

## Supplementary Materials

**Table S1.** Prediction of the *cis*-regulatory elements in the *TwTPS27a/b* promoters

Site name	Numbers of		Sequence	Function
	27aP	27bP		
TGACG-motif	2	2	TGACG	Cis-acting regulatory element involved in the meja-responsiveness
PYRIMIDINEBOXHVEPB1	1	1	TTTTTTCC	Required for GA induction, pyrimidine box
PYRIMIDINEBOXOSRAMY1A	1	0	CCTTTT	Gibberellin-response cis-element, pyrimidine box
W-box	3	7	TTGAC(T/C)	WRKY recognition site, salicylic acid (SA)-responsiveness
E-box	3	4	CANNTG	MYC recognition sequence, meja-responsiveness
T/G-box	1	0	CACGTT	MYC recognition sequence, meja-responsiveness
MYB1AT	1	2	(T/A)AACCA	MYB recognition site, dehydration-responsive
MYB2AT	1	0	TAACTG	MYB recognition sequence, dehydration-responsive
MYB1LEPR	1	1	GTTAGTT	Cis elements of Myb1
MYBPZM	1	1	CCAACC	Core of consensus maize P (myb homolog) binding site
MYBST1	3	2	GGATA	Core motif of mybst1 (a potato MYB homolog) binding site
MYBCORE	2	5	C(G/C)GTT(A/G)	CNGTTR, MYB recognition site, dehydration-responsive
ABRE	1	0	ACGTG	Abscisic acid responsiveness
RAV1AAT	2	6	CAACA	The AP2-like domain recognize the CAACA motif; ethylene-responsive
CAATBOX1	27	35	CAAT	Play a key role in transcription initiation
CTRMCAMV35S	0	1	TCTCTCTCT	CT-rich motif, can enhance gene expression
AAGAA-motif	1	1	GAAAGAA	Light responsive element
AE-box	2	2	AGAAACAA	Part of a module for light response
Box 4	2	1	ATTAAT	Part of a conserved DNA module involved in light responsiveness
GA-motif	1	1	ATAGATAA	Part of a light responsive element
GT1-motif	1	2	GGTTAA	Light responsive element
I-box	1	0	TAGATAACC	Part of a light responsive element
GATABOX	11	16	GATA	Light regulated, and tissue specific expression
IBOX	2	2	GATAAG	Light responsive element
IBOXCORE	5	6	GATAA	Light responsive element
SORLIP1AT	1	1	GCCAC	One of "Sequences Over-Represented in Light-Induced Promoters (sorlips) in Arabidopsis
SORLIP2AT	0	2	GGGCC	One of "Sequences Over-Represented in Light-Induced Promoters (sorlips)

SORLIP5AT	1	0	GAGTGAG	Light responsive element
TBOXATGAPB	0	1	ACTTTG	Mutations in the "Tbox" resulted in reductions of light-activated gene transcription
TCCC-motif	2	1	TCTCCCT	Part of a light responsive element
TCT-motif	0	1	TCTTAC	Part of a light responsive element
ACGTATERD1	6	4	ACGT	Required for etiolation-induced expression
ARE	1	1	TGGTTT	Essential for the anaerobic induction
CBFHV	1	2	RYCGAC	Dehydration-responsive element (DRE) binding proteins
CCAATBOX1	3	4	CCAAT	HSE (Heat shock element); CCAAT box
CURECORECR	3	2	GTAC	Copper-response element
ELRECOREPCR1	1	4	TTGACC	Fungal elicitor responsive element
GT1GMSCAM4	6	9	GAAAAA	Plays a role in pathogen- and salt-induced
LTRECOREATCOR15	1	1	CCGAC	Low-temperature response
SURE1STPAT21	1	2	AATAGAAAA	Sucrose responsive element (sure)
SURECOREATSULTR11	1	2	GAGAC	Core of sulfur-responsive element (SURE) found in the promoter of SULTR1
AACACOREOSGLUB1	1	1	AACAAAC	endosperm-specific expression
AACACOREOSGLUB1	1	1	AACAAAC	endosperm-specific expression
GCN4_motif	0	1	TGAGTCA	cis-regulatory element involved in endosperm expression
OSE1ROOTNODULE	3	4	AAAGAT	organ-specific elements, activated in infected cells of root nodules
OSE2ROOTNODULE	5	8	CTCTT	organ-specific elements, activated in infected cells of root nodules
ROOTMOTIFTAPOX1	14	12	ATATT	root-specific expression
RYREPEATBNNAPA	1	2	CATGCA	Seed-specific expression

**Table S2.** The results of local BLAST for query sequence of *TwTPS27* (KU948698)

Transcriptome	Matched sequence	Score(bits)	E-value	Length(bp)
SRX472292	<i>comp34029_c1_seq3</i>	1095	0.0	2562
SRX202900	<i>Tw_comp37092_c0_seq1_len=2086</i>	1180	0.0	2086
SRX472292	<i>comp27356_c0_seq1</i>	295	5e-080	375
SRX202900	<i>Tw_comp37092_c0_seq1_len=2086</i>	256	9e-068	2086

**Table S3.** Primers used in this study

Primers	Sequence (5' to 3')	Use for
<b>Full-length cDNA and gDNA PCR</b>		
<i>TwTPS27</i> -UTR-F	AAGTTTGGTTTCTTGCATCCAAAATC	cDNA-PCR and gDNA-PCR
<i>TwTPS27</i> -UTR-R	GATGTCCAAACTACTTATTTGCTAA	
<b>5'/3'-RACE PCR</b>		
<i>TwTPS27</i> -5'-R1-624	CTCTTTGGCTTCATCTAAAATAACT	1 <sup>st</sup> 5'-RACE PCR
<i>TwTPS27</i> -5'-R2-302	TCAGAGGTGGACGCAAGCAATC	2 <sup>nd</sup> 5'-RACE PCR
<i>TwTPS27</i> -3'-F1-974	CCAAAGCCAGAATAGCAGCAAC	1 <sup>st</sup> 3'-RACE PCR
<i>TwTPS27</i> -3'-F2-1422	GCTACTCTACTGGTCGTCGTCAT	2 <sup>nd</sup> 3'-RACE PCR
<b>Site Finding-PCR</b>		
Site Finder-1	CACGACACGCTACTCAACACACCACCTCGCACAGCGTCCTCAACCTGCAGGIBIHIGCTC	Initial PCR
Site Finder-2	CACGACACGCTACTCAACACACCACCTCGCACAGCGTCCTCAAGCGGCCGCNNNNNNNGCTC	Initial PCR
Site Finder-3	CACGACACGCTACTCAACACACCACCTCGCACAGCGTCCTCAACTCGAGNNNNNNNAGCT	Initial PCR
SFP1	CACGACACGCTACTCAACAC	1 <sup>st</sup> PCR
SFP2	ACTCAACACACCACCTCGCACAGC	2 <sup>nd</sup> PCR
SFP3	CACCTCGCACAGCGTCCTCA	3 <sup>rd</sup> PCR
27pro1	CGTAGGATGCGGAACCTCAATGC	1 <sup>st</sup> PCR
27pro2	GCAATCTCTTGGCATCTTGCCCTC	2 <sup>nd</sup> PCR
27pro3	TGTAGGGAGTGTTCAAGGAGTCG	3 <sup>rd</sup> PCR
27pro4	ATCATTGCGGAAGAAAAGAGAACTT	1 <sup>st</sup> PCR
27pro5	TCATCCAAACAAGTCATTCAACATA	2 <sup>nd</sup> PCR
27pro6	GCTGCCAGGGGCGAAACT	3 <sup>rd</sup> PCR
<b>FPNI-PCR</b>		
FP1	GTAATACGACTCACTATAGGGCACGCGTGGTNTCGASTWTSWGTT	1 <sup>st</sup> PCR
FP2	GTAATACGACTCACTATAGGGCACGCGTGGTNGTCGASWGANAWGAA	1 <sup>st</sup> PCR
FP3	GTAATACGACTCACTATAGGGCACGCGTGGTWGTGNAGWANCANAGA	1 <sup>st</sup> PCR
FP4	GTAATACGACTCACTATAGGGCACGCGTGGTAGWGNAGWANCAWAGG	1 <sup>st</sup> PCR
FP5	GTAATACGACTCACTATAGGGCACGCGTGGTNGTAWAASGTNTSCAA	1 <sup>st</sup> PCR
FP6	GTAATACGACTCACTATAGGGCACGCGTGGTNGACGASWGANAWGAC	1 <sup>st</sup> PCR
FP7	GTAATACGACTCACTATAGGGCACGCGTGGTNGACGASWGANAWGAA	1 <sup>st</sup> PCR

FP8	GTAATACGACTCACTATAGGGCACGCGTGGTGTNCGASWCANAWGTT	1st PCR
FP9	GTAATACGACTCACTATAGGGCACGCGTGGTNCAGCTWSCTNTSCTT	1st PCR
FSP1	GTAATACGACTCACTATAGGGC	2nd PCR
FSP2	ACTATAGGGCACGCGTGGT	3rd PCR
XXR494	CCCGTTTAGCTTTGCCCAATGTGAC	1st PCR
XXR410	TGAAGAGGGAGAGAGGCGTGAGGTA	2nd PCR
XXR358	AGAGGGGCTTGAGGTAGAAGATGAT	3rd PCR
<b>Full-length Promoter cloning</b>		
Pro-1-F	GTAAGTGAATAAATAAATTAATTTGCTACAGTTATCG	sense primer
Pro-2-F	TGGGCCCTCTTTATTGAAAACAAAAAT	sense primer
Pro-R	AATCCCAGAAGAAAGGTGTGATTTT	antisense primer
<b>Promoter::GUS construction</b>		
27aP-F	<u>GACCATGATTACGCCAAGCTT</u> GTAAGTGAATAAATAAATTTGCTACAGTTATCG	sense primer
27bP-1-F	<u>GACCATGATTACGCCAAGCTT</u> TGGGCCCTCTTTATTGAAAACAAAAAT	sense primer
27bP-2-F	<u>GACCATGATTACGCCAAGCTT</u> CTCTTCAATCTTTCTTTTATGTCAC	sense primer
27bP-3-F	<u>GACCATGATTACGCCAAGCTT</u> TAACTTGTAGGACAAATAGAGAAC	sense primer
27bP-4-F	<u>GACCATGATTACGCCAAGCTT</u> ATTAATAATTGTAGACTCGATTATTC	sense primer
27bP-5-F	<u>GACCATGATTACGCCAAGCTT</u> TGACTTTAAACTTGTGACATCGA	sense primer
27P-R	<u>ACCACCCGGGGATCCTCTAGAAATTCCCAGAAGAAAGGTGTGATTTT</u>	antisense primer
<b>Y1H assays</b>		
aPro-AbAi-F	<u>AAATGATGAATTGAAAAGCTTT</u> GAGTGAAATTTGATGTGTTTGACG	bait vector
aPro-AbAi-R	<u>AGCACATGCCTCGAGGTCGACCAAATAGTTTGAGAAGTGTACAACGTCA</u>	bait vector
aPro-m-AbAi-F	<u>AAATGATGAATTGAAAAGCTTT</u> GAGTGAAATTTGATGTGTTTctCt	bait vector
aPro-m-AbAi-R	<u>AGCACATGCCTCGAGGTCGACCAAATAGTTTGAGAAGTGTACAACGagA</u>	bait vector
bPro-AbAi-F	<u>AAATGATGAATTGAAAAGCTTT</u> GAGTCAAATTTGATGTGTTTGACG	bait vector
bPro-AbAi-R	<u>AGCACATGCCTCGAGGTCGACCAAATTGTTTGAGAAGTGGACAACGTCA</u>	bait vector
bPro-m-AbAi-F	<u>AAATGATGAATTGAAAAGCTTT</u> GAGTCAAATTTGATGTGTTTctCt	bait vector
bPro-m-AbAi-R	<u>AGCACATGCCTCGAGGTCGACCAAATTGTTTGAGAAGTGGACAACGagA</u>	bait vector
TwTGA1-AD-F	<u>GCCATGGAGGCCAGTGAATTC</u> ATGAACTCTCCGTCCACCC	prey vector
TwTGA1-AD-R	<u>ACGATTCATCTGCAGCTCGAGCT</u> ATTCTCCTTTAAACGACTGTGCAC	prey vector
<b>GUS transactivation assays</b>		
TwTGA1-OE-F	<u>TATAAAAAAAAAAAAAAGAATTC</u> ATGAACTCTCCGTCCACCC	effector vector

TwTGA1-OE-R	<u>ATTATTATGGAGAAAAAGCTTCTATTCTCCTTTAAACGACTGTGCAC</u>	effector vector
27aP-F	in section of Promoter::GUS construction	reporter vector
27aP-R	in section of Promoter::GUS construction	reporter vector
27bP-F	in section of Promoter::GUS construction	reporter vector
27bP-R	in section of Promoter::GUS construction	reporter vector

**Table S4.** Reaction system of Site Finding-PCR

Initial PCR		1 <sup>st</sup> PCR	
Components	Volume	Components	Volume
Genomic DNA	1.0 µL	Initial PCR product	20.0 µL
—	—	GSP1 (10 µM)	1.0 µl
Site Finer(n) (10 µM)	1.0 µl	SF1 (100 µM)	0.4 µl
Premix PrimeSTAR HS	10.0 µl	Premix PrimeSTAR HS	2.5 µl
ddH <sub>2</sub> O	8.0 µL	ddH <sub>2</sub> O	1.1 µL
Total	20.0 µl	Total	25.0 µl
2 <sup>nd</sup> PCR		3 <sup>rd</sup> PCR	
Components	Volume	Components	Volume
1 <sup>st</sup> PCR product	1.0 µl	Dilution of 2 <sup>nd</sup> PCR product	1.0 µl
GSP2 (10 µM)	1.0 µl	GSP3 (10 µM)	1.0 µl
SF2 (10 µM)	1.0 µl	SF3 (10 µM)	1.0 µl
Premix PrimeSTAR HS	12.5 µl	Premix PrimeSTAR HS	12.5 µl
ddH <sub>2</sub> O	9.5 µL	ddH <sub>2</sub> O	9.5 µL
Total	25.0 µl	Total	25.0 µl

**Table S5.** Reaction procedures of SiteFinding-PCR

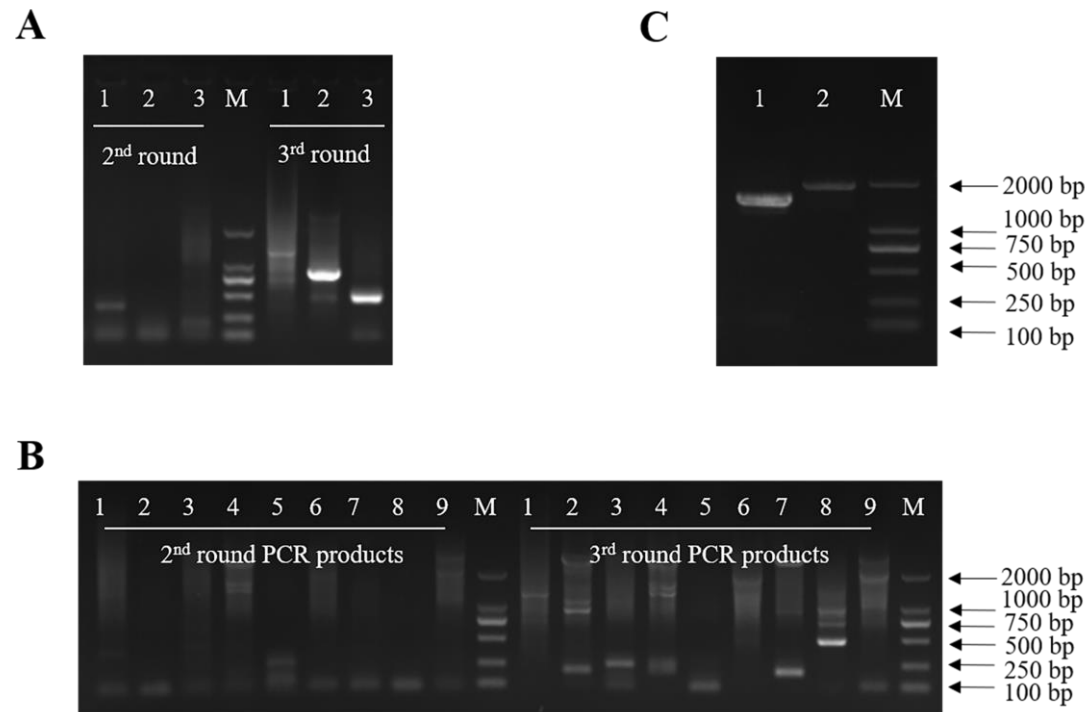
Reactions	Circles	Conditions of temperature
Initial PCR	1	94°C 5 min
	1	98°C 1 min; 25°C 1 min; 0.3°C /s heat up to 68°C
	1	68°C 10 min
1 <sup>st</sup> PCR	1	94°C 5 min
	30	98°C 10 s; 55°C 5 s; 68°C 4 min
	1	72°C 5 min
2 <sup>nd</sup> PCR	1	94°C 5 min
	30	98°C 10 s; 55°C 5 s; 68°C 3 min
	1	72°C 5 min
3 <sup>rd</sup> PCR	1	94°C 5 min
	30	98°C 10 s; 55°C 5 s; 68°C 2 min
	1	72°C 5 min

**Table S6.** Reaction system of fusion primer and nested integrated-PCR (FPNI-PCR)

1 <sup>st</sup> PCR		2 <sup>nd</sup> PCR		3 <sup>rd</sup> PCR	
Components	Volume	Components	Volume	Components	Volume
Genomic DNA	1.5 µL	1 <sup>st</sup> PCR product	1.0 µl	Dilution of 2 <sup>nd</sup> PCR product	1.0 µl
GSP1 (10 µM)	0.4 µl	GSP2 (10 µM)	1.0 µl	GSP3 (10 µM)	1.0 µl
FPn (10 µM)	2.0 µl	FSP1 (10 µM)	1.0 µl	FSP2 (10 µM)	1.0 µl
Premix PrimeSTAR HS	12.5 µl	Premix PrimeSTAR HS	12.5 µl	Premix PrimeSTAR HS	12.5 µl
ddH <sub>2</sub> O	8.6 µL	ddH <sub>2</sub> O	9.5 µL	ddH <sub>2</sub> O	9.5 µL
Total	25.0 µl	Total	25.0 µl	Total	25.0 µl

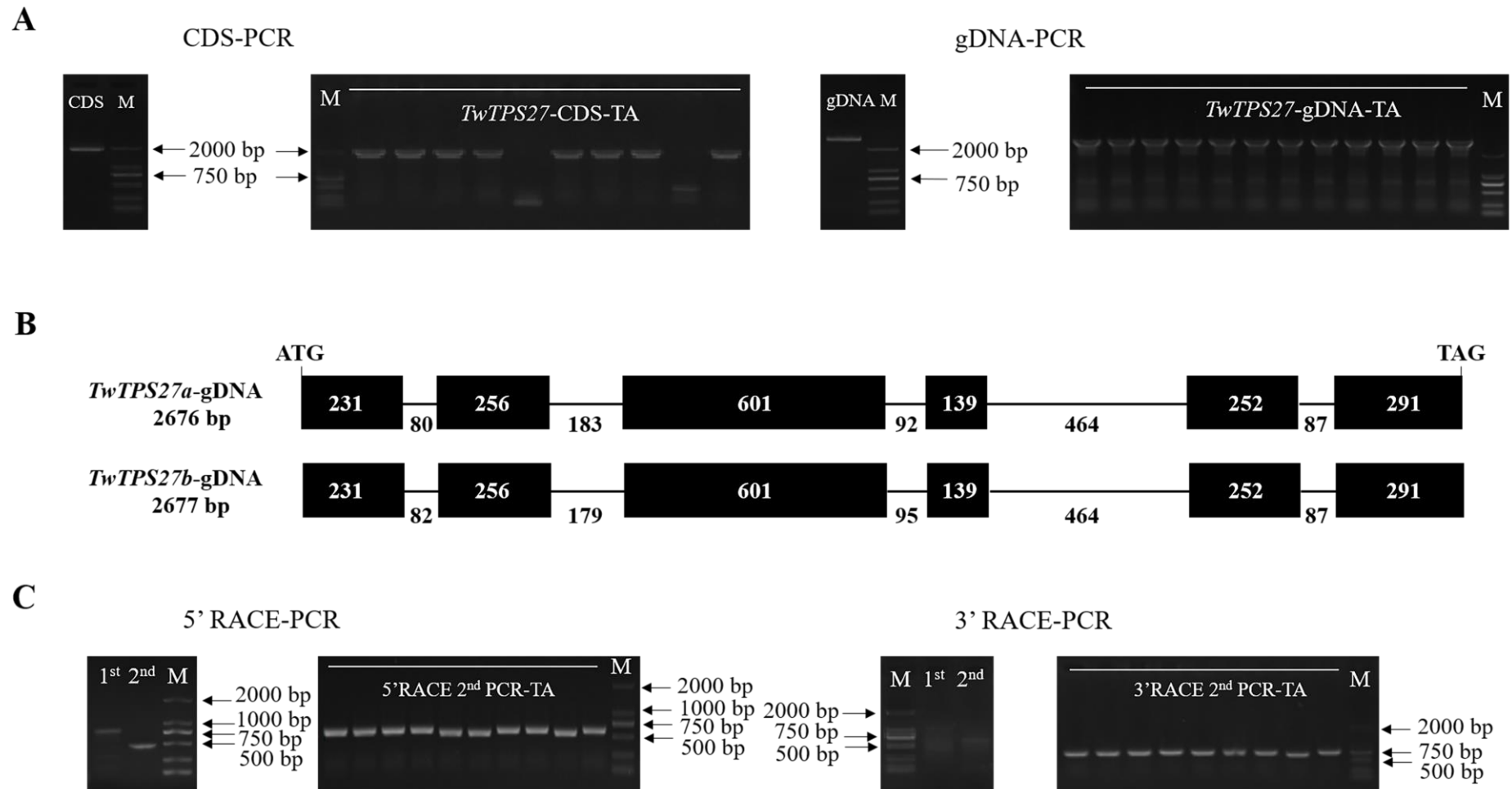
**Table S7.** Reaction procedures of FPNI-PCR

Reactions	Circles	Conditions temperature
1 <sup>st</sup> PCR	1	95°C 90 s
	2	94°C 10 s, 62°C 30 s, 72°C 2 min
	1	94°C 10 s, 25°C 2 min, 0.2°C/s, 72°C 2 min
	6	94°C 10 s, 62°C 30 s, 72°C 2 min, 94°C 10 s, 62°C 30 s, 72°C 2 min, 94°C 10 s, 44°C 30 s, 72°C 2 min
	1	72°C 5 min
2 <sup>nd</sup> PCR	1	95°C 90 s
	30	94°C 10 s, 62°C 30 s, 72°C 2 min
	1	72°C 5 min
3 <sup>rd</sup> PCR	1	95°C 90 s
	12	94°C 10 s, 62°C 30 s, 72°C 2 min
	1	72°C 5 min



**Figure S1.** Cloning of the 5'-flanking sequences of *TwTPS27a* and *TwTPS27b*. (A) Identification of the 2<sup>nd</sup> round and 3<sup>rd</sup> round PCR products in the SiteFinding-PCR assays. The PCR reaction systems and procedures are shown in Table S4-S5. All primers used here are shown in Table S3. M: DL2000 Marker. (B) Identification of the 2<sup>nd</sup> round and 3<sup>rd</sup> round PCR products in the FPNI-PCR assays. The PCR reaction systems and procedures are shown in Table S6-S7. All primers used here are shown in Table S3. M: DL2000 Marker. (C) Identification of the PCR products of 5'-flanking sequence of target genes. 1, the PCR product of the 1496 bp-length 5'-flanking sequence using the specific primers of Pro-1-F and Pro-1-R. 2, the PCR product of the 1862 bp-length 5'-flanking sequence using the specific primers of Pro-2-F and Pro-2-R. All primers used here are shown in Table S3. M: DL2000 Marker.





**Figure S2.** Identification of the PCR products for the full-length coding sequence (CDS), gDNA and 5'/3'-RACE of *TwTPS27a* and *TwTPS27b*. (A) Identification of the PCR product for full-length cDNA and gDNA of *TwTPS27*. Several positive clones of *TwTPS27*-cDNA-TA and *TwTPS27*-gDNA-TA were identified. M: DL2000 Marker. (B) Exon-intron structures of *TwTPS27a* and *TwTPS27b*. Exons and introns are represented by black boxes and straight lines, respectively. (C) Electrophoretogram analysis of 5'/3' RACE-PCR. 1<sup>st</sup> represents 1<sup>st</sup>-round 5'/3'RACE-PCR products, 2<sup>nd</sup> represents 2<sup>nd</sup>-round 5'/3'RACE-PCR products. M: DL2000 Marker. Several positive TA clones of 2<sup>nd</sup>-round PCR products (5'RACE 2<sup>nd</sup> PCR-TA and 3'RACE 2<sup>nd</sup> PCR-TA ) for 5'/3'RACE were identified.

**Nucleotide  
Identity  
=98.36%**

TwTPS27a	ATGGCACAATGTTCTCCCTCACCATCTCACACTTTGTTATACAGACTGGTTCAACAGCCCTTACACTACTCAGCTCTGCCTGAACCCAGAACAAAACATTTGTCATTCATCAAGACCAATTTGCATCGATCAACTCCAATTCGCTACAAATGAATCAACGGCCCTTGACTGACTACCGTCCGGGATCTGGAATCCGG	199
TwTPS27b	ATGGCACAATGTTCTCCCTCACCATCTCACACTTTGTTATACAGACTGGTTCAACAGCCCTTACACTACTCAGCTCTGCCTGAACCCAGAACAAAACATTTGTCATTCATCAAGACCAATTTGCATCGATCAACTCCAATTCGCTACAAATGAATCAACGGCCCTTGACTGACTACCGTCCGGGATCTGGAATCCGG	199
TwTPS27a	AGCTAATCGACTCCTTGACACTCCCTACAGTATCAATCACATGGAAACCAGCTGGAACAAGTTGAGCCAGATGCCAAGAGATTGCTTGGCTCCACTCTGATCTTGTCTCTCTTGAATCATGTTGATCGATGCAGCGATTAGGAATGCTTACCATTTTCAAGAAGAAATCGACTACTTGTCTAATACCTGATTT	399
TwTPS27b	AGCTAATCGACTCCTTGACACTCCCTACAGTATCAATCACATGGAAACCAGCTGGAACAAGTTGAGCCAGATGCCAAGAGATTGCTTGGCTCCACTCTGATCTTGTCTCTCTTGAATCATGTTGATCGATGCAGCGATTAGGAATGCTTACCATTTTCAAGAAGAAATCGACTACTTGTCTAATACCTGATTT	399
TwTPS27a	CAGCGTACTCTCCTGATGATCATGATCTCCACACAACTGCATTGAGGTTCCGCATCCTACGAGACAAACATTTCCCCATTAGCTCAGATGTGTTGAAAGTTTCATGAGCAGAGAAGGGAATTCCTGGACAGTTTGAGCAGAGATGTGAAAGGACTATTGAGTTTGTATGAAGCTTCATTCTTGGGAGTGGATGGAGA	599
TwTPS27b	CAGCGTACTCTCCTGATGATCATGATCTCCACACAACTGCATTGAGGTTCCGCATCCTACGAGACAAACATTTCCCCATTAGCTCAGATGTGTTGAAAGTTTCATGAGCAGAGAAGGGAATTCCTGGACAGTTTGAGCAGAGATGTGAAAGGACTATTGAGTTTGTATGAAGCTTCATTCTTGGGAGTGGATGGAGA	599
TwTPS27a	AGTTATTTTATGATGAAGCCAAAGAGTTCAAGTACAGAACTTAAGAGCCCTTACTGGGGAGATTGGAGATACGAGTATCGATCTGCGGAACAAGTCAACAGCTCTCAAAATTCCTGTTTTGGAGGATGCCAAGAGTGAAGCAAGGAATTTCAATGATTTCTACCAAGAAAGACCTGAAGAGCTCGACTTTGC	799
TwTPS27b	AGTTATTTTATGATGAAGCCAAAGAGTTCAAGTACAGAACTTAAGAGCCCTTACTGGGGAGATTGGAGATACGAGTATCGATCTGCGGAACAAGTCAACAGCTCTCAAAATTCCTGTTTTGGAGGATGCCAAGAGTGAAGCAAGGAATTTCAATGATTTCTACCAAGAAAGACCTGAAGAGCTCGACTTTGC	799
TwTPS27a	TTGAGCTGCCCAAGTTAGATTTCAATCTAGTCCAGCTCTACATATCTGCAGGAGCTGAAGAGCTATCAACTGGTGGGAAAACCTTGGGATTCAAAACAAGTAAAGCTTTACGAGGATCGATTGATCGAGAGCTACTTCTCGACGCAAGGATTACTTTCAAGCCCACTTTTCAAGCCAGAATAGCAGCAACAAG	999
TwTPS27b	TTGAGCTGCCCAAGTTAGATTTCAATCTAGTCCAGCTCTACATATCTGCAGGAGCTGAAGAGCTATCAACTGGTGGGAAAACCTTGGGATTCAAAACAAGTAAAGCTTTACGAGGATCGATTGATCGAGAGCTACTTCTCGACGCAAGGATTACTTTCAAGCCCACTTTTCAAGCCAGAATAGCAGCAACAAG	999
TwTPS27a	TTTATTAACATTGTTAATACCATTGATGACATACATGATTTATTTATGGATCACAAGATGATCTCAAACTCTTTCAGCGCTGTTAAGAGATGGGATTTGGCTGCCATGGAAGAAGCTCCGGATTACATGAAGATATGCTATTTTTCGGATGTACAATCTCGTTAACGAGCTGGCCTATGATGTTTTAATCAATCAAGGCAT	1199
TwTPS27b	TTTATTAACATTGTTAATACCATTGATGACATACATGATTTATTTATGGATCACAAGATGATCTCAAACTCTTTCAGCGCTGTTAAGAGATGGGATTTGGCTGCCATGGAAGAAGCTCCGGATTACATGAAGATATGCTATTTTTCGGATGTACAATCTCGTTAACGAGCTGGCCTATGATGTTTTAATCAATCAAGGCAT	1199
TwTPS27a	TGATGTTTTGCCCTGTCTTAGGGAAGCGTGGACAAGTTCTCGGGAGCAGCTTTTGTAGAATCTCAATGGTGTACACTGGGTATACACCAAGCATGGACGACTACCTGAAAATTTGTTGGATTTCAATAGTGTTCATGGAAGCTTAAACTTCGCTCGAGCCACCAGCAAGGATCAAGATCCCCCATGCTAATACAC	1399
TwTPS27b	TGATGTTTTGCCCTGTCTTAGGGAAGCGTGGACAAGTTCTCGGGAGCAGCTTTTGTAGAATCTCAATGGTGTACACTGGGTATACACCAAGCATGGACGACTACCTGAAAATTTGTTGGATTTCAATAGTGTTCATGGAAGCTTAAACTTCGCTCGAGCCACCAGCAAGGATCAAGATCCCCCATGCTAATACAC	1399
TwTPS27a	CACTCCACTGCTTGGAGATCGCTACTCTACTGGTCTCGCTCAITTTGCTGTTGAATAACGATTTGCAACTTTCACGATGAGAGCAAGCAGGGAGGTGGCAAGTTTTGTCAGTGTATATGGTTGAAAAGGTGATCGCAAGAGCAAGCATGTGATGAGATAAGGGAGTTGATAAAGCATGCATGGAAGATG	1599
TwTPS27b	CACTCCACTGCTTGGAGATCGCTACTCTACTGGTCTCGCTCAITTTGCTGTTGAATAACGATTTGCAACTTTCACGATGAGAGCAAGCAGGGAGGTGGCAAGTTTTGTCAGTGTATATGGTTGAAAAGGTGATCGCAAGAGCAAGCATGTGATGAGATAAGGGAGTTGATAAAGCATGCATGGAAGATG	1599
TwTPS27a	TTGAATACAGAGAGAAGGAGAAGTGAATCCACCATTAATGGTGAAGATGATGATGGACACCAAGCTTCCCAATGCCCTACACAGCAAGTGTGATGTTCCGGGTAGCCATCGAATTGACCAAGATGTCAATGCTCCTTGTATCTTTCCGCAATCTCTATTAG	1770
TwTPS27b	TTGAATACAGAGAGAAGGAGAAGTGAATCCACCATTAATGGTGAAGATGATGATGGACACCAAGCTTCCCAATGCCCTACACAGCAAGTGTGATGTTCCGGGTAGCCATCGAATTGACCAAGATGTCAATGCTCCTTGTATCTTTCCGCAATCTCTATTAG	1770
TwTPS27a	MAEYVWVSLTISHFVIQTGSTALHYSALPETRTRKHCHSSRPFASINSNSLQMNQRPLDYRPAIWNPELIDSLNTPYSYQSHGTQLDKLRQDAKRLLASTSDPCLLNHVESMQRLGIAYHFQEEIDVLLNTRIQPYSFDDHDLHTLALRFRILRDNNFISSEVFGKFSREGKFLDLSRDVKLLSLYEASFLGVDG	199
TwTPS27b	MAEYVWVSLTISHFVIQTGSTALHYSALPETRTRKHCHSSRPFASINSNSLQMNQRPLDYRPAIWNPELIDSLNTPYSYQSHGTQLDKLRQDAKRLLASTSDPCLLNHVESMQRLGIAYHFQEEIDVLLNTRIQPYSFDDHDLHTLALRFRILRDNNFISSEVFGKFSREGKFLDLSRDVKLLSLYEASFLGVDG	199
TwTPS27a	EVILDEAREFSSKNLRALLGRLESTSIDVAEQVQSLQIPLFWRMFRVEARNFIDFYQKRDVKSSTLLELAKLDFNLVQSTYQGELELSRWENLGFQKLSFRDRMLQSYFSTHGITFRPQFSKARIAATRFINIVNTIDDIHDYYSQDDLLKLSAVKRWDLAAMEELPDYMKICYFAMYNLVNELAYDVLINQG	399
TwTPS27b	EVILDEAREFSSKNLRALLGRLESTSIDVAEQVQSLQIPLFWRMFRVEARNFIDFYQKRDVKSSTLLELAKLDFNLVQSTYQGELELSRWENLGFQKLSFRDRMLQSYFSTHGITFRPQFSKARIAATRFINIVNTIDDIHDYYSQDDLLKLSAVKRWDLAAMEELPDYMKICYFAMYNLVNELAYDVLINQG	399
TwTPS27a	IDVLPCLRREAWTKFCGAAFVESQWCYTGTPSMDDYLKNCWISIGVHGSINLFARAHQCGSRSPNANTPLHCLELFLYSSVICRLNNDLATFCHESKTGEVSEVRCVMVEKGVSGECACDEIRELIKHWKMLNTERRSIDLPLMVMCMCDTPKLSQCLYCHGDDGFVAIDLTKDVMSSLIFRCHSI	589
TwTPS27b	IDVLPCLRREAWTKFCGAAFVESQWCYTGTPSMDDYLKNCWISIGVHGSINLFARAHQCGSRSPNANTPLHCLELFLYSSVICRLNNDLATFCHESKTGEVSEVRCVMVEKGVSGECACDEIRELIKHWKMLNTERRSIDLPLMVMCMCDTPKLSQCLYCHGDDGFVAIDLTKDVMSSLIFRCHSI	589

Figure S3. The full-length CDSs and protein sequences alignment between *TwTPS27a* and *TwTPS27b*.

TwIPS27a	ATGGCACC	ATGGCACC	200
gDNA-27a	ATGGCACC	ATGGCACC	200
TwIPS27a	GCTAATCGACTCCTTGAACACTCCCTACAGC	GCTAATCGACTCCTTGAACACTCCCTACAGC	320
gDNA-27a	GCTAATCGACTCCTTGAACACTCCCTACAGC	GCTAATCGACTCCTTGAACACTCCCTACAGC	400
TwIPS27a	TCATGTTGAGTCGATGCAGCGATTAGGAATCGCTTACCAATTTTCAAGAAGAAATCGACTACTGCTTAATACTCGTATTACAGCCGACTCTCCTGATCATGATCTCCACACACTGCATTGAGGTTCCGCATCCTACGAGACAAATTTCCCATAGCTCAG	TCATGTTGAGTCGATGCAGCGATTAGGAATCGCTTACCAATTTTCAAGAAGAAATCGACTACTGCTTAATACTCGTATTACAGCCGACTCTCCTGATCATGATCTCCACACACTGCATTGAGGTTCCGCATCCTACGAGACAAATTTCCCATAGCTCAG	487
gDNA-27a	TCATGTTGAGTCGATGCAGCGATTAGGAATCGCTTACCAATTTTCAAGAAGAAATCGACTACTGCTTAATACTCGTATTACAGCCGACTCTCCTGATCATGATCTCCACACACTGCATTGAGGTTCCGCATCCTACGAGACAAATTTCCCATAGCTCAG	TCATGTTGAGTCGATGCAGCGATTAGGAATCGCTTACCAATTTTCAAGAAGAAATCGACTACTGCTTAATACTCGTATTACAGCCGACTCTCCTGATCATGATCTCCACACACTGCATTGAGGTTCCGCATCCTACGAGACAAATTTCCCATAGCTCAG	600
TwIPS27a	.....ATGTTGGAAAGTTTCATGAGCAGAGAAGGAAATTCCTGGACGTTTG	.....ATGTTGGAAAGTTTCATGAGCAGAGAAGGAAATTCCTGGACGTTTG	537
gDNA-27a	TCITTTTATTTTTTTTTATTTTATAGATCAGATATATTTAAAGAGACTTTATGCAAGCCTAAGCAAGAAATGCCAAGGAGCCCAAGGCAACANTTTGCTTGTAAATTACTGATTAACTTACTATACAAATTAAGCAGATGTTGGAAAGTTTCATGAGCAGAGAAGGAAATTCCTGGACGTTTG	TCITTTTATTTTTTTTTATTTTATAGATCAGATATATTTAAAGAGACTTTATGCAAGCCTAAGCAAGAAATGCCAAGGAGCCCAAGGCAACANTTTGCTTGTAAATTACTGATTAACTTACTATACAAATTAAGCAGATGTTGGAAAGTTTCATGAGCAGAGAAGGAAATTCCTGGACGTTTG	800
TwIPS27a	AGCAGAGATGTAAGGACTATTGAGTTTGTATGAAGCTTCATTCTGGGAGTGGATGGAGAAGTTATTTAGATGAAGCCAAAGATTCAAGTACGAAAGCTTAAAGCCTTACTGGGAGATTGGAGAGTACGATATCGATGTTGCGGAACAAGTGAAGCAGTCGCTACAAATTCCTCTGTTTGGAGGATGCCAAG	AGCAGAGATGTAAGGACTATTGAGTTTGTATGAAGCTTCATTCTGGGAGTGGATGGAGAAGTTATTTAGATGAAGCCAAAGATTCAAGTACGAAAGCTTAAAGCCTTACTGGGAGATTGGAGAGTACGATATCGATGTTGCGGAACAAGTGAAGCAGTCGCTACAAATTCCTCTGTTTGGAGGATGCCAAG	737
gDNA-27a	AGCAGAGATGTAAGGACTATTGAGTTTGTATGAAGCTTCATTCTGGGAGTGGATGGAGAAGTTATTTAGATGAAGCCAAAGATTCAAGTACGAAAGCTTAAAGCCTTACTGGGAGATTGGAGAGTACGATATCGATGTTGCGGAACAAGTGAAGCAGTCGCTACAAATTCCTCTGTTTGGAGGATGCCAAG	AGCAGAGATGTAAGGACTATTGAGTTTGTATGAAGCTTCATTCTGGGAGTGGATGGAGAAGTTATTTAGATGAAGCCAAAGATTCAAGTACGAAAGCTTAAAGCCTTACTGGGAGATTGGAGAGTACGATATCGATGTTGCGGAACAAGTGAAGCAGTCGCTACAAATTCCTCTGTTTGGAGGATGCCAAG	1000
TwIPS27a	AGTGGAAAGCAAGGAAATTCATTGATTTTACCAAAGAAAGACGTGAAGAGCTCGACTTTGCTTGAGCTTGCACAGTTAGATTTCAATCTAGTCCAGCTACATATCAACAGGAGCTGAAGAGCTTCAAAAGTGGTGGGAAACTTGGGATTCAAAACAAAGTTAAGCTTTACGAGGATCGATTGATCGAGAGCTACT	AGTGGAAAGCAAGGAAATTCATTGATTTTACCAAAGAAAGACGTGAAGAGCTCGACTTTGCTTGAGCTTGCACAGTTAGATTTCAATCTAGTCCAGCTACATATCAACAGGAGCTGAAGAGCTTCAAAAGTGGTGGGAAACTTGGGATTCAAAACAAAGTTAAGCTTTACGAGGATCGATTGATCGAGAGCTACT	937
gDNA-27a	AGTGGAAAGCAAGGAAATTCATTGATTTTACCAAAGAAAGACGTGAAGAGCTCGACTTTGCTTGAGCTTGCACAGTTAGATTTCAATCTAGTCCAGCTACATATCAACAGGAGCTGAAGAGCTTCAAAAGTGGTGGGAAACTTGGGATTCAAAACAAAGTTAAGCTTTACGAGGATCGATTGATCGAGAGCTACT	AGTGGAAAGCAAGGAAATTCATTGATTTTACCAAAGAAAGACGTGAAGAGCTCGACTTTGCTTGAGCTTGCACAGTTAGATTTCAATCTAGTCCAGCTACATATCAACAGGAGCTGAAGAGCTTCAAAAGTGGTGGGAAACTTGGGATTCAAAACAAAGTTAAGCTTTACGAGGATCGATTGATCGAGAGCTACT	1200
TwIPS27a	ICTCGACGACAGGATTACTTTCAAGCCCCAGTTTTCCAAAGCCAGAATAGCAGCAACAAGTTTATTAACATTTGTAATACCATTGATGACATACATGATTATTTGGATCACAAGATGATCTCAAACCTTTTGATAGCGCTGTTAAGAG	ICTCGACGACAGGATTACTTTCAAGCCCCAGTTTTCCAAAGCCAGAATAGCAGCAACAAGTTTATTAACATTTGTAATACCATTGATGACATACATGATTATTTGGATCACAAGATGATCTCAAACCTTTTGATAGCGCTGTTAAGAG	1088
gDNA-27a	ICTCGACGACAGGATTACTTTCAAGCCCCAGTTTTCCAAAGCCAGAATAGCAGCAACAAGTTTATTAACATTTGTAATACCATTGATGACATACATGATTATTTGGATCACAAGATGATCTCAAACCTTTTGATAGCGCTGTTAAGAG	ICTCGACGACAGGATTACTTTCAAGCCCCAGTTTTCCAAAGCCAGAATAGCAGCAACAAGTTTATTAACATTTGTAATACCATTGATGACATACATGATTATTTGGATCACAAGATGATCTCAAACCTTTTGATAGCGCTGTTAAGAG	1400
TwIPS27a	.....ATGGGATTGGCTGCCATGGAAAGACTTCCGGATTACATGAAGATATGCTATTTTGGCATGTACAATCTCGTTAACGAGCTGGCCTATGATGTTTTAATCAATCAAGGCATTGATGTTTTGCCCTGTCTTAGGGAAGCC	.....ATGGGATTGGCTGCCATGGAAAGACTTCCGGATTACATGAAGATATGCTATTTTGGCATGTACAATCTCGTTAACGAGCTGGCCTATGATGTTTTAATCAATCAAGGCATTGATGTTTTGCCCTGTCTTAGGGAAGCC	1227
gDNA-27a	AGTGTATGATCGAAGCTTTCCITTTTTGATTGAATTTGCAGATGGGATTGGCTGCCATGGAAAGACTTCCGGATTACATGAAGATATGCTATTTTGGCATGTACAATCTCGTTAACGAGCTGGCCTATGATGTTTTAATCAATCAAGGCATTGATGTTTTGCCCTGTCTTAGGGAAGCC	AGTGTATGATCGAAGCTTTCCITTTTTGATTGAATTTGCAGATGGGATTGGCTGCCATGGAAAGACTTCCGGATTACATGAAGATATGCTATTTTGGCATGTACAATCTCGTTAACGAGCTGGCCTATGATGTTTTAATCAATCAAGGCATTGATGTTTTGCCCTGTCTTAGGGAAGCC	1600
TwIPS27a	.....	.....	1227
gDNA-27a	ATCATGTTAATATATACTTGATGGTGTGTTTACCATTGTGTTTGCACCTTCAAACCTCTCAAATGCACTGCTTTTGGTGTAACTACCCGCACTGCGATGAGTTGCAAGCTGAGGCTGATAGGAGCTGCTCCCACTCCAAACGTAATGCTATTGACCGCATTTTCGATATTAACACAGAGATTTTTCCCAATTTTGT	ATCATGTTAATATATACTTGATGGTGTGTTTACCATTGTGTTTGCACCTTCAAACCTCTCAAATGCACTGCTTTTGGTGTAACTACCCGCACTGCGATGAGTTGCAAGCTGAGGCTGATAGGAGCTGCTCCCACTCCAAACGTAATGCTATTGACCGCATTTTCGATATTAACACAGAGATTTTTCCCAATTTTGT	1800
TwIPS27a	.....	.....	1227
gDNA-27a	TCTCAATCAATTTTATTTTAAATATATTTCTTACGAAATAAATGATTTGAATGAAGATATCTAATTTTATCCTCATTGACAAAGTATTCTTAGTGACGTGTCAAAAACACTTTTGTACCGCAATTCACCTCACTAGAGTTTCAAACTCGCTGACCTCAATATAGGAGTCAAAACACAACCTTTGTCCCA	TCTCAATCAATTTTATTTTAAATATATTTCTTACGAAATAAATGATTTGAATGAAGATATCTAATTTTATCCTCATTGACAAAGTATTCTTAGTGACGTGTCAAAAACACTTTTGTACCGCAATTCACCTCACTAGAGTTTCAAACTCGCTGACCTCAATATAGGAGTCAAAACACAACCTTTGTCCCA	2000
TwIPS27a	.....TGGACAAGTTCTCGGAGCAGCTTTTGTAGAATCTCAATGGTGTACTACTGGGTATACCAAGCATGGACGACTACCTGAAAAATTTGTTGGATTCAATAGGTGTTTCATGGAAGCTTAAACTTCGCTCGAGCGCACCAGCAAGGATCAAGAT	.....TGGACAAGTTCTCGGAGCAGCTTTTGTAGAATCTCAATGGTGTACTACTGGGTATACCAAGCATGGACGACTACCTGAAAAATTTGTTGGATTCAATAGGTGTTTCATGGAAGCTTAAACTTCGCTCGAGCGCACCAGCAAGGATCAAGAT	1381
gDNA-27a	AACAGTCTATGTTAAACTATTGGTAACCAAGACCTTGTGGATGCAGTGGACAAGTTCTCGGAGCAGCTTTTGTAGAATCTCAATGGTGTACTACTGGGTATACCAAGCATGGACGACTACCTGAAAAATTTGTTGGATTCAATAGGTGTTTCATGGAAGCTTAAACTTCGCTCGAGCGCACCAGCAAGGATCAAGAT	AACAGTCTATGTTAAACTATTGGTAACCAAGACCTTGTGGATGCAGTGGACAAGTTCTCGGAGCAGCTTTTGTAGAATCTCAATGGTGTACTACTGGGTATACCAAGCATGGACGACTACCTGAAAAATTTGTTGGATTCAATAGGTGTTTCATGGAAGCTTAAACTTCGCTCGAGCGCACCAGCAAGGATCAAGAT	2200
TwIPS27a	CCCCATAGCTAATACACCCTCCACTGCTTGAAGATCCGCTACTCTACTGGTCTGCTCGCTCATTGTGCGTTTGAATAACGATTGGCAACTTTCCAG	CCCCATAGCTAATACACCCTCCACTGCTTGAAGATCCGCTACTCTACTGGTCTGCTCGCTCATTGTGCGTTTGAATAACGATTGGCAACTTTCCAG	1494
gDNA-27a	CCCCATAGCTAATACACCCTCCACTGCTTGAAGATCCGCTACTCTACTGGTCTGCTCGCTCATTGTGCGTTTGAATAACGATTGGCAACTTTCCAG	CCCCATAGCTAATACACCCTCCACTGCTTGAAGATCCGCTACTCTACTGGTCTGCTCGCTCATTGTGCGTTTGAATAACGATTGGCAACTTTCCAG	2400
TwIPS27a	GGGAGTGGTAACTTTTTCAGTGTATATGGTTGAAAAGGTGTATCGCAAGAGCAAGCATGTGATGAGATAAGGGAGTTGATAAAGCATGCATGGAAGATGTTGAATACAGAGAGGAGGAAAGTATCTCCACCATTAAATGGTGGAAATGTGTATGGACACCAAAAGCTTTCCCAATGCCCTTACCAGCATGG	GGGAGTGGTAACTTTTTCAGTGTATATGGTTGAAAAGGTGTATCGCAAGAGCAAGCATGTGATGAGATAAGGGAGTTGATAAAGCATGCATGGAAGATGTTGAATACAGAGAGGAGGAAAGTATCTCCACCATTAAATGGTGGAAATGTGTATGGACACCAAAAGCTTTCCCAATGCCCTTACCAGCATGG	1694
gDNA-27a	GGGAGTGGTAACTTTTTCAGTGTATATGGTTGAAAAGGTGTATCGCAAGAGCAAGCATGTGATGAGATAAGGGAGTTGATAAAGCATGCATGGAAGATGTTGAATACAGAGAGGAGGAAAGTATCTCCACCATTAAATGGTGGAAATGTGTATGGACACCAAAAGCTTTCCCAATGCCCTTACCAGCATGG	GGGAGTGGTAACTTTTTCAGTGTATATGGTTGAAAAGGTGTATCGCAAGAGCAAGCATGTGATGAGATAAGGGAGTTGATAAAGCATGCATGGAAGATGTTGAATACAGAGAGGAGGAAAGTATCTCCACCATTAAATGGTGGAAATGTGTATGGACACCAAAAGCTTTCCCAATGCCCTTACCAGCATGG	2600
TwIPS27a	TGATGGTTTCGGGGTAGCCATCGATTGACCAAAAGATGTCATGTCCCTTGATCTTTGCCCCAATCCCTATTTA	TGATGGTTTCGGGGTAGCCATCGATTGACCAAAAGATGTCATGTCCCTTGATCTTTGCCCCAATCCCTATTTA	1769
gDNA-27a	TGATGGTTTCGGGGTAGCCATCGATTGACCAAAAGATGTCATGTCCCTTGATCTTTGCCCCAATCCCTATTTA	TGATGGTTTCGGGGTAGCCATCGATTGACCAAAAGATGTCATGTCCCTTGATCTTTGCCCCAATCCCTATTTA	2675

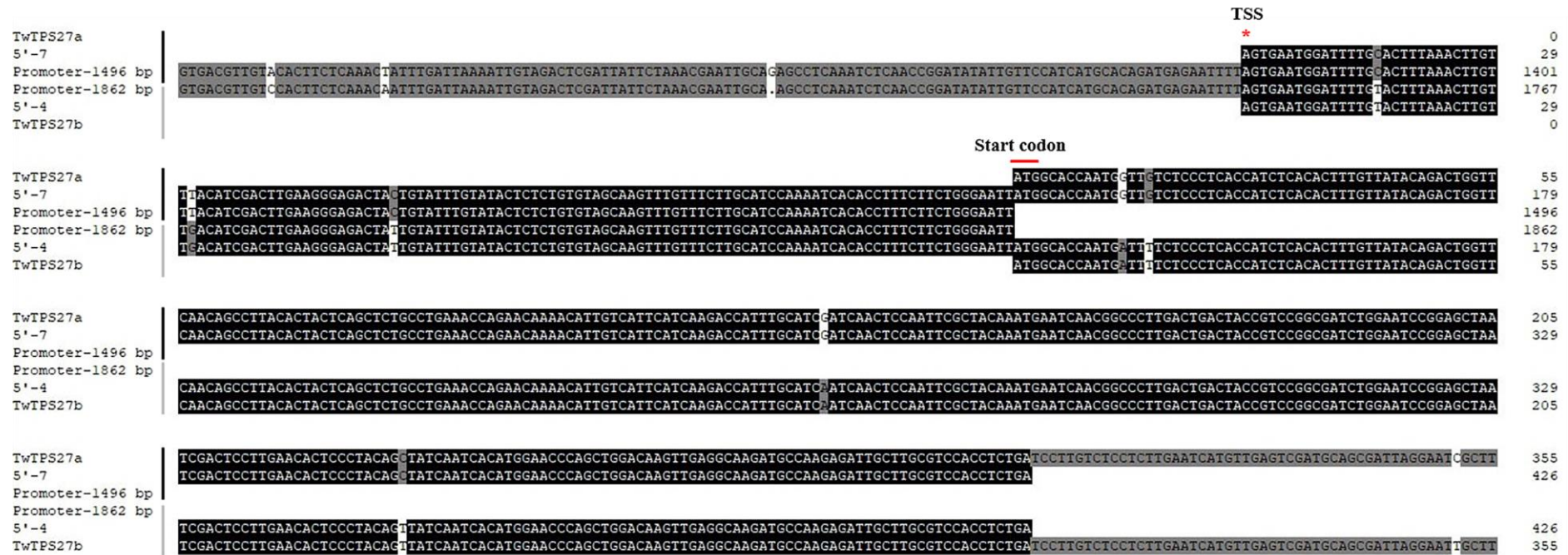
Figure S4. Sequence alignment between the full-length CDS and gDNA of *TwIPS27a*.

TwTPS27b	ATGGCACC	200
gDNA-27b	ATGGCACC	200
TwTPS27b	GCTAATCGACTCCCTTGAACACTCCCTACAGT	318
gDNA-27b	GCTAATCGACTCCCTTGAACACTCCCTACAGT	400
TwTPS27b	AATCATGTTGAGTCGATGCGAGGATTAGGAATTCCTACCAATTTCAAGAGAAATCGACTACTTGCCTAATCTGCTATTCAAGCCGCTACTCTGATGATCATGATCTCCACRCACTGCTTGGAGTCCGCTACTACGAGACAACATTTCCCATTAGCTCAG	487
gDNA-27b	AATCATGTTGAGTCGATGCGAGGATTAGGAATTCCTACCAATTTCAAGAGAAATCGACTACTTGCCTAATCTGCTATTCAAGCCGCTACTCTGATGATCATGATCTCCACRCACTGCTTGGAGTCCGCTACTACGAGACAACATTTCCCATTAGCTCAG	600
TwTPS27b	ATGTGTTTGGAAAGTTCATGAGCAGAGAAGGAAATTCCTGGACAGTTTGAG	539
gDNA-27b	ATGTGTTTGGAAAGTTCATGAGCAGAGAAGGAAATTCCTGGACAGTTTGAG	800
TwTPS27b	CAGAGATGTAAGGACTATTGAGTTTGTATGAAGCTTCACTTGGGAGTGGATGGAGAAGTTATTTAGATGAAGCCAAAGAGTTCAGTAGCAAGAACTTAAGAGCCCTTACTGGGGAGATTGGAGAGTACGAGTATCGATGTCGCGGAACAAGTAAAGCAGTCACTGCAAAATCCCTGTTTTGGAGGATGCCAAGAG	739
gDNA-27b	CAGAGATGTAAGGACTATTGAGTTTGTATGAAGCTTCACTTGGGAGTGGATGGAGAAGTTATTTAGATGAAGCCAAAGAGTTCAGTAGCAAGAACTTAAGAGCCCTTACTGGGGAGATTGGAGAGTACGAGTATCGATGTCGCGGAACAAGTAAAGCAGTCACTGCAAAATCCCTGTTTTGGAGGATGCCAAGAG	1000
TwTPS27b	TGGAAGCAAGGAATTCATTGATTTCTACCAGAAGAAGACGCGAAGAGCTCGACTTTCCTTGGAGTGGATGGAGAAGTTATTTAGATGAAGCCAAAGAGTTCAGTAGCAAGAACTTAAGAGCCCTTACTGGGGAGATTGGAGAGTACGAGTATCGATGTCGCGGAACAAGTAAAGCAGTCACTGCAAAATCCCTGTTTTGGAGGATGCCAAGAG	939
gDNA-27b	TGGAAGCAAGGAATTCATTGATTTCTACCAGAAGAAGACGCGAAGAGCTCGACTTTCCTTGGAGTGGATGGAGAAGTTATTTAGATGAAGCCAAAGAGTTCAGTAGCAAGAACTTAAGAGCCCTTACTGGGGAGATTGGAGAGTACGAGTATCGATGTCGCGGAACAAGTAAAGCAGTCACTGCAAAATCCCTGTTTTGGAGGATGCCAAGAG	1200
TwTPS27b	TCGACGATAGGGATTACTTTCAAGCCCAAGTATTAACCAATGTTAATACCAATGATGACATACATGATTTATGATCAACAGATGATCTCAAACTCTTTAACAGCCGCTGTTAAGAG	1088
gDNA-27b	TCGACGATAGGGATTACTTTCAAGCCCAAGTATTAACCAATGTTAATACCAATGATGACATACATGATTTATGATCAACAGATGATCTCAAACTCTTTAACAGCCGCTGTTAAGAG	1400
TwTPS27b	ATGGGATTGGCTGCCATGGAAGAACTTCCGGATTACATGAAGATATGCTATTTTGGCATGACAACTCCTTAAACGAGCTGGCCTATGATGTTTTAATCAATCAGGGCATTGATGTTTTGCCCTGCTTAGGGAAGCG	1227
gDNA-27b	ATGGGATTGGCTGCCATGGAAGAACTTCCGGATTACATGAAGATATGCTATTTTGGCATGACAACTCCTTAAACGAGCTGGCCTATGATGTTTTAATCAATCAGGGCATTGATGTTTTGCCCTGCTTAGGGAAGCG	1600
TwTPS27b	CATTATGTTAATATATACTGATGGTGGCTTTGACCGTGTGTTTGGCCCTTCAACCGCTCAAAGACATGCTTTTGGTGTGAAGTATGCTATTTTGGCATGACAACTCCTTAAACGAGCTGGCCTATGATGTTTTAATCAATCAGGGCATTGATGTTTTGCCCTGCTTAGGGAAGCG	1227
gDNA-27b	CATTATGTTAATATATACTGATGGTGGCTTTGACCGTGTGTTTGGCCCTTCAACCGCTCAAAGACATGCTTTTGGTGTGAAGTATGCTATTTTGGCATGACAACTCCTTAAACGAGCTGGCCTATGATGTTTTAATCAATCAGGGCATTGATGTTTTGCCCTGCTTAGGGAAGCG	1800
TwTPS27b	ATCCTCAATAAATTTTATTTTAAATATATTTTACGAAAAAATGATTTGAATGAAAAATATCTAATTTTACCCTCATTGACAAAGTATTTAGTAACTGTCAAAACACTTTTATCACCACACTCACCTCCTAGAGTTTCAAACTCGCTTGACCTCCTACAGGAGGTCAAAACACACTTGCTCCC	1227
gDNA-27b	ATCCTCAATAAATTTTATTTTAAATATATTTTACGAAAAAATGATTTGAATGAAAAATATCTAATTTTACCCTCATTGACAAAGTATTTAGTAACTGTCAAAACACTTTTATCACCACACTCACCTCCTAGAGTTTCAAACTCGCTTGACCTCCTACAGGAGGTCAAAACACACTTGCTCCC	2000
TwTPS27b	TGGACAAAGTTCGCGGAGCAGCTTTGTAGAATCTCAATGGTGTACACTGGGTATACACCAAGCATGGAGACTACCTGAAAAATTTGTTGATTTCAATAGGTGTTCAIGGAAGCTTAAACTTCGCTCGAGCGCACCCAGGATCAAGA	1380
gDNA-27b	TGGACAAAGTTCGCGGAGCAGCTTTGTAGAATCTCAATGGTGTACACTGGGTATACACCAAGCATGGAGACTACCTGAAAAATTTGTTGATTTCAATAGGTGTTCAIGGAAGCTTAAACTTCGCTCGAGCGCACCCAGGATCAAGA	2200
TwTPS27b	TCGCCATGGCTAATACCACTCCACTGCTTGGAAAGTACAGTACTACTGGTTCGCTGCTCATTGTCGTTTGAATAACGATTTGGCAACTTTCAG	1493
gDNA-27b	TCGCCATGGCTAATACCACTCCACTGCTTGGAAAGTACAGTACTACTGGTTCGCTGCTCATTGTCGTTTGAATAACGATTTGGCAACTTTCAG	2400
TwTPS27b	AGGGAGGTGGCAAGTTTGTCAACTGTTATATGTTGAAAAAGTGTATCGCAAGACAAACATGATGATGATGATAGGGAGTTGATAAAGCATGATGGAAGTGTGTAATACGAGAGAGGAGAGTGTATCCACCATTAAATGCTGGAATGTGTTGGACACACCAAGCTTTCCCAATGCCTTACCAGCAGC	1693
gDNA-27b	AGGGAGGTGGCAAGTTTGTCAACTGTTATATGTTGAAAAAGTGTATCGCAAGACAAACATGATGATGATGATAGGGAGTTGATAAAGCATGATGGAAGTGTGTAATACGAGAGAGGAGAGTGTATCCACCATTAAATGCTGGAATGTGTTGGACACACCAAGCTTTCCCAATGCCTTACCAGCAGC	2600
TwTPS27b	GTGATGGATTGGGGTAGCCATCGAGTTGACCAAGATGTCATGTCCTCCTTGTATCTTTCGCCAATCTCTATTTA	1769
gDNA-27b	GTGATGGATTGGGGTAGCCATCGAGTTGACCAAGATGTCATGTCCTCCTTGTATCTTTCGCCAATCTCTATTTA	2676

Figure S5. Sequence alignment between the CDS and gDNA of *TwTPS27b*.



**Figure S6.** Sequence alignment between 5'/3'-RACE sequences and CDSs of *TwTPS27ab*. The primers used for 2<sup>nd</sup> round 5'/3'-RACE PCR are marked with two straight lines. The start codon (ATG) and stop codon (TAG) are marked with a single line.



**Figure S7.** Sequence alignment for the determination of the *TwIPS27a* and *TwIPS27b* promoters. The 5'-7 and 5'-4 represent the 5'-RACE sequences of *TwIPS27a* and *TwIPS27b* from 5'-RACE assays, respectively. The TwIPS27a and TwIPS27b represent the coding sequences of *TwIPS27a* and *TwIPS27b*, respectively. The red asterisk represents the transcription start site (TSS). The start codons (ATGs) of *TwIPS27a/b* are marked with a red sigle line. After sequences alignment, the 1496 bp promoter sequence belongs to the *TwIPS27a* gene, whereas the 1862 bp promoter sequence belongs to the *TwIPS27b* gene.

27aPro-1239bp TAAACATAAGTCTGCTGAAATTTATTTGGAAAAAATTTTGTATATGAAACATCTCTTAAAGGTACACTTTCTATCATCTTCTACCTCAAGCCCTCTCTTTTAAACTAACATCTCTCTCTCTCTACCTCACGCTCTCTCCCT  
 27bPro-1212bp TAAACATAAGTCTGCTGAAATTTATTTGGAAAAAATTTTGTATATGAAACATCTCTTAAAGGTACACTTTCTATCATCTTCTACCTCAAGCCCTCTCTTTTAAACTAACATCTCTCTCTCTCTACCTCACATCTCTTCCCT

27aPro-1239bp CTTCTATATTAGATTCTCACCTTCTCTCTAAGATTTCGACCTCTCTTCAATCTTCTTTTATGTACATGGGCAAGCTTAAACGGGATCCGGAGGCAAATTTTATAGGGTTATCTATTAATTATATTATTGAAAGTATAAAAAA  
 27bPro-1212bp CTTCTATATTAGATTCTC.....TCTCTTCAATCTTCTTTTATGTACATGGGCAAGCTTAAACGGGATCCGGAGGCAAATTTTATAGGGTTATCTATTAATTATATTATTGAAAGTATAAAAAA.

27aPro-1239bp ATATTAAATCAAATTTTATAAAATATGATAAGTAATAATTGTCACATGTCATCTTGGTTTAAATCATGATTTTTCATATGATGGACGTTTAAATGAATATTGAGGAGGCTTTTATATAAATTATCTATATATAAGGTTATTAAAA  
 27bPro-1212bp TACTTAAATCAAATTTTATAAAATATGATAAGTAATAATTGTCACATGTTTCTTGGTTTAAATCATGATTTTTCATATGATGGACGTTTAAATGAATATTGAGGAGGCTTTTATATAAATTATCTATATATAAGGTTATTAAAA

27aPro-1239bp ACAATTTGAGTAGTTTCGCCCTGGCAGCGGTTAAAGATGAATTTGAGTCAAATTTGATGTGTTGACGTTCTTTTCATCCAATATGTTGAATGACTTGTGGATGAAAAGTATTAGATGATCCATTTTTCAAATTTCTCTTTCT  
 27bPro-1212bp ACAATTTGAGTAGTTTCGCCCTGGCAGCGGTTAAAGATGAATTTGAGTCAAATTTGATGTGTTGACGTTCTTTTCATCCAATATGTTGAATGACTTGTGGATGAAAAGTATTAGATGATCCATTTTTCAAATTTCTCTTTCT

27aPro-1239bp TCCGCAATGATTCTTAACTTTAAGACTAATTGCCACAATGAGGTTTGAATGTAACGTTTTTCAACAATGTCCACCATCTTACTATAACTTAAGATGACAAGATTTTCAGATTGTTTATACCTATAACCTTGCTAGGACAAATAGAGAA  
 27bPro-1212bp TCCGCAATGATTCTTAACTTTAAGACTAATTGCCACAATGAGGTTTGAATGTAACGTTTTTCAACAATGTCCACCATCTTACTATAACTTAAGATGACAAGATTTTCAGATTGTTTATACCTATAACCTTGCTAGGACAAATAGAGAA

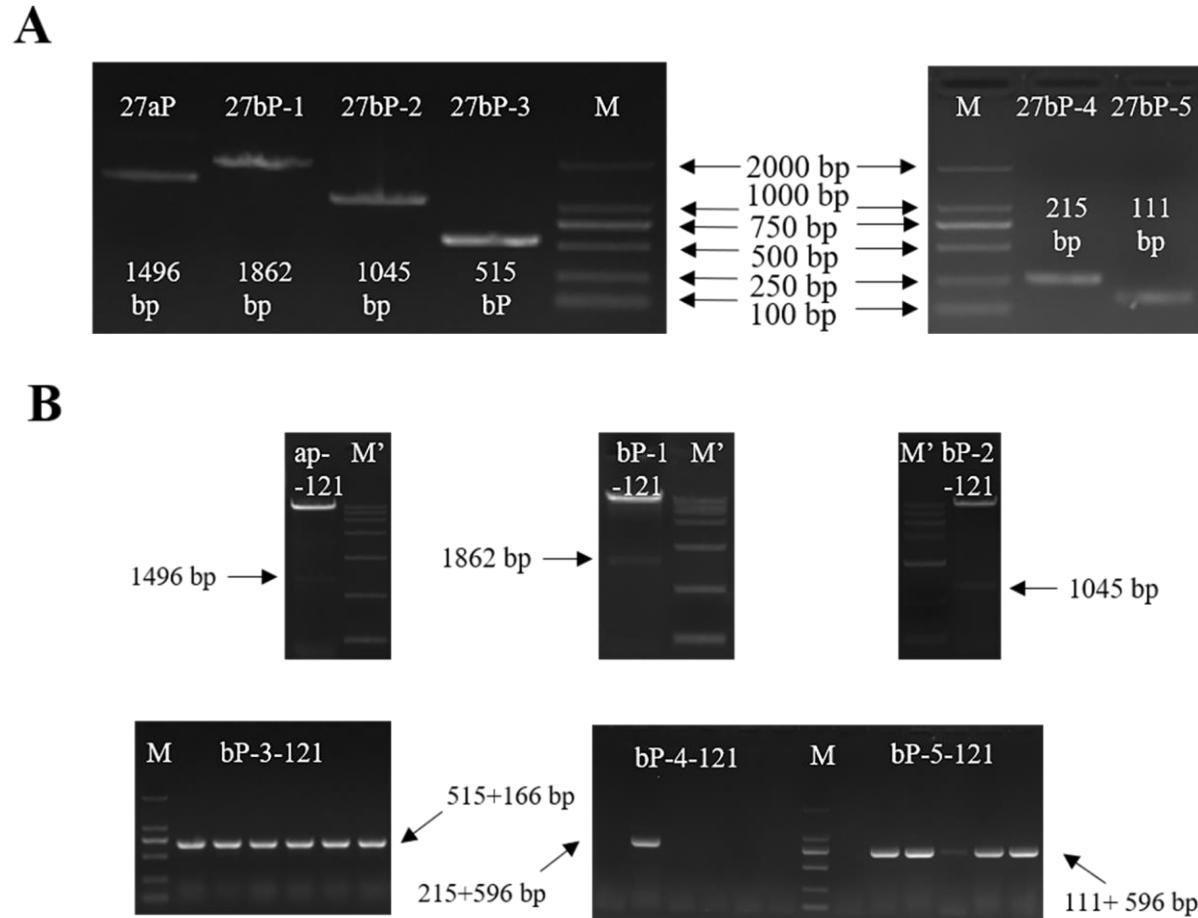
27aPro-1239bp CAATATCATTTCGCATACATTGTTATAATAAGGATTCAAATGGTCTAATTTGTCATGGTTGGTCAATTTACGGAATCTACAAGTCAATCTGCTAGCTAGTCTTTCAAACCAAATGTTTACCTACCTTCTAAGGATATACGGGTGGGA  
 27bPro-1212bp CAATATCATTTCGCATACATTGTTATAATAAGGATTCAAATGGTCTAATTTGTCATGGTTGGTCAATTTACGGAATCTACAAGTCAATCTGCTAGCTAGTCTTTCAAACCAAATGTTTACCTACCTTCTAAGGATATACGGGTGGGA

27aPro-1239bp TTTGGAGGCTCCCAATTCCCTAGAGTTTACAATTCATGTAATATGGAGAAAAAGTCAAGTAAGTATTAAAAATGAAAAATGAAGTGTGGTGTGACGTTGTCACCTTCTCAAACATTGATTAAAAATGTAGACTCGATTATTC  
 27bPro-1212bp TTTGGAGGCTCCCAATTCCCTAGAGTTTACAATTCATGTAATATGGAGAAAAAGTCAAGTAAGTATTAAAAATGAAAAATGAAGTGTGGTGTGACGTTGTCACCTTCTCAAACATTGATTAAAAATGTAGACTCGATTATTC

27aPro-1239bp TAAACGAATTGCAAGCCTCAAATCTCAACCGGATATATTGTTCCATCATGCACAGATGAGAATTTTGTGAATGGATTTTGCACCTTAAACTTGTTCACATCGACTTGAAGGGAGACTATGTTATTGTATACTCTCTGTGTAGCAAGT  
 27bPro-1212bp TAAACGAATTGCAAGCCTCAAATCTCAACCGGATATATTGTTCCATCATGCACAGATGAGAATTTTGTGAATGGATTTTGCACCTTAAACTTGTTCACATCGACTTGAAGGGAGACTATGTTATTGTATACTCTCTGTGTAGCAAGT

27aPro-1239bp TTGTTTCTTGATCCAAAATCACACCTTTCTTCTGGGAAT  
 27bPro-1212bp TTGTTTCTTGATCCAAAATCACACCTTTCTTCTGGGAAT

**Figure S8.** Sequence alignment between *TwTPS27a* promoter from -1115 to +124 bp and *TwTPS27b* promoter from -1088 to +124 bp. The two sequences showed 93.0 % nucleotide identity.



**Figure S9.** Verification of various promoter::GUS vectors. The vectors of aP-121, bP-1-121 and bP-2-121 were verified by double digestion with the restriction enzymes of *Hind* III and *Xba* I. The vector of bP-3-121 was verified by the primers of M13R-4921: RCAGGAAACAGCTATGACC and 121-GUS-R: CAACGCTGATCAATTCCACAG. The vectors of bP-4-121 and bP-5-121 were verified by the primers of 121-cx-F4703: TCGCCCTTTTGTCTTTGGCCCAATAC and 121-cx-R6157: TCACTTCCTGATTATTGACCCACACTTTG.



TwIPS27	.....ATGG	4
comp34029	CTCTGTGTAGCAAGTTTGTTCCTTGCATCCAAAATCACACCTTTCTTCTGGGAATTATGG	120
comp37092	CTCTGTGTAGCAAGTTTGTTCCTTGCATCCAAAATCACACCTTTCTTCTGGGAATTATGG	107
<b><i>TwIPS27</i>-UTR-F</b>		
TwIPS27	CACCACTGGTTCCTCCCTCACCATCTCACACTTTGTTATACAGACTGGTTC AACAGCCT	64
comp34029	CACCACTGGTTCCTCCCTCACCATCTCACACTTTGTTATACAGACTGGTTC AACAGCCT	180
comp37092	CACCACTGGTTCCTCCCTCACCATCTCACACTTTGTTATACAGACTGGTTC AACAGCCT	167
TwIPS27	TGGTTTCGGGGTAGCCATCGAATTGACCAAAGATGTCATGTCCTCCTTGATCTTTCGCCA	1757
comp27356	TGGTTTCGGGGTAGCCATCGAATTGACCAAAGATGTCATGTCCTCCTTGATCTTTCGCCA	164
comp37092	TGGTTTCGGGGTAGCCATCGAATTGACCAAAGATGTCATGTCCTCCTTGATCTTTCGCCA	1860
TwIPS27	AATCCCAATTTAG.....	1770
comp27356	AATCCCAATTTAGTGACCAATTAGCAAATAAGTCGTTTGGATTTTCGATCTTTGGCAATAT	224
comp37092	AATCCCAATTTAGTGACCAATTAGCAAATAAGTAGTTTGGACATC AATCTTTGGCAATAT	1920
<b><i>TwIPS27</i>-UTR-R</b>		

**Figure S10.** Primers designed for cloning the CDSs and gDNA sequences of *TwIPS27a/b*. The primers were designed in the 5'/3'-untranslated region (5'/3'-UTR) of the candidate genes. Single line represents the start/stop codons. The black boxes represent the sense and antisense primers.