SUPPLEMENTAL DATA

Supplementary tables

Table S1. Phosphinothricin resistance of F_2 progenies of the *ltpg1* heterozygotes (F_1), which were generated by crossing the *ltpg1* mutant with the wild-type.

Cross[a]	Independent lines	Phosphinothricin resistance		
		[b]PPT^R	[c]PPT^S	Ratio
WT X *ltpg1*	1	82	28	2.9
	4	163	54	3.0
	7	63	21	3.0

[a] The parental genotype (ecotype Columbia background)
[b] PPT^R: Number of phosphinothricin-resistant seedlings
[c] PPT^S : Number of phosphinothricin-sensitive seedlings

Table S2. Oligonucleotide sequences used in this study.

Reactions	Primer name	Sequence information	Annealing Tm for PCR (℃)	Enzyme site
Mutant isolation, RT-PCR and Real-time RT-PCR	LB1	5'-GCC TTT TCA GAA ATG GAT AAA TAG CCT TGC TTC C-3	60	
	AtLTPG-1 cDNA F2	5'-GCC CGG GAT AAT GAA GGG TCT TCA T-3'	58	*Sma*I
	AtLTPG-1 cDNA R2	5'-CGG ATC CTT ACA TCC CTA ATG TGA C-3'	58	*Bam*HI
	actin2 F1	5'-CAT CCA AGC TGT TCT CTC CTT GTA C-3	58	
	actin2 R1	5'-CAG ACA CTG TAC TTC CTT TCA GGT G-3'	58	
	actin2 F1 (real-time)	5'-GGT AAC ATT GTG CTC AGT GGT GG-3	58	
	actin2 R1(real-time)	5'-AAC GAC CTT AAT CTT CAT GCT GC-3'	58	
	actin7 F1	5'-CGC GGT TCT TGA GAA GAC CGG TGT GA -3	58	
	actin7 R2	5'-GAG CTT CTC CAG CTA TCG CCA TTA GG-3'	58	
	AtLTPG-1 cDNA F1	5'-CGG ATC CTG ATA ATG AAG GGT CTT CA-3'	58	*Bam*HI
	AtLTPG-1 cDNA R1	5'-CGG ATC CAC ATC CCT AAT GTG ACA TG-3'	58	*Bam*HI
Promoter analysis, and Complementation	AtLTPG-1 GUS F1	5'-CTC TAG AAG GAT ACG TAG ACA ATT GGT AG-3'	58	*Xba*I
	AtLTPG-1 GUS R1	5'-GCC CGG GGC TTG TTG AAG ATC TTG TTT G-3'	58	*Sma*I
	AtLTPG-1 R3	5'-ACC CGG GGG ACT TGG GAT TGG CTG AGG TT-3'	58-60	*Sma*I
	NPTII F	5'-GGG GCA GGA TCT CCT GTC ATC TC-3'	58	
	NPTII R	5'-GCG CTG CGA ATC GGG AGC GGC G-3'	58	
Subcellular localization	YFP-F1	5'-GGC CGG CCT GGA GGT GGA GGT GGA GCT GTG AGC AAG GGC-3'	52	*Fse*I
	YFP-R1	5'-GGC CCC AGC GGC CGC AGC AGC ACC AGC AGG GTC CTT GTA CAG CTC-3'	52	*Sfi*I
	AtLTPG-1 P1	5'-TCC ACC TCC ACC TCC AGG CCG GCC TGA AGC TGA TCC TCC CTT-3'	64-58	
	AtLTPG-1 P2	5'-GGT GCT GCT GCG GCC GCT GGG GCC GCA AAG GAT GGT CAC GCA-3'	64-58	

Supplementary figures

Figure S1. Expression of the *LTPG1* transcripts in various tissues (A) and 10-day-old seedlings after exogenous applications of abiotic stresses and the stress hormone, ABA (B). R, roots; S, 10-day-old seedlings; L, rosette leaves; C, cauline leaves; F, flowers; Si, siliques. (B) Ten-day-old Arabidopsis seedlings were incubated in liquid MS medium supplemented with H_2O (control), 200 mM NaCl, 200 mM mannitol, 20% PEG or 1 μM ABA for 6 h. Total RNA (0.1 μg) was used for the RT-PCR analysis. The *actin7* (At5g09810) gene was used to determine the quantity and quality of the cDNAs. The *rd29A* gene (At5g52310) was used as a drought stress-inducible marker.

Figure S2. Complementation of the *ltpg-1* mutants by introduction of the *LTPG1* genomic clone. (A) Schematic diagram of binary vectors containing the *LTPG1* genomic DNA. The resultant binary vector was transformed into the *ltpg1* mutants. (B) Chromosomal DNA was isolated from wild-type, *ltpg1* mutants and transgenic *ltpg1* lines and then subjected to PCR. (C) RT-PCR analysis of *LTPG1* transcripts from wild-type, *ltpg1* mutants and transgenic *ltpg1* lines.