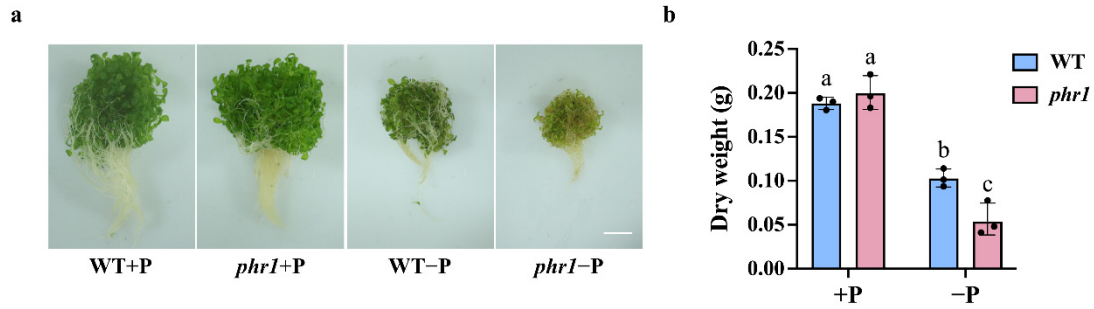
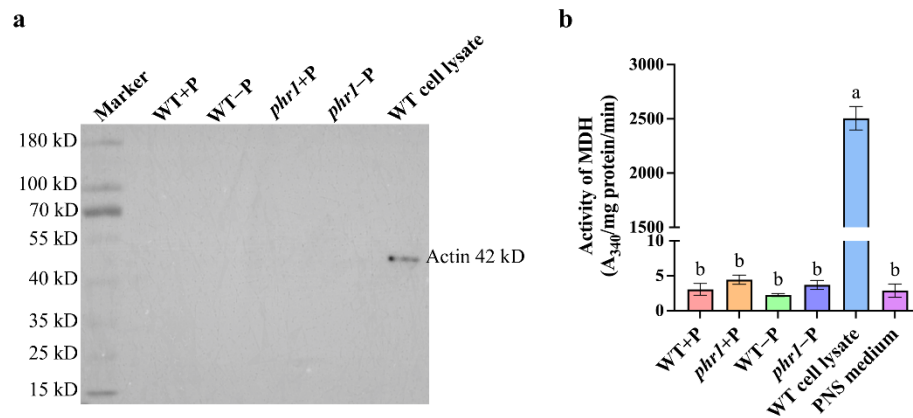
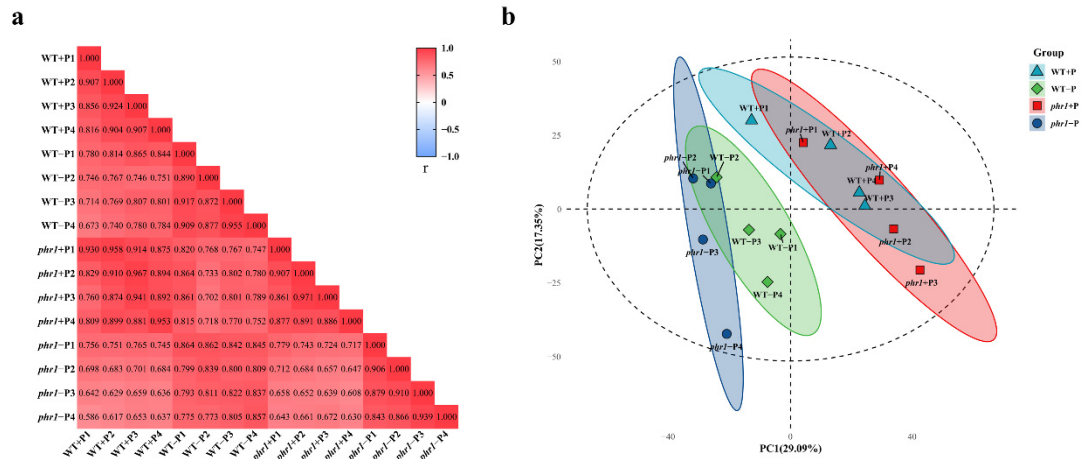




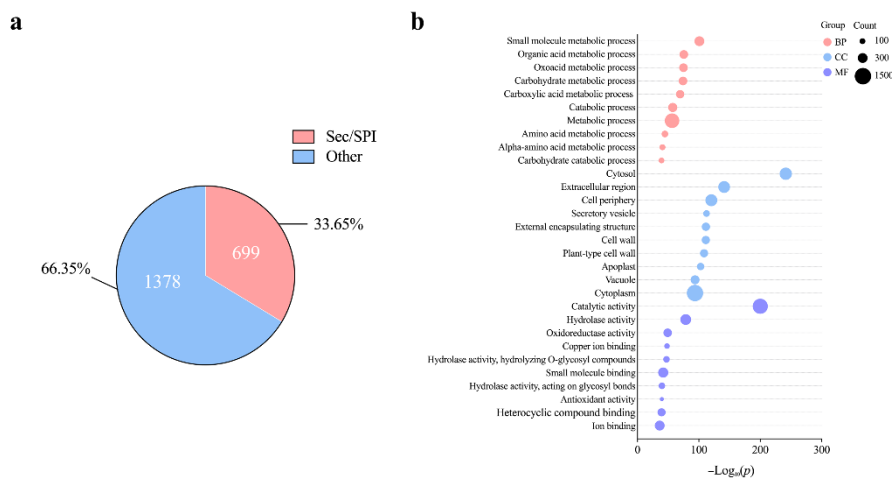
Supplementary Figure S1. Growth phenotypes of Arabidopsis seedlings in Pi sufficient and starvation media. **(a)** Phenotypes of WT and *phr1* seedlings after different Pi treatments. 6.0 mg of seeds were germinated and cultured in +Pi media for 4 days, followed by transferring into +Pi and -Pi medium for another 9 days. **(b)** Dry weight of seedlings in (a). Data are presented as means $\pm$ standard deviation (SD) of three independent biological replicates. Statistical significance was analyzed by two-way ANOVA analysis with Turkey test and represented by different letters ($p < 0.05$).



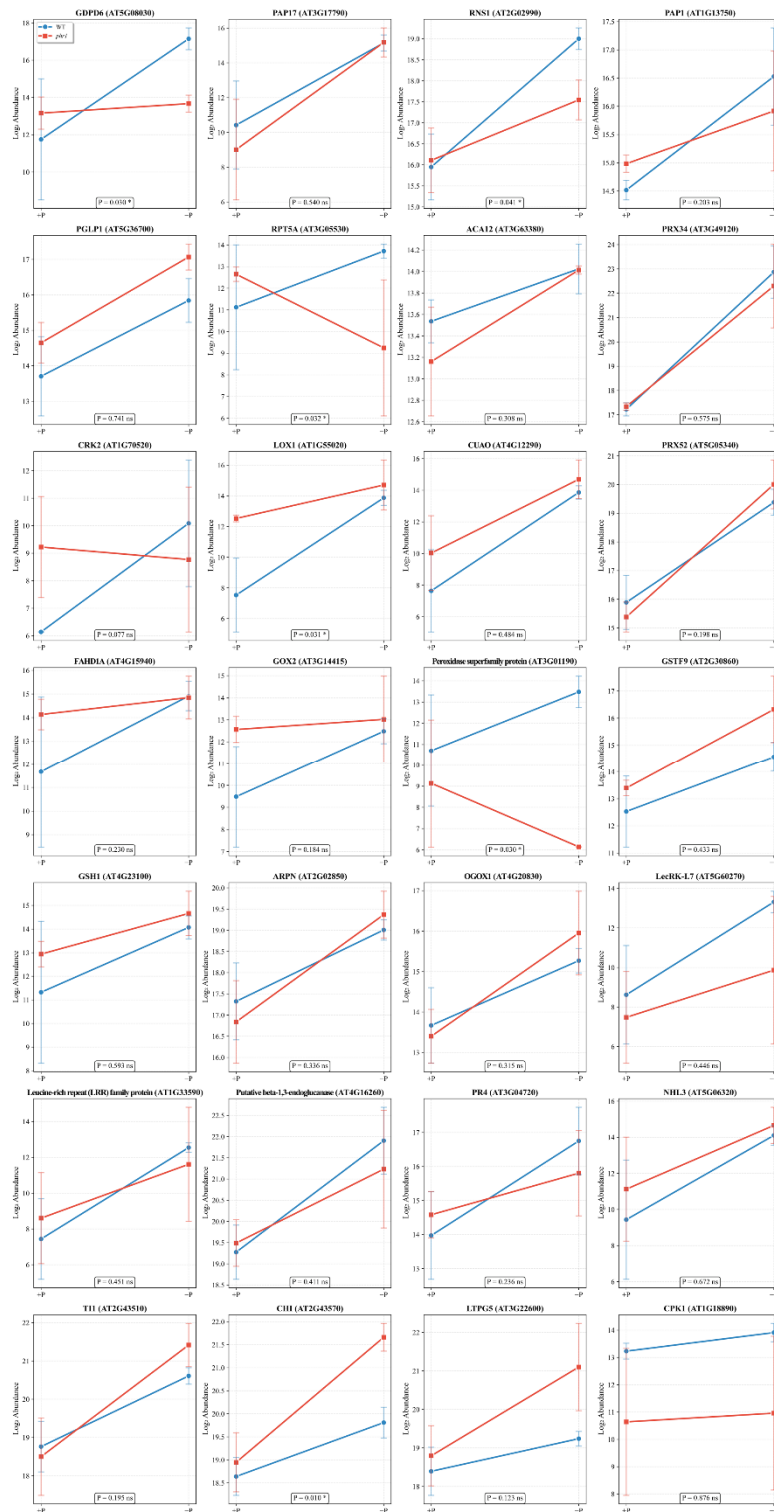
Supplementary Figure S2. Assessment of intracellular protein contamination in secretome fractions from hydroponic cultures. **(a)** Immunoblot analysis was applied using anti-Actin antibody to secretome samples (8 μg each) and total cell lysate (2 μg) of WT Arabidopsis seedlings as a positive control. **(b)** Enzymatic activity assay of intracellular malate dehydrogenase (MDH) in the same protein fractions. The PNS culture medium was used as a negative control. Data are presented as mean $\pm$ SD ($n = 3$ technical replicates). Different lowercase letters indicate statistically significant differences among groups ($p < 0.05$, one-way ANOVA followed by Tukey's post-hoc test). This experiment was repeated twice with consistent results.



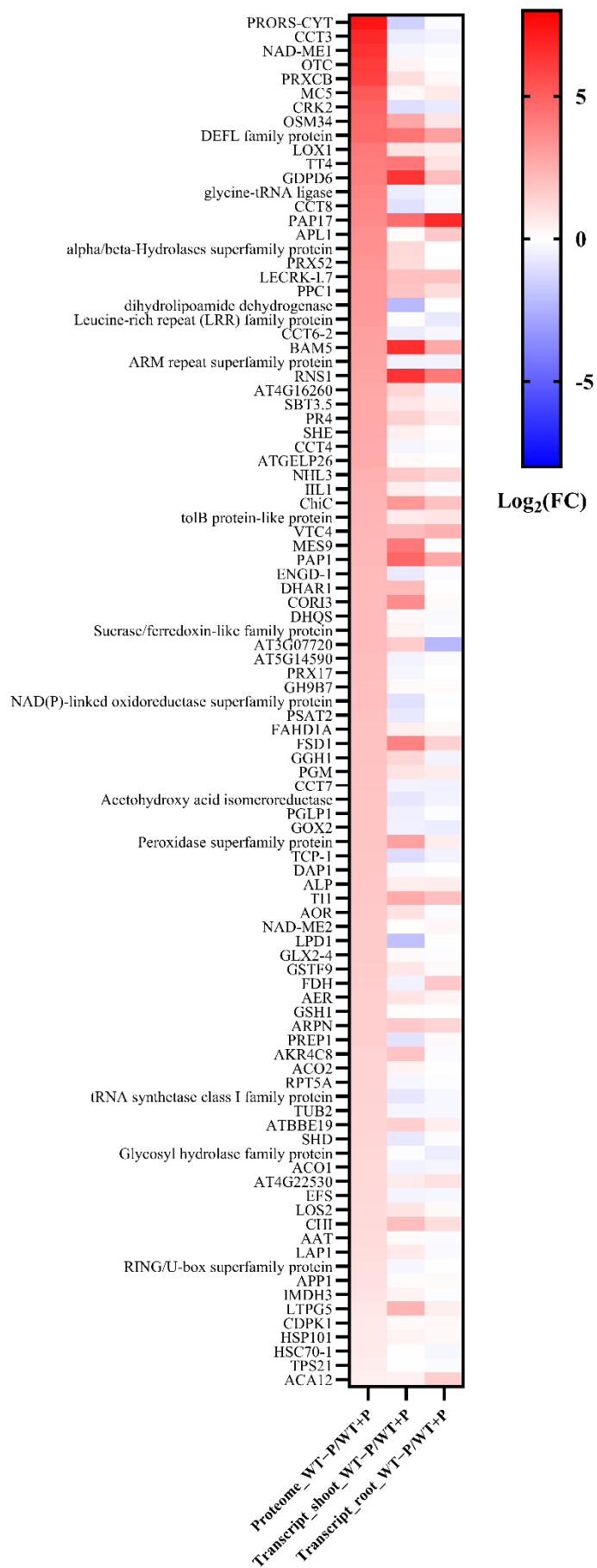
Supplementary Figure S3. Validation of sample repeatability. **(a)** Correlation heatmap of experimental samples. **(b)** Principal component analysis (PCA) analysis of experimental samples.



Supplementary Figure S4. Functional analysis of all the secreted proteins in the secretome. **(a)** Signal peptide prediction for the secretome proteins by SignalP-6.0. **(b)** GO functional enrichment of the secretome proteins. The top 10 most significantly enriched terms in each category (Biological Process, BP; Cellular Component, CC; and Molecular Function, MF) are presented. The p -value indicates the degree of enrichment, and values less than 0.05 represent significant functional enrichment.



Supplementary Figure S5. Interaction analysis of genotype and phosphate treatment on proteins of tables 1-3. The genotype (WT and *phr1*) $\times$ phosphate (+P and -P) interaction was determined by two-way ANOVA analyses. Error bars indicate standard deviations (SD) from four biological replicates per treatment condition. The lines connecting the two phosphate treatments for the same genotype are used to visualize the direction and magnitude of phosphate responsiveness. The *p*-value for the interaction term is shown within each subpanel, with $p < 0.05$ considered statistically significant.



Supplementary Figure S6. Integrated analyses of up-regulated secretome and transcriptomics in WT-P/WT+P.