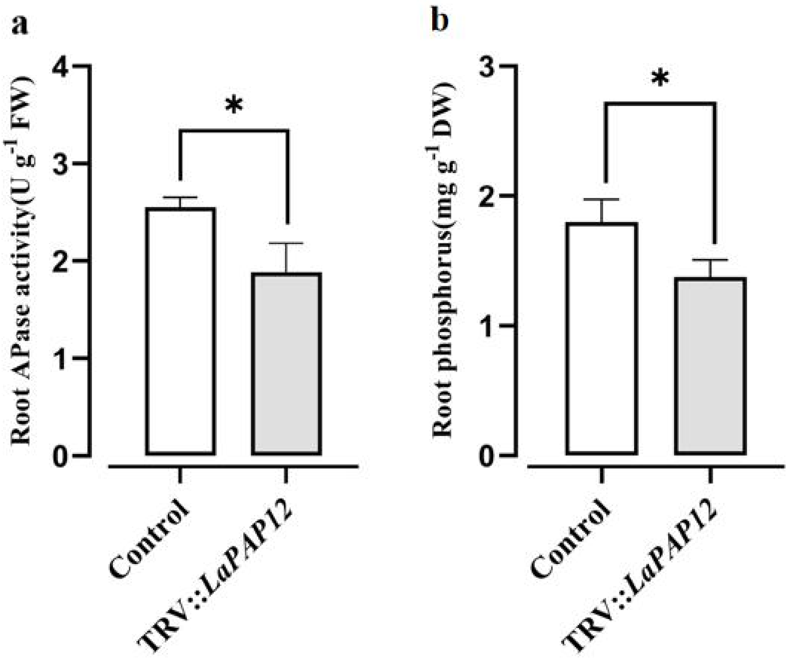

Supplemental Figure S1 Root-secreted APase activity (a) and root phosphorus content (b) in knock-down plant of *LaPAP12* (TRV::*LaPAP12*) and control. Data are means ± standard error (n = 3), the signifificant differences are indicated $*p < 0.05$, unpaired two-tailed Student's t test.

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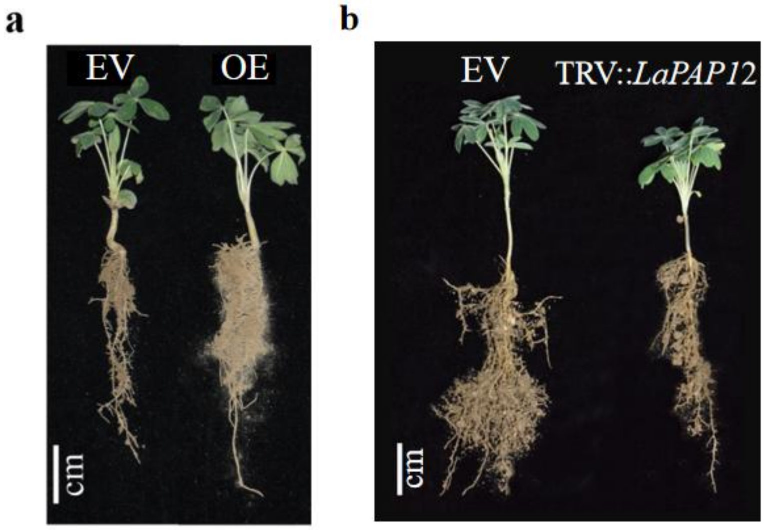
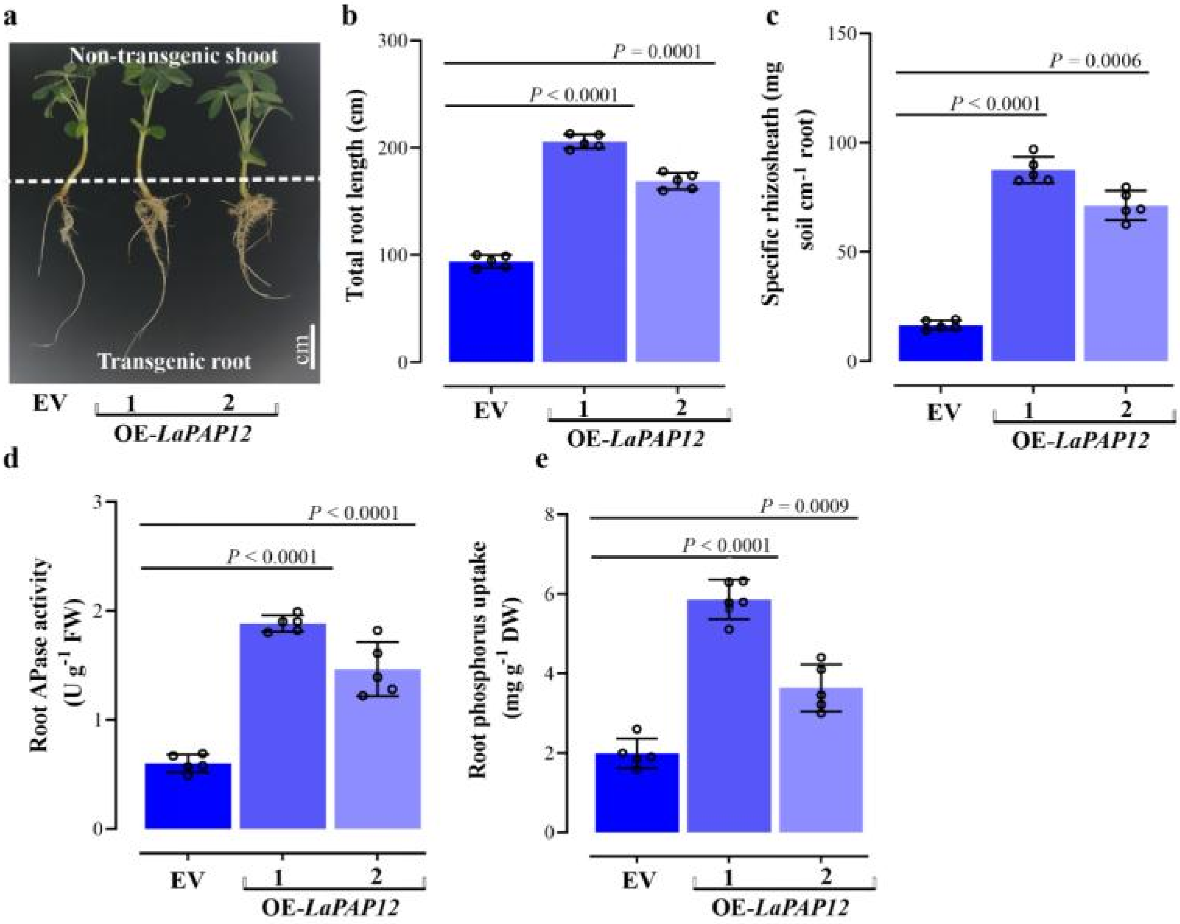
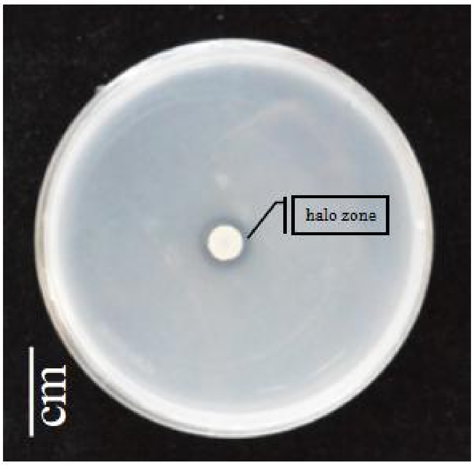


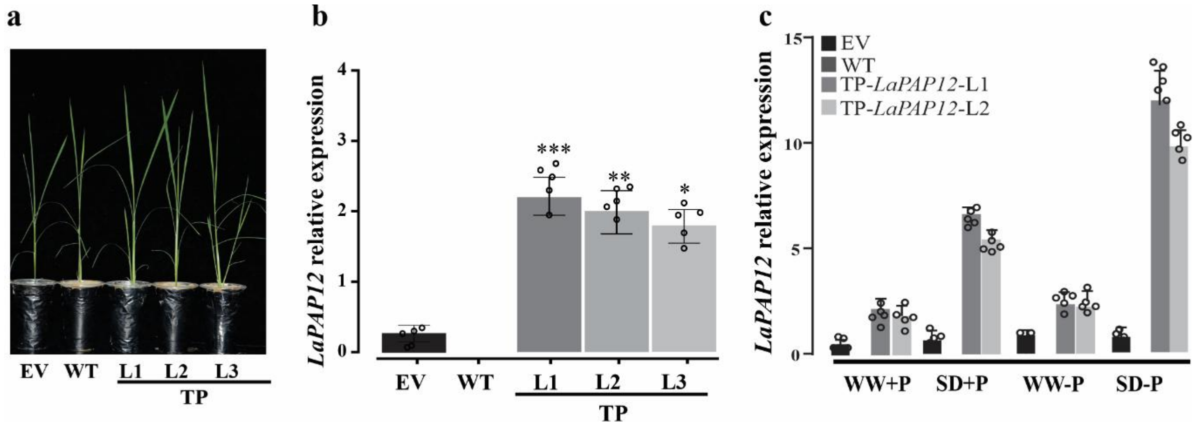
Supplemental Figure S2 Rhizosheath formation in white lupin OE-*LaPAP12* and the empty vector (EV) control (a), knock-down plant of *LaPAP12* (TRV::*LaPAP12*) and the empty vector (EV) (b). Scale: 5 cm.



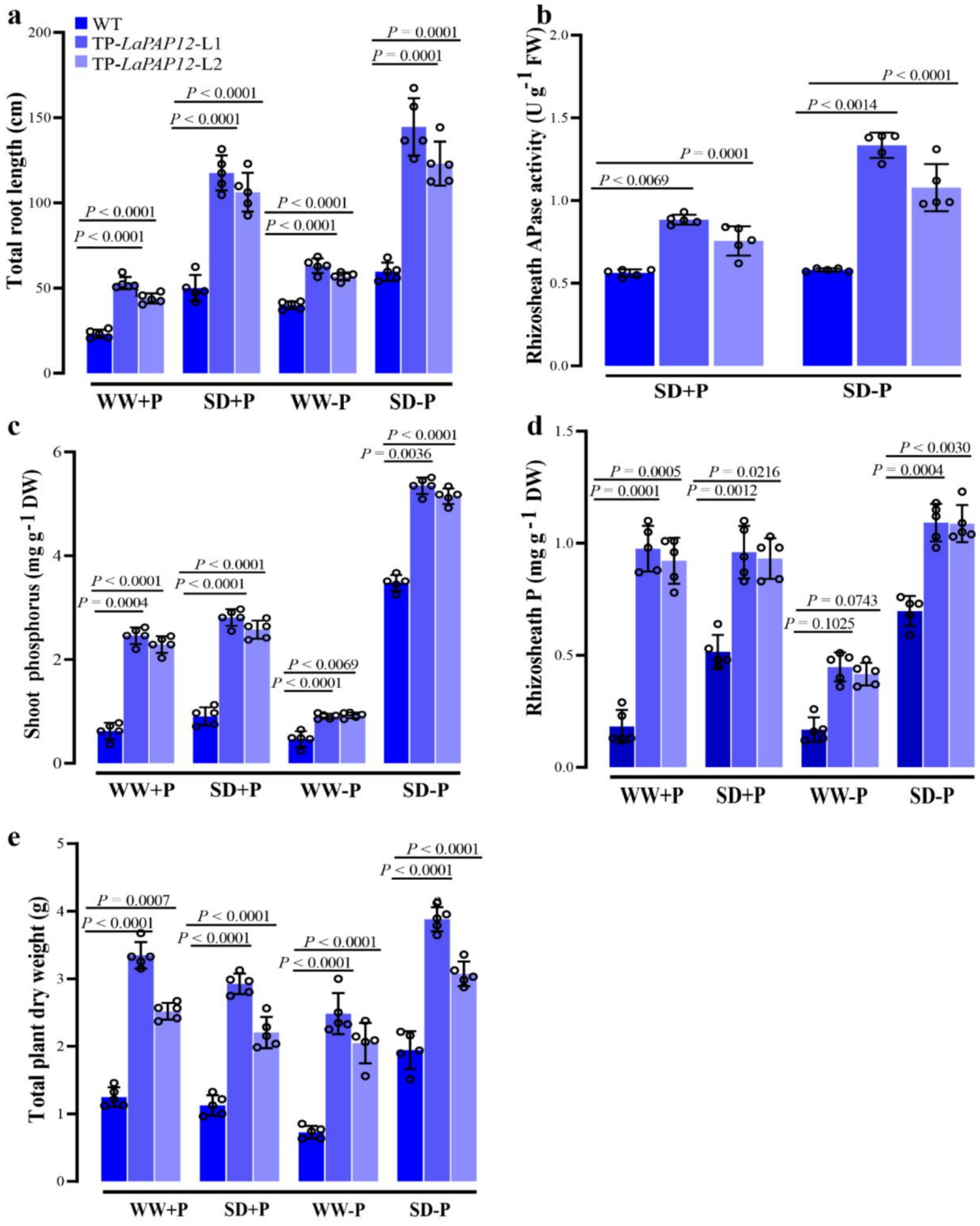
Supplemental Figure S3 White lupin transgenic hairy root initiation and other root-related traits under low P soil drying conditions. (a) Initiation of white lupin hairy root in nutrient solution before being transplanted into the soil; (b) Total root length (cm), (c) Specific rhizosheath weight (mg soil cm^{-1} root) of *LaPAP12*-overexpressing (OE- *LaPAP12*) and control plants (EV), (d) Root APase activity (Ug^{-1} FW), (e) Root phosphorus content (mg g^{-1} DW). Data were collected after the root system along with the attached rhizosheath soil were harvested from the pots. Different letters at the top of bars indicate significant differences among OE-*LaPAP12* and EV hairy roots. OE-*LaPAP12*, roots overexpressing *LaPAP12*; EV, empty vector; FW, fresh weight; DW, dry weight.



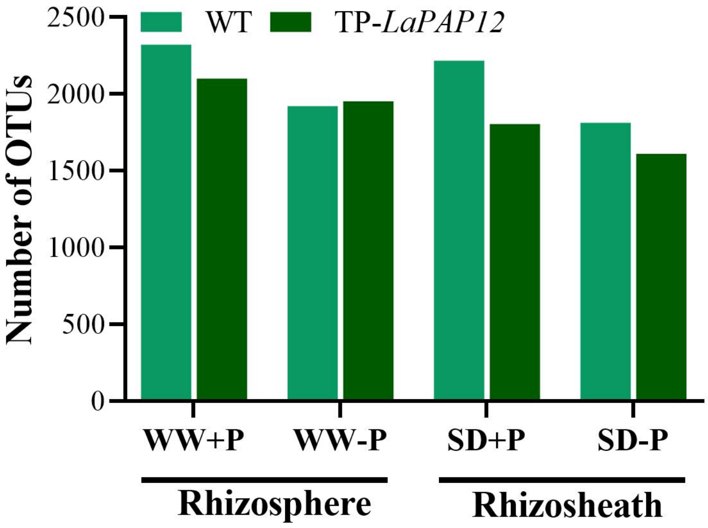
Supplemental Figure S4 $Ca_3(PO_4)_2$ solubilization by *Bacillus megaterium* strain (scale: 1 cm).



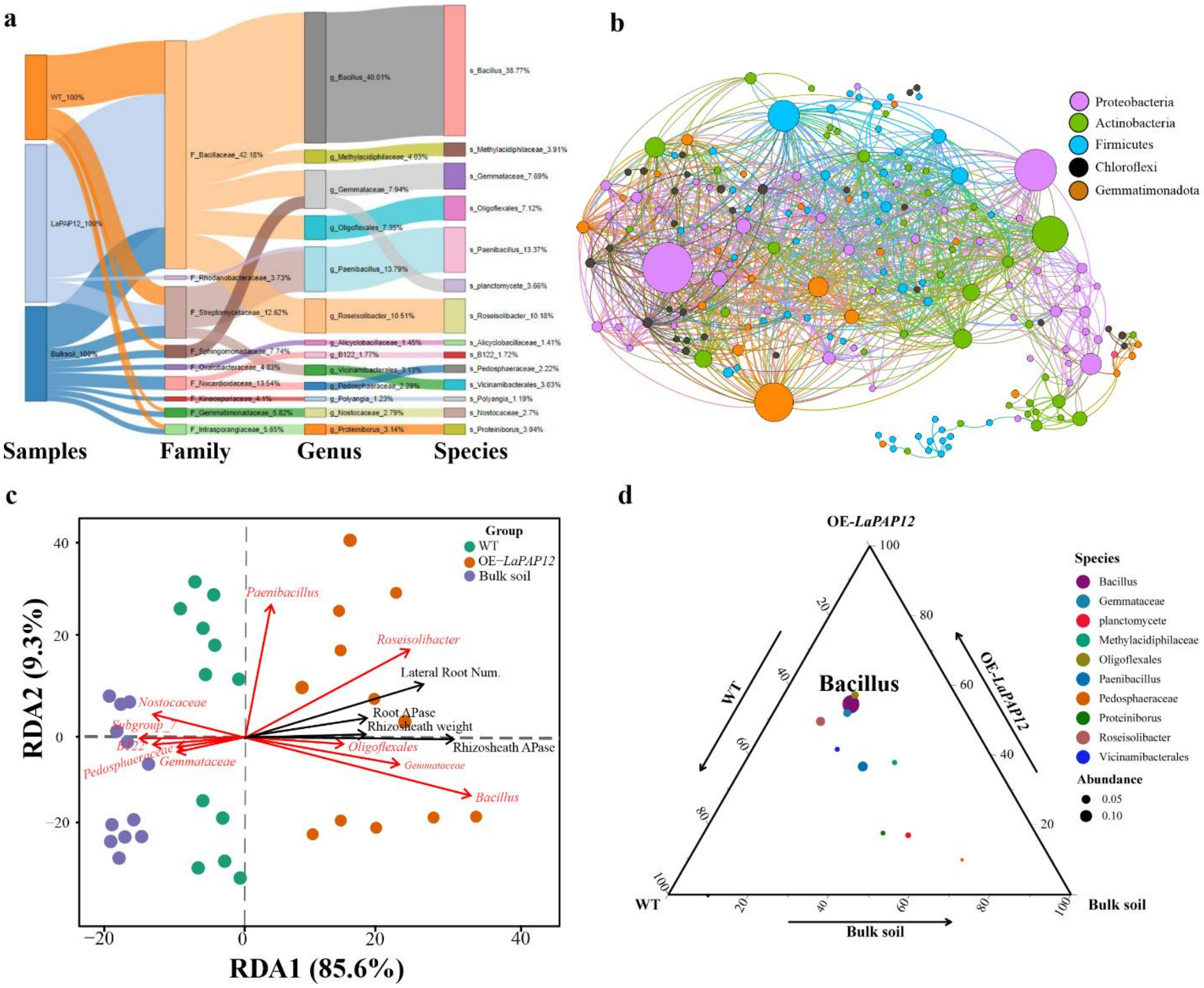
Supplemental Figure S5 Phenotypic observation and expression analysis of transgenic overexpressing TP-*LaPAP12* and WT rice plants. (a) Phenotype of EV, WT and transgenic rice lines; (b) RT-qPCR analysis of EV, WT and TP-*LaPAP12* rice lines; (c) RT-qPCR analysis of *LaPAP12* in EV, WT, and transgenic rice lines under four different treatments. Data are means ± standard error (n = 5). TP- *LaPAP12*, *LaPAP12*-overexpressing lines; EV, empty vector; WT, wild-type; WW+P, well-watered with sufficient phosphorus (P); SD+P, soil drying with sufficient P; WW–P, well-watered with P deficiency; SD–P, soil drying with P deficiency.



Supplemental Figure S6 Physiological and biochemical traits displayed by rice plants overexpressing *LaPAP12* under four different treatments. (a) Total root length (cm plant^{-1}), (b) Rhizosheath APase activity (U g^{-1} DW), (c) Shoot P content (mg g^{-1} DW), (d) Rhizosheath P accumulation (mg g^{-1} DW), (e) Total plant dry weight (g). All the measurements include five independent biological replicates and error bars represent standard error. Different letters at the top of bars indicate significant differences among WT and TP-*LaPAP12* lines under both WW and SD treatments. WW+P, well-watered with sufficient P; SD+P, soil drying with sufficient P; WW–P, well-watered with P deficiency; SD–P, soil drying with P deficiency.

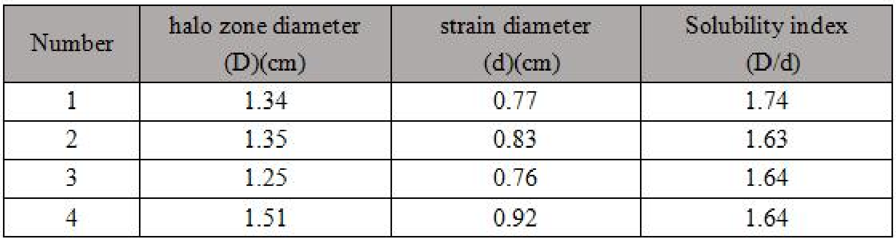


Supplemental Figure S7 The total number of bacterial OTUs (operational taxonomic units) identified in WT and TP-*LaPAP12* rice lines. Rhizosphere samples were collected from the WW+P and WW–P treatments, while rhizosheath samples were collected from SD+P and SD–P treatments. WW+P, well-watered with sufficient phosphorus (P); SD+P, soil drying with sufficient P; WW–P, well-watered with P deficiency; SD–P, soil drying with P deficiency.



Supplemental Figure S8 *Bacillus*-enriched rice microbial community of TP-*LaPAP12*-L1 rhizosheath and rhizosphere soils. (a) Sankey diagram of proportional OTUs at the family to genus and genus to species level, (b) Co-occurrence network analysis of top five phylum, nodes (OTUs) colored by phylum. Each node represents a taxon, with a size proportional to its relative abundance across all samples, while different color edges between the nodes represent positive and negative correlations between taxa. Pearson coefficient correlations with a score lower than −0.7 and higher than 0.7, and q-value <0.01 were considered significant, (c) Redundancy Analysis (RDA) showing the relationship between environmental variables and biological variables, (d) Ternary plot representing the proportion and connection of bacterial taxa (at the species level) among WT, TP-*LaPAP12*, and bulk soil.

Supplemental Table S1. Solubility index for $Ca_3(PO_4)_2$ solubilization by *Bacillus megaterium* strain.



Number	halo zone diameter (D)(cm)	strain diameter (d)(cm)	Solubility index (D/d)
1	1.34	0.77	1.74
2	1.35	0.83	1.63
3	1.25	0.76	1.64
4	1.51	0.92	1.64

Supplemental Table S2. Estimation of indole acetic acid (IAA) by the *Bacillus megaterium* after 24, 48, and 96 h of incubation using spectrophotometry.

Bacterial strain	**Cultured medium**	**Incubation period**	**IAA concentration (µg/mL)**
Bacillus megaterium	LB medium	24h	2.34 ± 0.27
	LB medium + tryptophan	24h	6.32 ± 1.11
Bacillus megaterium	LB medium	48h	14 ± 0.39
	LB medium + tryptophan	48h	52.36 ± 2.14
Bacillus megaterium	LB medium	96h	1.67 ± 0.98
	LB medium + tryptophan	96h	10.78 ± 0.76

Data represent the average value of three replicates ± standard deviation.

Supplemental Table S3. List of primers used in this study.

Name	Strand	Sequence	Purpose
LaPAP12	Forward	GAGCTCGGTACCCGGGGATCCATGTCCTCTTTATGTACATGTAAGTGTATCG	Vector construction
LaPAP12	Reverse	CAGGTCGACTCTAGAGGATCCTCACATTTTTGTTACAGTGGGTAAGATTTTGATTTTTG	
LaPAP12	Forward	TACCGAATTCTCTAGATGCTTATGAGCGATCTGAACGTGT	VIGS
LaPAP12	Reverse	ATGGAGGCCTTCTAGAACTGGCTTCACGGTATGCTGA	
388F	Forward	ACTCCTACGGGAGGCAGCAG	16S sequencing
806R	Reverse	GGACTACHVGGGTWTCTAAT	
27-F	Forward	AGAGTTTGATCCTGGCTCAG	*Bacillus* detection
492-R	Reverse	GGCTACCTTGTTACGACTT	
*Os*Actin	Forward	CCAGCAGATGTGGATTGCCA	Normalize expression
*Os*Actin	Reverse	CGGCGATAACAGCTCCTCTT	
*La*Actin	Forward	AGATTTGGCATCACACTTTCTAC	Normalize expression
*La*Actin	Reverse	ATTTGGGTCATCTTCTCTCTGTT	
LaPAP12	Forward	CAGCATACCGTGAAGCCAGT	qPCR
LaPAP12	Reverse	GCCTCCACTGCGTATCCATC	
LaPAP22	Forward	TGCCCTTTGAAGAAAGTGGGT	qPCR
LaPAP22	Reverse	CCAAGGTGCATGCAATAGAGC	
LaPAP18b	Forward	CTGGTCATGTGCACGCTTAT	qPCR
LaPAP18b	Reverse	GCTTCACGGAATTCGGACCA	
LaPAP16	Forward	GTCGGATCATCAACCCGTCA	qPCR
LaPAP16	Reverse	GTCCGTCCATGCGTTCTCTC	
LaPAP9b	Forward	ACTACAGCCATGCATCGGAAT	qPCR
LaPAP9b	Reverse	GTGACGGTGACTGTGACGAA	
LaPAP18a	Forward	TACCGATGTGGCGGTTATGG	qPCR
LaPAP18a	Reverse	GATGTTGCATTCGATCGGCA	
LaPAP7a	Forward	TGCCTCTCTCATCACCTACCT	qPCR
LaPAP7a	Reverse	TCCCATCTGAGTGGCAACAA	
LaPAP17	Forward	ACAGTGGTACAGTGTGTTGGG	qPCR
LaPAP17	Reverse	GGGATAATGCCCTGCCAGTC	
LaPAP27c	Forward	TTCTGCGCAACGTGTAGTCA	qPCR
LaPAP27c	Reverse	GCTCAATCTGCGCCGTAAAC	
LaPAP18c	Forward	TGTTCGACCTCCTCCTCGAA	qPCR
LaPAP18c	Reverse	GCTACGGCGTCATATCTCCC	
LaPAP7b	Forward	GATCTAAGGCATGGAGGGGC	qPCR
LaPAP7b	Reverse	TGCTGGATTGAGATCTTTGGGT	
LaPAP27d	Forward	GCACTTCACAGTTCCGCTTC	qPCR
LaPAP27d	Reverse	TTGAACTCGAGTGGTTCGCA	
LaPAP9a	Forward	TTGCCCTTTGGGGTCATGTT	qPCR
LaPAP9a	Reverse	CCAGATGGGTTGCCAGTCTT	
LaPAP27a	Forward	CAATTTCCAGCCTGGCTCAC	qPCR
LaPAP27a	Reverse	TGGTTGCCACTTGCTGTCAT	
LaPAP29a	Forward	TTGGAGCGGGAGATGTGAAG	qPCR
LaPAP29a	Reverse	TACCCCAACTACCTTTCACCG	

LaPAP27b	Forward	GTGGGACCAATTCACAGCTC	qPCR
LaPAP27b	Reverse	GTCTGAGCCAGAACTCCACA	
LaPAP7c	Forward	TCGCTACTTCGAGGATCCAG	qPCR
LaPAP7c	Reverse	ACAGTACTACCATGATGCCCTC	
LaPAP26	Forward	CTCATGCACGTGCCACTCTA	qPCR
LaPAP26	Reverse	ACCGGTGACCGCTTGTTATG	
LaPAP27e	Forward	GAACAGTGGGATGGCGTGAT	qPCR
LaPAP27e	Reverse	GGACCCATCAACTTCGTCCT	
LaPAP29b	Forward	TTCTGTGGGAAGCTAACCGA	qPCR
LaPAP29b	Reverse	TGTTGATCGTCGAGGCGTTT	
LaPAP10a	Forward	TGAAGCGGAGTTGCCAAAAG	qPCR
LaPAP10a	Reverse	TGACACGCGTTCAGATCGTT	
LaPAP20c	Forward	GCGTGTTCGAAGCCTCATTT	qPCR
LaPAP20c	Reverse	ATTGAACTGTCGCAGGGGTT	
LaPAP10b	Forward	TGAGCGCTTTACTCGGGTTT	qPCR
LaPAP10b	Reverse	TGTCCAAAGTTAGCCTCCCTG	
LaPAP20e	Forward	TGGGACTCATTTGGTCGCTT	qPCR
LaPAP20e	Reverse	ACACCCGCCACATCAAAAGA	
LaPAP20d	Forward	CCACACGGCAGTTTTGGTTT	qPCR
LaPAP20d	Reverse	GTAGGGCCGTTCCGTTACTG	
LaPAP10d	Forward	CCACACGGCAGTTTTGGTTT	qPCR
LaPAP10d	Reverse	AAAACTGCCGTGTGGTGTTT	
LaPAP10c	Forward	CCACACGGCAGTTTTGGTTT	qPCR
LaPAP10c	Reverse	TCCAACATACAGTAGGGCCG	
LaPAP23	Forward	AACCACTGGTGGCAAAGGAG	qPCR
LaPAP23	Reverse	GCAGGAACCGCAAATCTTGA	
LaPAP29c	Forward	ACAAAGAATCTGTGCGCGTG	qPCR
LaPAP29c	Reverse	GCTTCAAGAAGCGAGTGGTG	