

Figure S1. Heatmaps showing the DEGs in wild-type rice roots at different time points of P starvation and +P resupply.

(a) the log₂FC of the top 10 phosphate starvation response (PSR) genes. **(b)** the log₂FC of the genes involved in SL biosynthetic and signaling pathway. PS1, PS3, PS7 and PS8 represent DEGs of comparisons -P1 vs +P1, -P3 vs +P3, -P7 vs +P7 and -P8 vs +P8, respectively. RP represents DEGs of 1 day of +P resupply after 7 days of -P (RP vs -P8). *p*-value < 0.05; log₂FC ≥ 1.2.

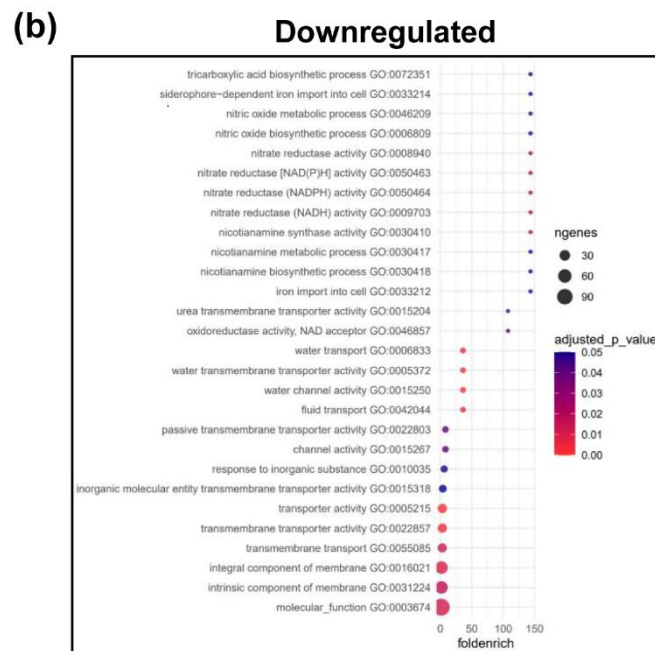
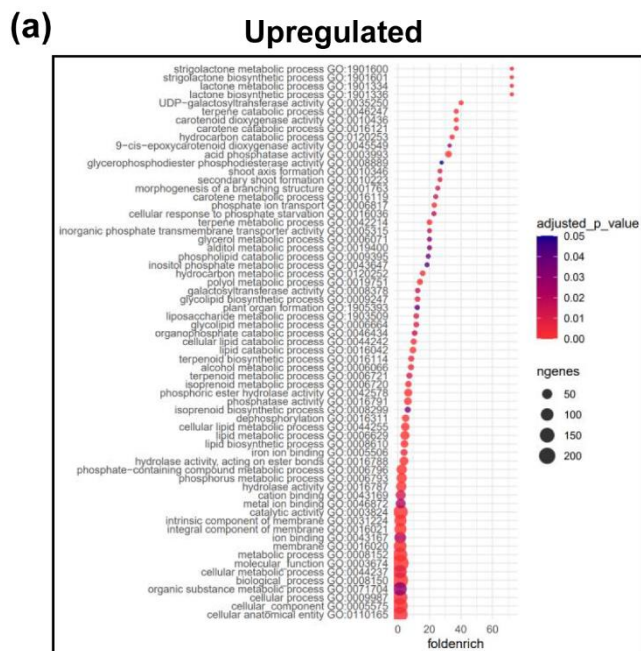


Figure S2. GO enrichment analysis of common DEGs after 7 days and 8 days of P starvation compared to control P sufficient treatment in wild-type rice roots.

(a) Dot plot of upregulated genes. **(b)** Dot plot of downregulated genes. The size of the dots represents the number of enriched genes associated with GO term and the color of the dots represents adjusted p -values.

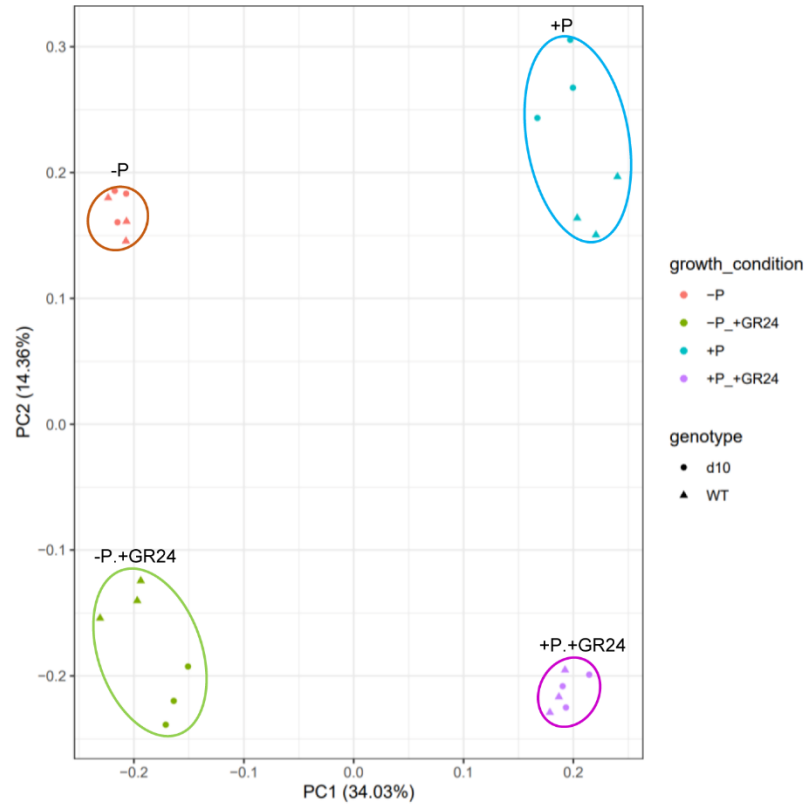


Figure S3. PCA of rice roots transcript profiles using DEseq2 transformed counts in wild-type and *d10* mutant in response to GR24 under both +P and -P at day 8.

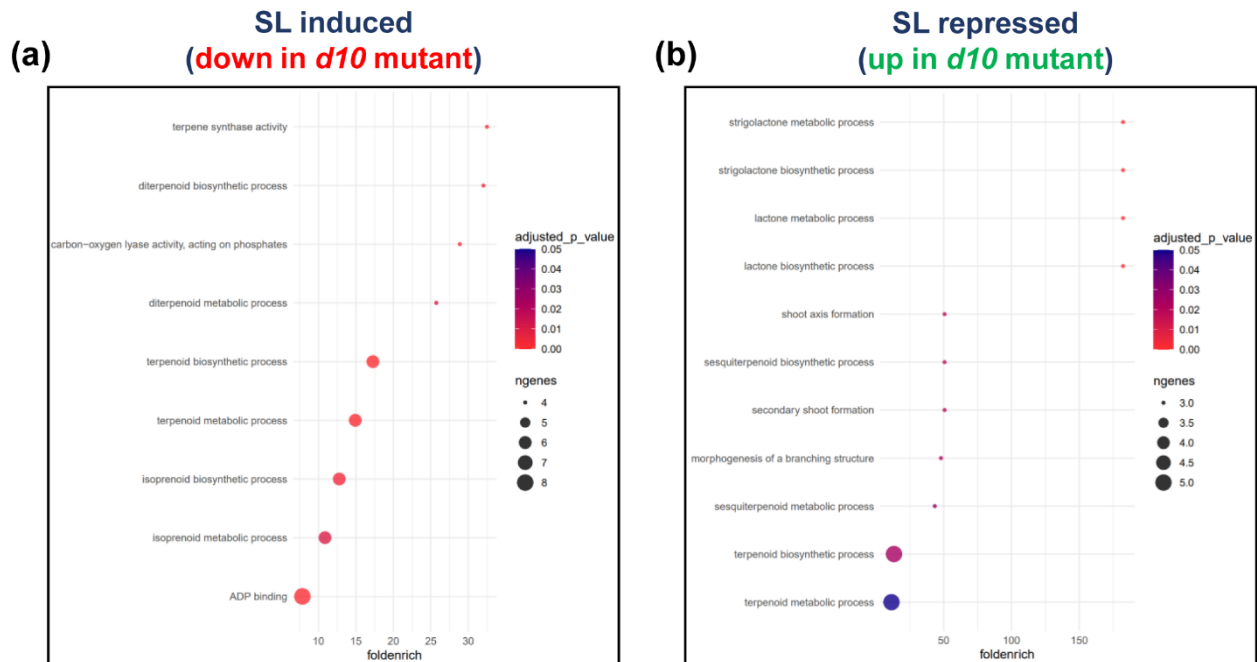


Figure S4. GO enrichment analysis of SL DEGs independent of P starvation at day 8.

(a) SL induced genes which are downregulated in *d10* mutant compared with wild-type. **(b)** SL repressed genes which are upregulated in *d10* mutant compared with wild-type. The size of the dots represents the number of enriched genes associated with GO term and the color of the dots represents adjusted *p*-values.

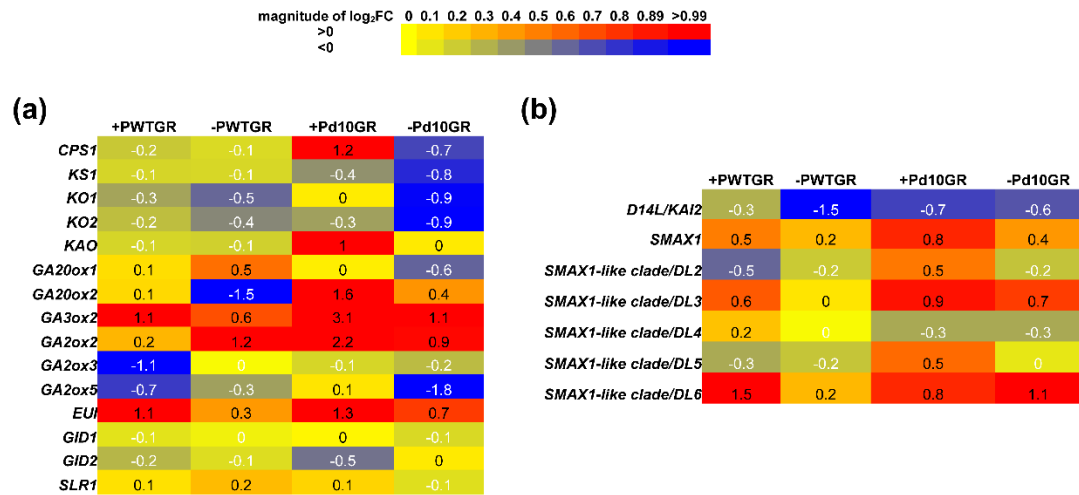
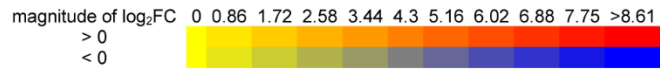


Figure S5. Heatmaps analysis of DEGs involved in (a) gibberellin pathway and (b) karrikin signaling in wild-type and *d10* mutant roots in response to GR24 treatment under both +P and -P at day 8.

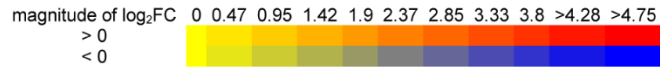
+PWTGR, -PWTGR, +Pd10GR and -Pd10GR represent the comparisons of +PWTGR24 vs +PWT, -PWTGR24 vs -PWT, +Pd10GR vs +Pd10 and -Pd10GR vs -Pd10, respectively. For details: gibberellin pathway genes (Data S9); karrikin signaling genes (Data S10).

(a)



Transcript_ID	Annotation	WT.PS8	WT.RP	d10.PS8
Os06t0570566-00	Similar to Ent-kaurene oxidase	7.8	-8.1	8.6
Os10t0116800-01	Similar to Purple acid phosphatase	6.7	-5.8	5.7
Os11t0151700-01	Purple acid phosphatase	5.1	-3.2	5.9
Os07t0106000-01	Metallophosphoesterase domain containing protein	4.7	-4.7	4
Os03t0287100-01	Similar to Phosphatidylinositol transfer protein, expressed	3.5	-2.8	3.3
Os01t0376700-01	Similar to Sucrose-phosphatase	3.2	-3.1	3.1
Os09t0397800-01	Hypothetical gene	3.2	-3.8	3.2
Os02t0514326-00	Hypothetical protein	3.1	-3.6	3.5
Os08t0156600-01	Vacuolar phosphate efflux transporter, Pi homeostasis	2.7	-3	3
Os04t0110600-01	Salt tolerance level 1	1.9	-1.9	1.7

(b)



Transcript_ID	Annotation	WT.PS8	WT.RP	d10.PS8
Os08t0120600-01	Similar to Fructose-bisphosphate aldolase	-3.2	3.1	-4.7
Os06t0146800-01	Conserved hypothetical protein	-3.2	3.5	-4
Os04t0507950-01	Hypothetical conserved gene	-3.2	2	-2.7
Os02t0620600-01	Ammonium transporter, Ammonium uptake	-3.1	3.6	-2.6
Os05t0114400-01	Zinc finger, C2H2-type domain containing protein	-2.7	2.6	-2.7
Os03t0835150-01	Conserved hypothetical protein	-2.2	2.4	-2.1
Os02t0782900-01	Conserved hypothetical protein	-2.2	1.6	-2
Os01t0681900-01	NADH-dependent Glutamate Synthase 1	-1.9	2.2	-2.3
Os04t0665600-01	OsRLI1	-1.8	2.2	-1.6
Os03t0684700-01	HPP family protein	-1.7	1.7	-1.8

Figure S6. Heatmaps showing a strongest upregulated and downregulated DEGs in the roots of wild-type and *d10* mutant at day 8.

(a) the \log_2FC of the top 10 strongest P starvation-upregulated DEGs and its repression by P resupply in wild-type, and DEGs in *d10* mutant by P starvation at day 8. **(b)** the \log_2FC of the top 10 strongest P starvation-downregulated DEGs and its induction by +P resupply in wild-type, and DEGs in *d10* mutant by P starvation at day 8. Values represent adjusted p -value < 0.05 .

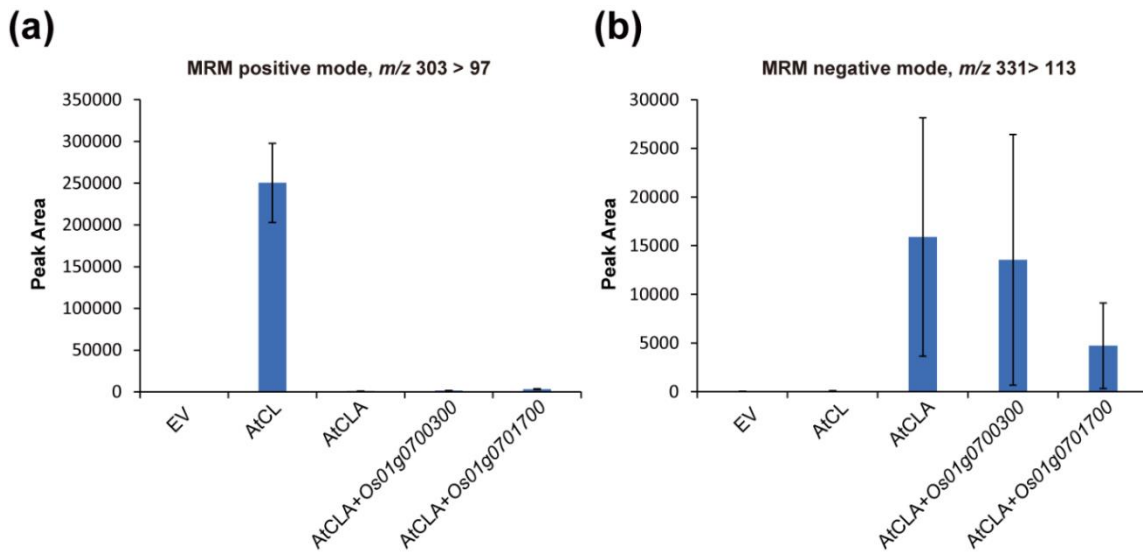


Figure S7. Production of carlactone (CL) and carlactonoic acid (CLA) in transient expression assays using *Nicotiana benthamiana*.

(a) Quantification of CL (transition $[M+H]^+$ m/z 303 > 97) in *N. benthamiana* leaf samples. **(b)** Quantification of CLA (transition $[M-H]^-$ m/z 331 > 113) in *N. benthamiana* leaf samples. Data are shown as mean \pm SE (n=5). EV, empty vector control. AtCL, *Arabidopsis* CL pathway genes (*AtD27*, *AtMAX3*, *AtMAX4*). AtCLA, *Arabidopsis* CLA pathway (AtCL pathway + *AtMAX1*).

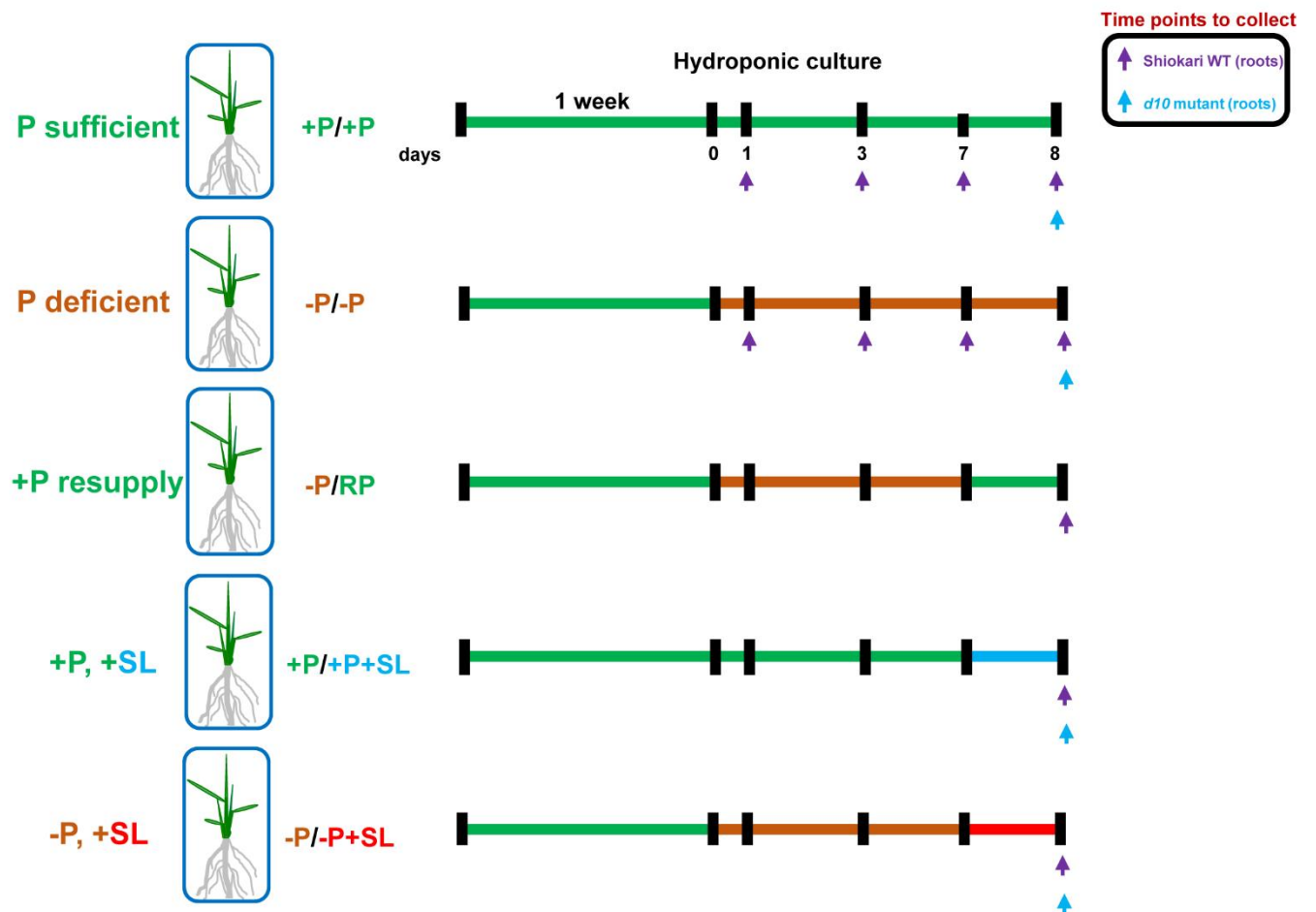


Figure S8. Schematic representation of the experimental design for RNA-seq. Germinated rice seedlings were transferred to P sufficient (+P), half-strength Hoagland hydroponic solution for 1 week. Then, seedlings were continued to grow for another 7-days either on +P or P deficient (-P) solution. In parallel, at day 7, -P seedlings were supplied with +P for up to day 8 (+P resupply). Further, both +P and -P seedlings were treated with 5 μ M of synthetic strigolactone (SL), *rac*-GR24 for up to day 8 (1 day treatment). The purple arrows indicate sample collection time points of wild-type (WT) rice Shiohari roots and blue arrows represent sample collection time points of rice SL mutant *d10*.