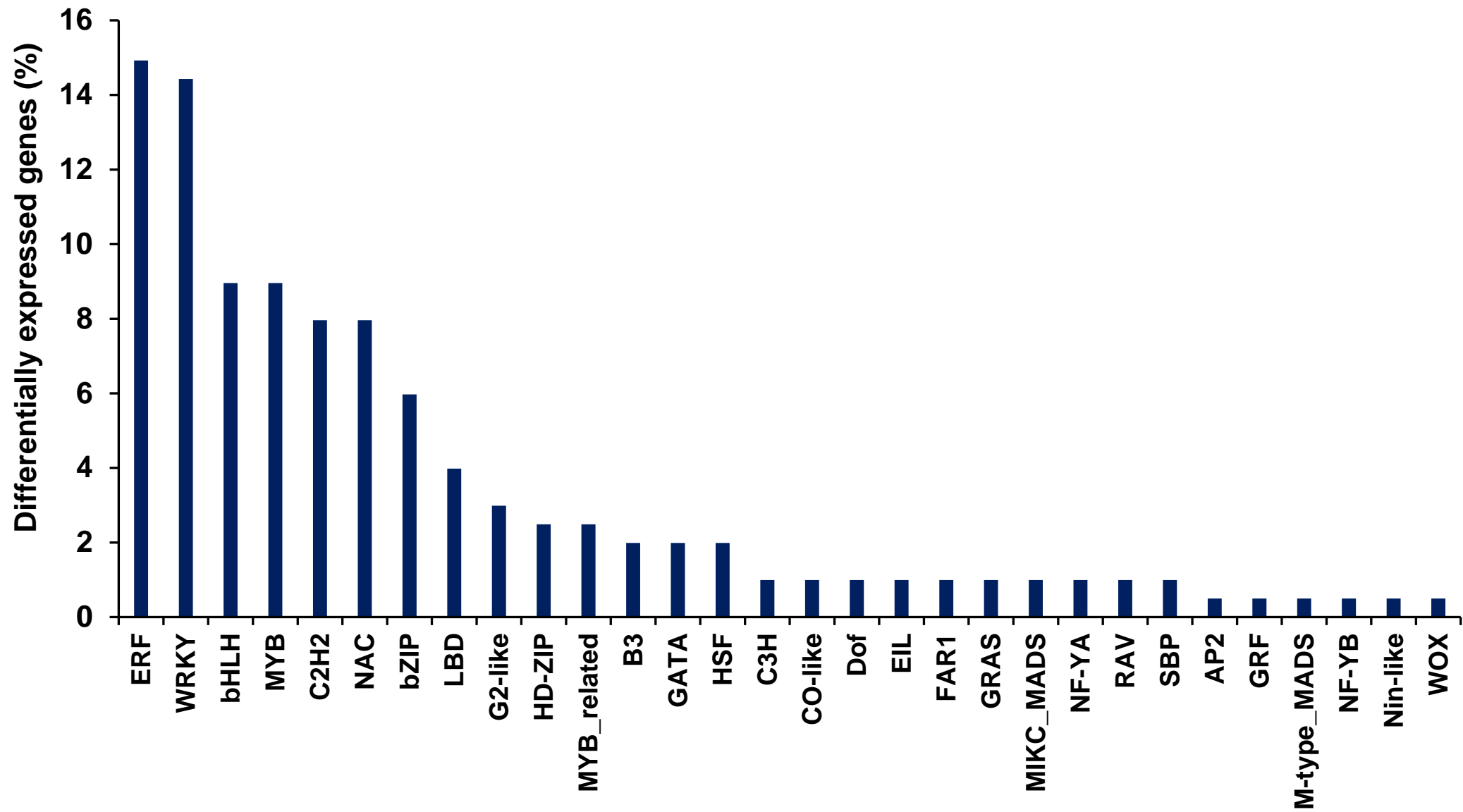
Figure S7. Number of differentially expressed genes (DEGs) (in percent) identified per transcription factor family (combined DEGs from all N conditions).
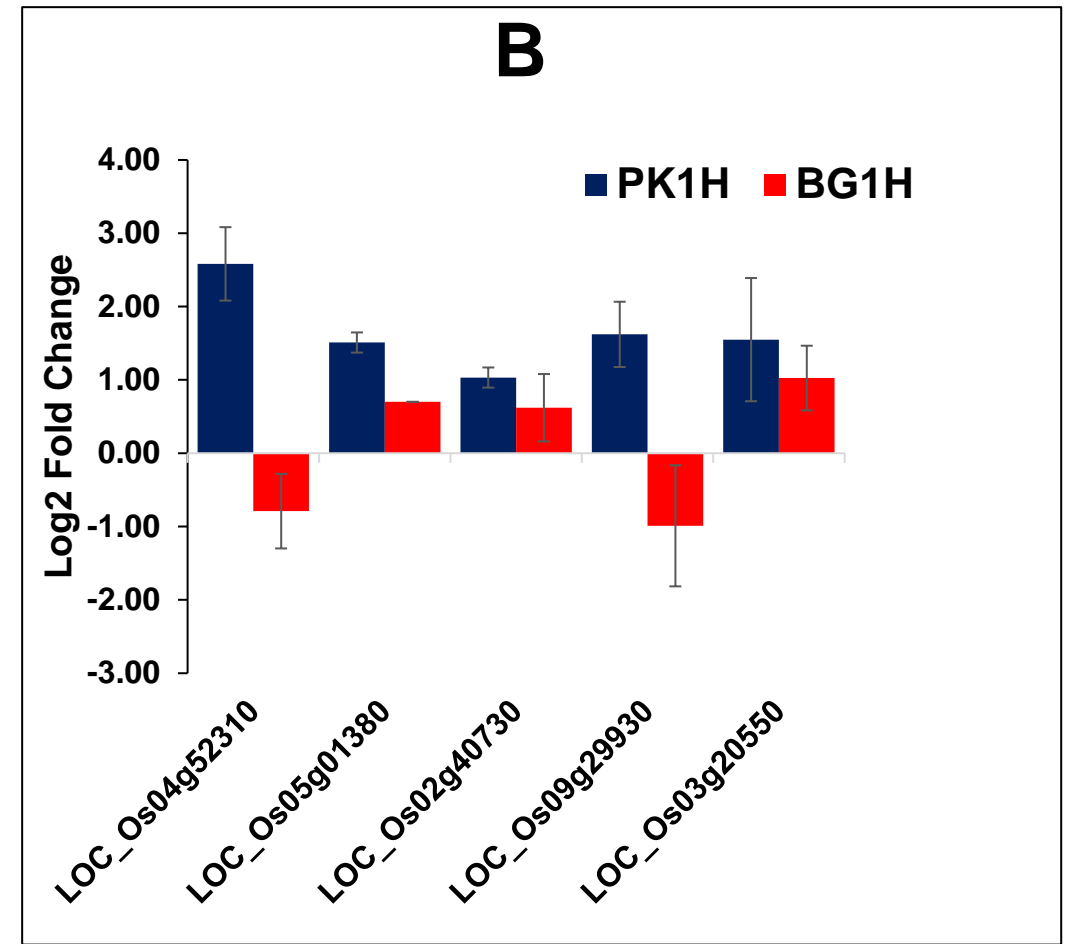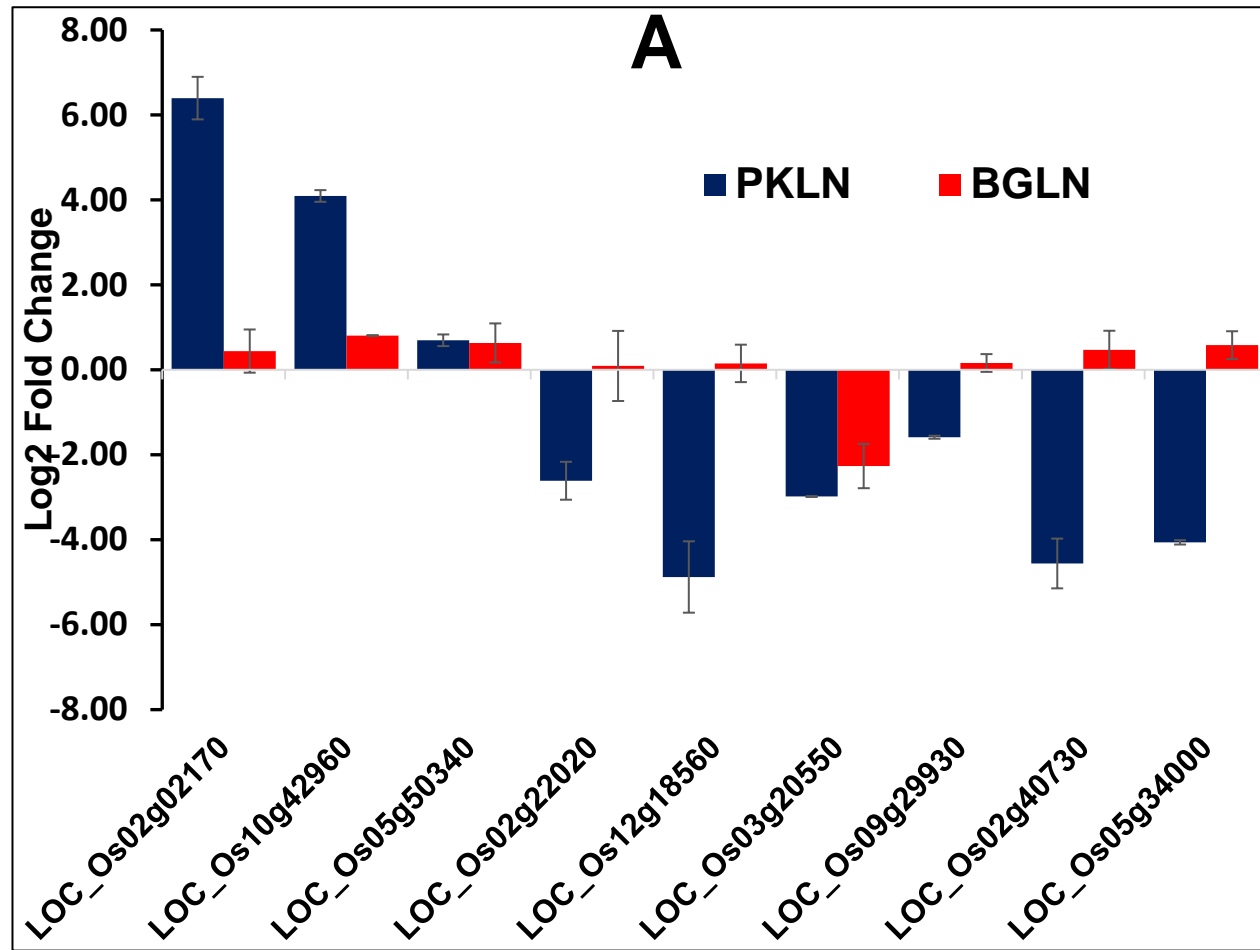
Figure S8. Validation of RNA-seq data *via* qRT-PCR. Bar plot showing relative transcript abundance of selected genes in Bengal and Pokkali under different N treatments are shown. *EF1α* was used as the reference gene. (A) Pokkali/Bengal in full nitrogen was used as reference sample for low nitrogen stress (PKLN or BGLN). (B) and Pokkali/Bengal in low nitrogen (PKLN and BGLN) as reference sample for 1-h recovery treatments (PK1H and BG1H).
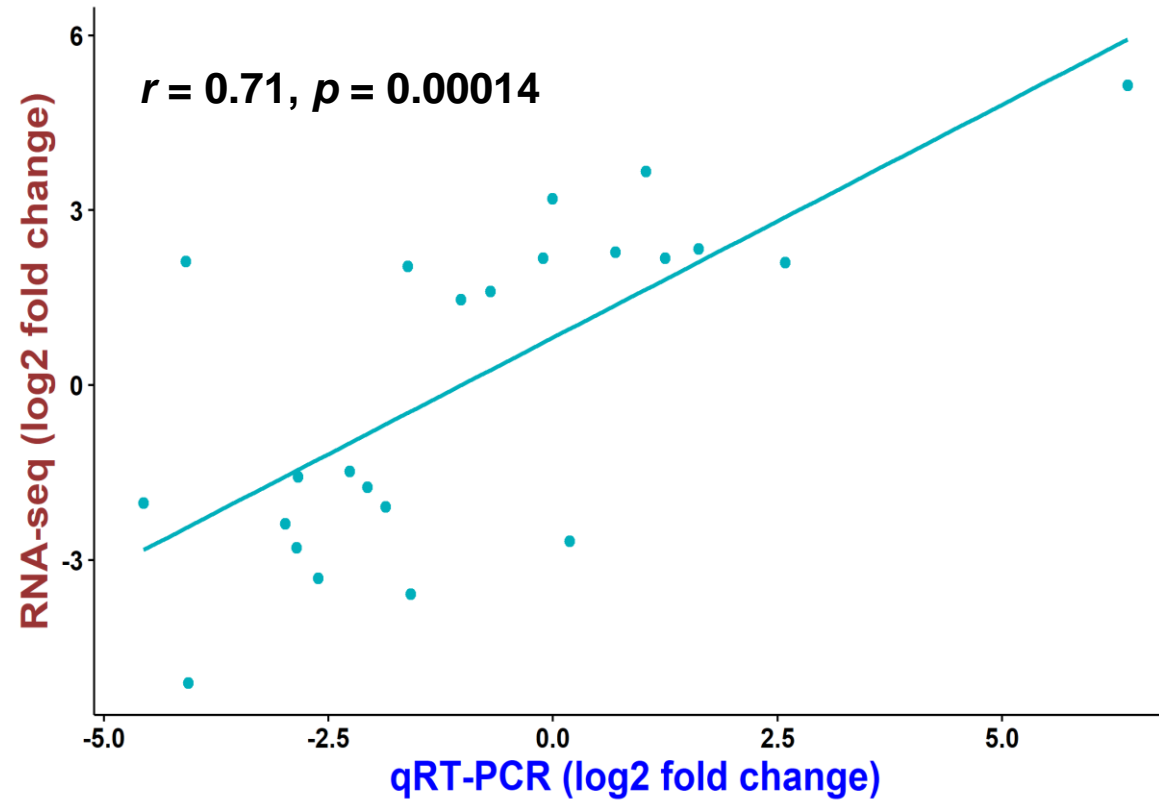
Figure S9. Pearson correlation analysis between RNA-seq and qRT-PCR results is shown (C). Each dot (blue green) represents $\log_2$ fold change for the selected genes in each corresponding sample (11 genes and 6 samples).