

Table S1. DNA sequences of primers used in this study.

Gene	Primer (5'→ 3')		Note
	Forward	Reverse	
<i>PpTST1</i>	TTTACATCTCTAGGACTGGCAGGA	CGTTGGAATAGGAATCCAGATTCTGCA	dCAPS
<i>TEF2</i>	GGTGTGACGATGAAGAGTGATG	TGAAGGAGAGGGAAGGTGAAAG	RT-qPCR
<i>PpTST1</i>	CATGGATATCTCTGGTAGAAGGACG	CAGAGGCCACGTACCCTTGTC	RT-qPCR
<i>PpTST1</i>	AATTACATTTACAATTACGATGAGGGGAGCTGT GATGGTGGCTATTG	CTCCTCGCCCTTGCCCATCTCACTTTTGGCTGC GGCAAC	Subcellular location
<i>PpTST1</i>	GTGAGTAAGGTTACCGAATTCCTGATCGTCAG CAAGTTCA	CGTGAGCTCGGTACCGGATCCATTAAATACTC TTCCACAGT	VIGS

Table S2. Identification of *Cis*-elements in 2kb upstream region of *PpTST1*.

<i>Cis</i> - Element	Motif	Position	Function
AAGAA-motif	GAAAGAA	-1010(+), -1432(-)	Unknown
AP-1	TGAGTTAG	-1883(+)	Stress response element
ARE	AAACCA	-23(+), -90(+), -1054(-), -1243(+)	<i>Cis</i> -acting regulatory element essential for the anaerobic induction
as-1	TGACG	-1372(+)	SA-responsive element
Box 4	ATTAAT	-1921(-)	Part of a conserved DNA module involved in light responsiveness
Box III	atCATTTTCA Ct	-71(-)	Protein binding site
CAAT-box	CCAAT/CAAT T/CAAAT	-49(-), -83(+), -125(+), -141(+), -153(+), -176(+), -283(+), -300(-), -312(+), -399(+), -423(+), -506(-), -514(+), -534(+), -543(-), -571(+), -591(+), -600(-), -628(+), -648(+), -723(-), -831(-), -882(+), -897(-), -942(-), -953(+), -998(+), -1029(+), -1048(+), -1280(+), -1462(-), -1497(+), -1513(-), -1534(-), -1798(+), -1968(-)	Common <i>cis</i> -acting element in promoter and enhancer regions
CGTCA-motif	CGTCA	-1372(-)	MeJA-responsive element
GARE-motif	TCTGTTG	-1810(+)	Gibberellin-responsive element
HD-Zip 1	CAAT(A/T)AT TG	-953(+)	Element involved in differentiation of the palisade mesophyll cells
MBS	CAACTG	-1208(-), -1325(-), -1368(-), -1719(-)	MYB binding site involved in drought-inducibility
MYB	CAACAG	-1811(-), -1869(-)	MYB binding site
Myc	TCTCTTA	-1443(+)	Unknown
P-box	CCTTTTG	-1852(+)	Gibberellin-responsive element
STRE	AGGGG	-1782(-)	Stress response element
TATA-box	TATAA	-39(-), -166(-), -250(-)	Core promoter element around -30 of transcription start
TCCC-motif	TCTCCCT	-1828(-)	Part of a light responsive element
TCT-motif	TCTTAC	-1445(+)	Part of a light responsive element
W box	TTGACC	-307(+)	WRKY binding site
WUN-motif	AAATTTCTT	-195(+)	Stress response element

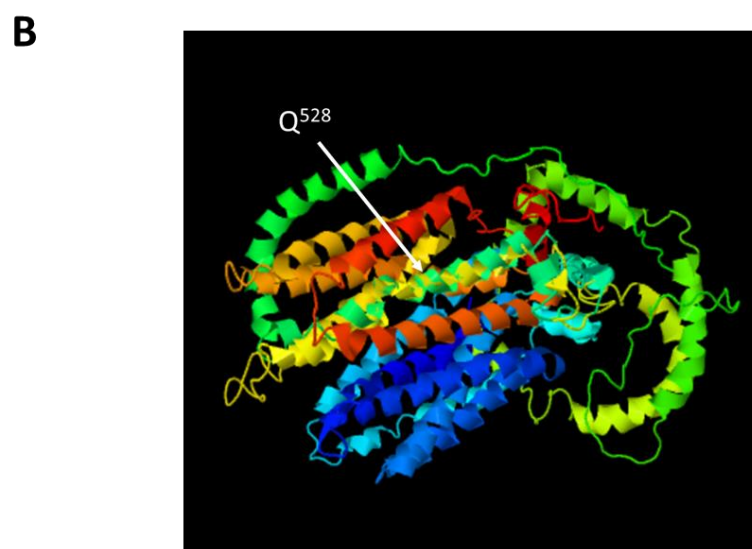
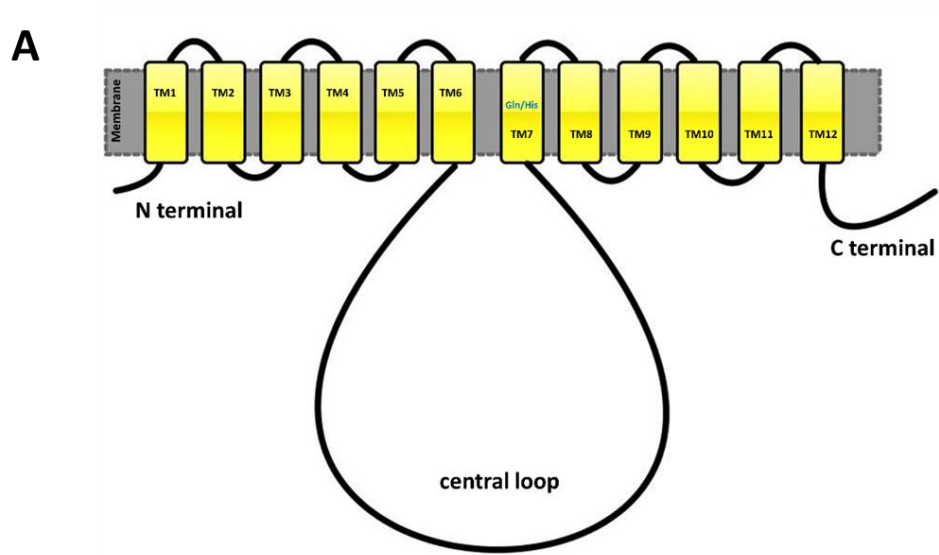


Figure S1. The predicted structure of PpTST1. **(A)**, The predicted schematic topology of PpTST1. TM, transmembrane domain. Blue character Gln/His indicates one amino acid substitution resulting from a G/T SNP. **(B)**, The tertiary structure of PpTST1 predicted using Protein Homology/analogy Recognition Engine V 2.0 [45]. Q⁵²⁸ indicates Gln which could be replaced with His resulting from a G/T SNP.