Table S1. Primers used in recombinant pYLCRISPR/Cas9 vector construction

Purpose	Primers	Sequence (5'→3')
1st PCR	U-F	CTCCGTTTTACCTGTGGAATCG
	gR-R	CGGAGGAAAATTCCATCCAC
	A5gRT1^{+}	GAGGCAGGTACCCAATTCGGTTTTAGAGCTAGAAAT
	A5AtU3bT1^{-}	CGAATTGGGTACCTGCCTCTGACCAATGTTGCTCC
	A5gRT2^{+}	TGGAGCGCCAGAGTTCTAATGTTTTAGAGCTAGAAAT
	A5AtU3dT2^{-}	ATTAGAACTCTGGCGCTCCATGACCAATGGTGCTTTG
2nd PCR	Pps-GGL	TTCAGAGGTCTCTCTCGACTAGTATGGAATCGGCAGCAAAGG
	Pgs-GG2	AGCGTGGGTCTCGTCAGGGTCCATCCACTCCAAGCTC
	Pps-GG2	TTCAGAGGTCTCTCTGACACTGGAATCGGCAGCAAAGG
	Pgs-GGR	AGCGTGGGTCTCGACCGACGCGTATCCATCCACTCCAAGCTC

The restriction enzyme *Bsa*I site was underlined.

Table S2. Oligonucleotide primers used in mutation detection

Purpose	Primer	Sequence (5'→3')
Transgenic plant identification	Hyg for	CTTGACATTGGGGAGTTTAGCGAGA
	Hyg rev	CCCTTATCTGGGAACTACTCACACA
Mutation detection	ATG5-T1-F	CTCTCCACCAGACTCTCTCT
	ATG5-T1-R	TCCAGTACAATCCACGTACT
	T1 seq	CACACACACACATATATATAGAGAG
	ATG5-T2-F	CTGTGGGACTATGTAGGTTG
	ATG5-T2-R	TTTTGTGTTCTGATGGTGTT
	T2 seq	AGATGTGCGATTGGGTTTTACAATC

Table S3. Sequences of Specific Primers Used for qPCR Analysis

name	accession no.	forward primer (5′ → 3′)	reverse primer (5′ → 3′)
β-actin	NM_001308447	CAGCAGATGTGGATCTCAAA	CTGTGGACAATGGAAGGAC
SlEDS1	NM_001320249	GGAATTGAAGTCAGAGATGAGCTAA	AAAGTTCCAGCAAAAGCAAAAA
SlPAD4	XM_019212160	CCGTGATCAGATGGTAGAAATAATG	CGGCAGAGAAGCCAGAGAGT
SlPR1	NM_001247429	TGGTATTAGCCATATTTCAC	CCAGTTGCCTACAGGATC
SlJAZ1	NM_001247954	CGAGACGGAATTCACTTACAAGA	TGAGCACCTAATCCCAACCAT
SlMYC2	NM_001324483	GGAGGCGAAGACTCTGAACATT	GCTGGCTTTCTACCTCGCTTC
SlLOXD	NM_001320292	CGAACTTGAAAACAGAGCGA	GTAATACTCTCCAGAAAGAACTCCT
SlNPR1	NM_001247629	TGTTTTATGTGGATTGGTGGCT	CTTCTGCTTGATGGGATGACTG
SlATG5	XM_010317407	AAGAGCAACACGGAACGAAGT	TACCACCCATGCAAAAGGAAT

Table S4. Editing type of *slatg5* mutants in T0 generation

CR-ATG5-2 (Biallelic)	Target 1	Reference: ATTGCAGATTTTAGCTCCTCGAATTGGGTACCTGCCTCTTTTAGCACAAAAAGTA Allele1: ATTGCAGATTTTAGCTCCTCCAATTGGGTACCTGCCTCTTTTAGC (substitution) Allele2: ATTGCAGATTTTAGCTCCTC (12-bp del) CTGCCTCTTTT (573-bp del) ATCAC (deletion)
CR-ATG5-3 (Biallelic)	Target 2	Reference:ATATGTCCCAATCTGACCAATTAGAACTCTGGCGCTCCATTATGG Allele1:ATATGTCCCAATCTGACCAA--AGAACTCTGGCGCTCCATTATGG(deletion) Allele2:ATATGTCCCAATCTGACCAATTTCAGCCCCGCCAT (complicated variant)
CR-ATG5-7 (heterozygous)	Target 2	Reference:TGAATATGTCCCAATCTGACCAATTAGAACTCTGGCGCTCCATTATGG Allele1:TGAATATGTCCCAATCTGACCAATTAGAACTCTGGCGCTCCATTATGG (WT) Allele2:TGAATATGTCCCAATCT----------CTGGCGCTCCAT (deletion)

Target sequences are shown in red letters. Deletion is denoted in green. Insertion is expressed with a green letter and substitution is shown in a blue letter. Complex variant regions marked yellow.

Table S5. CRISPR/Cas9-Mediated Mutagenesis and Transmission from T0 to T1 Generation

Transgenic line	T0		T1 mutation segregation				
	Zygosity	Genotype	No. of plants tested	Wt	Biallele	Homozygote	Heterozygote
L2	T1 (Bia)	s1, d585	20	7	8 (s1, d585)	0	3 (wt, s1) 2 (wt, d12)
L3	T2 (Bia)	d1, variant	8	8	0	0	0
L7	T2 (He)	wt, d14	10	3	3 (d14, s1)	0	4 (wt, d14)

d#, the number of bases deleted from the target sequences; s#, the number of bases substituted origin target sequences; wt, wild-type sequence without mutations detected at target sequences.