

Os01g0974800		0
Os01g0866500		0
Os02g0704900		0
Os04g0687100		0
Os05g0114000		0
Os05g0438500		0
Os02g0768600	ATGGCAGCGCGGGACGGCGTCTGGCTACGGCGGCCACCCGCTTCAACGCGGTGCGGGGGGTGGGGTCTCGGCGCAGCGCCCGCTCCCCACGGCCGTGTC	100
target sequence	GGCGACGGCGTCTGGCTACGG.....	20
Consensus		
Os01g0974800	ATGGCTCCCTTCTCCAAGTCGCGACCACCGCTGAGC	36
Os01g0866500	ATGAGCGAGGCGGACGAGCGGAGGGCGAAACCGC	36
Os02g0704900	ATGGTGGAGAAAGC..TGATGGAAAACCCC	28
Os04g0687100	ATGAGTGAAGA..GGACACCAATGCT	24
Os05g0114000	ATGGCTCCCTGTTGAAGCCGTGGAGAAGAGACA	36
Os05g0438500	ATGAGCAGCGAGAATGGAGAGAACGGACACGGCGC.CGCCAGCAGGTGGTGGAGCGC	57
Os02g0768600	GGTTCCAGCGCCGGGTGCTCGCCACCACCGCGCTCTCAGGACCGCCGAGCTCCGCGCCAAGGAGCAGGGCTGCGCCGAGACCT.CGACTACCGCGTGT	199
target sequence		20
Consensus		
Os01g0974800	TCTCTCACCCGAGGGGAAGGCACCACTCTCAACTGTGTTCATCGAAATACCGAGGGCAGCAAGGTCAAGTATGAACCTTGATAAGAAAACCGGGCTCTTA	132
Os01g0866500	AAGCGGCCGCGCGCGCGG.....TGAACGAGAGGATCTCTCGTCGCTGTGGCGGAGCTTCCAAGGGAAGCAAGGTGAAGTACGAGCTCGACAAGAAAACGGGGTTTCATCA	120
Os02g0704900	CATCTGGATCAAGATAC.CCCCTGTGTCTCTCAACGAGCGCATCTTCTTCTCCATGTCTCAAAAACATGTTGCTGTCTCATCCATGGCACCAGTATCTG..	123
Os04g0687100	GCTGTGGGCGAGCCAGGGCGCCCTTAAGCTCAACGAGAGGATCTGTCTCTCTTGTGTGAGATCAACCAAGGAAGCAAGGTGAATATGAGCTTGACAAGAACTGGACTGATTT..	120
Os05g0114000	GGTCTAGCCCCCTG..AAGGCCCTGTCTCTCAATGAAGAGGATCTGTCTCTATATGTCTCCGAGATCTATTTCAGACACATCCATGGCAGTATCTT..	129
Os05g0438500	TATCAGCAGACGCGCGCGCGCGGCGGAAGCTGAACGAGAGGATCTCTCTCTGCTGTCTCGCGGAGTCTCTCTCCCGCGCACTCCGTGGCAGCACCTC..	153
Os02g0768600	TCTCTCGTCGACGGCGGGCGCGCA..AGGTGTCTGCGCTGGCAGCAGTCTCCCTGCGCCGCAAGGCGCGGGGTCTTCCACTCTCTCTGAGATCCCAAG	297
target sequence		20
Consensus		
Os01g0974800	GAGATTGGACCTGAGGCACCCACCATCTTCAACTGTGTTCATCGAAATACCGAGGGCAGCAAGGTCAAGTATGAACCTTGATAAGAAAACCGGGCTCTTA	232
Os01g0866500	GACACGGGCGGTGACGCTCCGGCTGTGTTCAAAGCTTGTGTGGAGATCTCCAAGGGAAGCAAGGTGAAGTACGAGCTCGACAAGAAAACGGGGTTTCATCA	220
Os02g0704900	GAGATAGGTCCAGGAGCTCCACGAGTTTCAACTGTGTGGTTGAATCTCTTNGAGGCGCAAGGTGAAGTATGAGTTGGATAGAGGCAACTGGTCTAATTA	223
Os04g0687100	GAGATCGGCCCTGTCTCTCTCTCTCTTCAACCTTGTGTGAGATCAACCAAGGAAGCAAGGTGAATATGAGCTTGACAAGAACTGGACTGATTA	220
Os05g0114000	GAGATTGGACCTGTGTGACCAACTATATTCAACTGCGTCTATTGAGATTCCTAGGGGCGCAAGGTTAAATATGAACCTTGACAAGAAAACCTGGACTGATAG	229
Os05g0438500	GAGATCGGCCCTGTATGCTCCCGCGCTGTTCAAAGCTCTGCTGGAGATCAACCAAGGCGAGCAAGGTGAAGTACGAGCTGGACAAGAAAGCGGGGCTCATCA	253
Os02g0768600	GAGAGCAGCGCAAGATGGAGGTCGCCACGACGAGTGATCTTCAACCTCTTCAACCTCTTCAAGCAGGACCAAGGAGGCAACCTCCGATCTACTCCGTACAACATTA	397
target sequence		20
Consensus		
Os01g0974800	AAGTAGAC..GAGTTCTTACTCTTTCAGTCGTCTATCTCTCACAACCTATGGGTTTCATCTCTCGCACGC..TGTGCGACGATAGTGATCTTTGGATGTGCT	329
Os01g0866500	TGGTTGATC..GGGTCTTGTACTCTGTCAGTGGTTTACCCCCACAACCTACGGCTTCATCTCTCGAACGC..TCTGCGAAGACAACGATCCCAATGGATGTGCT	317
Os02g0704900	AGGTTGATC..GTGTTCTTTACTCATGTGTTGTTTACCCACACAACCTATGGTTTCATCTCCAGCGCACAC..TTTGTGAGGACGGTGACCCCATGGACGTCTCT	320
Os04g0687100	AGGTGACAC..GTGTCCTTACTCATCAGTTGTGTATCCCAATAATATGGTTTCATCTCCAAGGACAC..TTTGTGAAGACAATGATCCCAATGGATGTGCT	317
Os05g0114000	TGTTGGAC..GTGTGCTTATTCATCAGTTGTGTACCTTCAACCTATGGATTTCATCTCTCGCACGC..TGTGTGAAGACAGATGATCCGTTGGATGTGCT	326
Os05g0438500	AGGTTGATC..GGATTCTTACTCTCTCTGGTCTTACCTTCAACAACCTACGTTTCATCTCCGAGAACGC..TTTGTGAGGACACGACCCCATGGATGTCTCT	350
Os02g0768600	ATTGGAAATTATGATTTATTTCCTCAACAATGGGAGGACCAACTCTTGCAACAACCGATGTGCAAGGAGCATTTGGGATTAATGATCTCTGTGTATGTGTG	497
target sequence		20
Consensus		
Os01g0974800	GGTCAATATGCAGGAGCCAGTTATCCAGGATGCTTCTACGGGCAAAAGGCCATCGGTGTCTATGCCAATGATCGATCAGGGAGAGGCAATGATAAGATT	429
Os01g0866500	AGTGCTCATGCGAGGACCAAGTGATTCGGGCTGCTTTCTCCGAGCTAGGGCCATCCGACTCATGCCCATGATCGATCAGGGAGAGAAGGACGACAAGATC	417
Os02g0704900	CGTCCGTGATGCGAGGAACAAGTTGTCCTCGGATTTCTCTCGAGGCTCGGTGCTATTGGGCTCATGCCATGATGATGATCAGGGTGAGAAAGATGACAAGATC	420
Os04g0687100	GGTCCGATGCGAGGACCTGTTATTCCTGGTTCTTCTCTCGGTGTAGAGAAATTTGGCCTTATGCCCATGATTGACCAAGGGTGAGAAAGATGACAAGATA	417
Os05g0114000	GGTTAATATGCAGGAGCCGTTATACCAAGGATGCTTCTACGAGCAAAAGGCCATTTGGTCTCATGCCATGATGATGACCAAGGGAGAGGACAGATGACAAGATT	426
Os05g0438500	TGTCCTCATGCGAGGAACAGTTCTTCTGGTTTCTTCTCTCGAGCCAGGGCCATTGGTCTCATGCCATGATGATGACCAAGGGAGAGAAGGATGACAAGATC	450
Os02g0768600	TGAGATTGGTGAAAGAGCTGCTTAACATTGGAGATGCTTCTTAAGGTAAAACGTTGGCAGCTTTAGCAATGATTGATGAGGGTGAGCTTGACTGGAAAATT	597
target sequence		20
Consensus		
Os01g0974800	ATTTCAGTCTGTGCTGATGATCCTGAGTACAAGCATTACAACGATATCAAGGACCTCCACCTCACCGCTTAGCTGAATCAGGCGTTTCTTTCAGAGACT	529
Os01g0866500	ATAGCCGCTCTGCTGGACGATCCTGAGTACCGCCACTACAACGATCTCAGTGAAGCTTTGCGCTCATCGCGTCCAGGAAATCCGGCGTTTCTTTGAAGACT	517
Os02g0704900	ATAGCTGTTTGTGCTGATGACCTGAATACCGCCACTTCAGGGACATCAAGGAAATCCCCCTCACCGCCTTCAAGAGATCCGCGCTTCTTTGAAGACT	520
Os04g0687100	ATAGCAGTATGTCTGATGATCCTGAATACCGTCAATACAATGACATCAGTGAAGCTGTCTCTCTCACCGCCTCCAAGAGATTAAACGCTTCTTTGAAGACT	517
Os05g0114000	ATTGCCGTTTGTGCTGATGATCCTGAGTACAAGCATTAACATGATATCAAGGAGCTCCCACTCACCGCTTGGCTGAATCAGGCGCTTTTGAAGACT	526
Os05g0438500	ATAGCTGTCTGCGCGATGATCCTGAGTACCGCCATTTCAATAATCTCAGGAGCTTTCTCTCTCATCGCTTGAAGAAATCCGGCGCTTCTTTGAAGACT	550
Os02g0768600	GTGCTATTTCCTTTGGATGATCCTTAAGCATCTCTGTGAATGATGTGGATGATGTGAGAAGCATTTTCCGGGAACATTGACTGCTACGAGACTGCT	697
target sequence		20
Consensus		
Os01g0974800	ACAAGAAGAATGAGA..ATAAGGAGGTG..GCTGTCAACGACTTTCATGCCTGCCACTTCTGCTTATGAGACCATACGCCATTCCATGGATC..TATATGCTAC	626
Os01g0866500	ACAAGAAGAATGAAA..ACAAGGAGGTC..GCCGTGAATGAGCTACTGCCGTGACCGTGCTCTGGGATGCCATCCAGTATTCATGGATC..TGATGTCTCA	614
Os02g0704900	ACAAGAAGAATGAGA..ACAAGAAGATT..GCTGTCAATGACTTTCTCCAGCAGAAAGTGCATCAACGCAATCAAGTACTCAATGGAC..TCTACGCGCG	617
Os04g0687100	ACAAGAAGAATGAGA..ACAAGGAGGTT..GCTGTTGATGCATTCTTGCTTGCACACACTGCTCTGTGAGCGCAATTGACTCTCCATGGAC..TGATGTGCA	614
Os05g0114000	ACAAGAAGAATGAGA..ACAAGGAGGTT..GCTGTCAATGACTTCTTGCTTGCAGAGTGCTGCTTATGAGGCCATAAAGCACTCCATGGATC..TCTATGCTAC	623
Os05g0438500	ACAAGAAGAATGAGA..ACAAGGAGGTT..GCTGTCAATGACTTCTTGCTTGCCTGCTCCGACAGCTCTGTGAAGCAATCCAGTACTCTATGGATC..TGATCGGACA	647
Os02g0768600	TCAGGCACTACAAGTACAGACGGTAAGCCTCAACAGATTGCTCTGCGGCAACAAACCCACAGCAAGGAATATGCTCTGAAAGGTCTAGAAAGAAAC	797
target sequence		20
Consensus		
Os01g0974800	TTAC..ATCCTTGAAGGCTTACGCAGATAG.....	654
Os01g0866500	GTAC..ATTGAGCA..CTTGGGCGAGTAG.....	639
Os02g0704900	CTAC..ATCATTTGAGAGCTTGAGGAAGTGA.....	645
Os04g0687100	ATAT..ATCTTGCRAAGCTTGAGGCGAGTAG.....	642
Os05g0114000	TTAC..ATCGTGGAGGCTTGAGGAGGTAG.....	651
Os05g0438500	GTAC..ATTCTGCAGAGCTTGAGCGGTAG.....	675
Os02g0768600	CACAGAAATATGGGAGAAAATGCTGTAAGGAATATCCCTGCTGGAGAGCTCTCACTAGCCTA	860
target sequence		20
Consensus		

Fig. S2 Nucleotide sequences alignment of the seven putative gene encoding sPPase in rice.

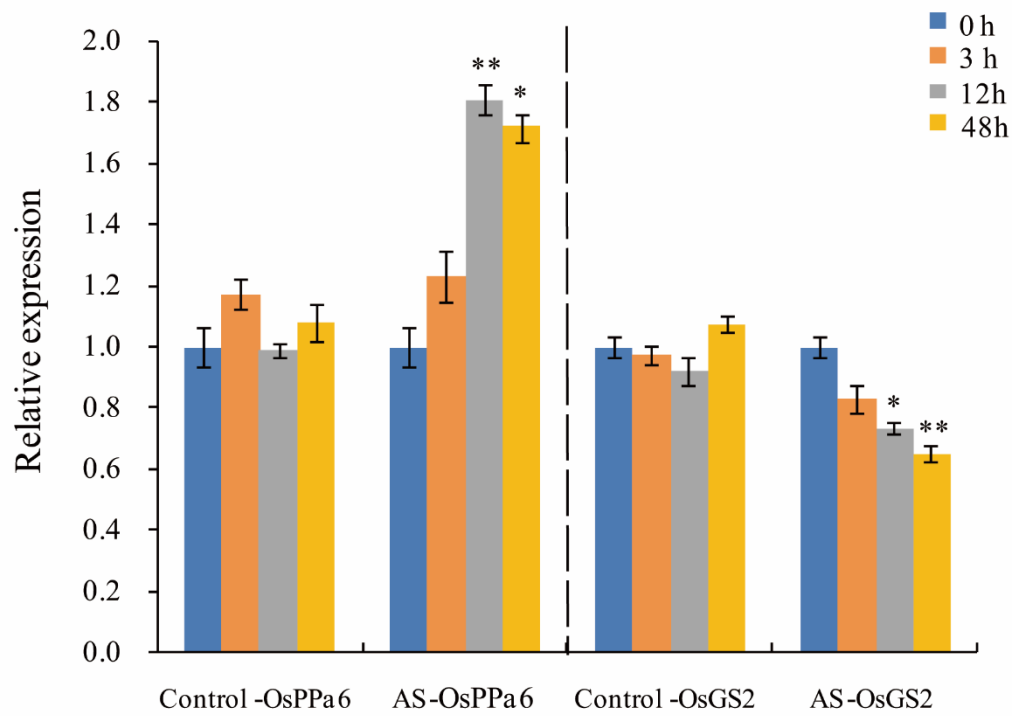


Fig. S3 Relative expression levels of the *OsPPa6* gene and the *OsGS2* gene in shoots of the wild type. Values are mean $\pm$ SD of three replications and asterisks denote Student's test significance at level of $P \leq 0.05$ (*) or $P \leq 0.01$ (**).

Table S1Primers used of PCR and qRT-PCR in this study

Primer name	Primer sequences
sgRNA-F	5'-GGCAGGCGACGGCGTCGGCTACGG-3'
sgRNA-R	5'-AAACCCGTAGCCGACGCCGTCGCC-3'
U3-F	5'-GTCGTTTCCCGCCTTCAGTTTTGCATGCCTGCAGGTCGACG-3'
U3-R	5'-CTGTCAAACACTGATAGTTTGGATCCTCTAGAGATTATG-3'
OsPPa6-F	5'-TCCCACTTTCCAGTCTCC-3'
OsPPa6-R	5'-GTTGCCCTTCTTGGTGTC-3'
Cas9-F	5'-AGAGGACTTCTACCCGTTCC-3'
Cas9-R	5'-CCTTCTGTGTGGTCTGGTTC-3'
qOsPPa6-F	5'-TGAGCTTGACTGGAAAATTGTG-3'
qOsPPa6-R	5'-GCTTCTCAACATCATCCACATC-3'
qOsGS2-F	5'-CAGGCTATATTCAAGGACCCAT-3'
qOsGS2-R	5'-AGCCCTGTTACGTTTGTTAGTA-3'
OsActin1-F	5'-CTAAGCCAAGAGGAGCTGTTAT-3'
OsActin1-R	5'-ATAACAGATAGGCCGTTGAAA-3'