

```

AtU6-26: -----*-----960-----*-----920-----*-----880-----
Ghu6-9 : ATGTCATTGCTACAAATTGCGAGTAGGCTTTGCAATTAATAACATTAATCCAAACCATTAGATGATGCTTAGTATTIAATATTTATCCTCAGCCCATGATGGCTGAGGCCCTCGAGATCAIAAACCCAG 127
Ghu6-7 : CTTCTAGATTAATCGATGCTCCACCTGCTTTTTCATTTCTTTATGGAAAGGCTTAAAGAGATATGTAAGTACTCATACAGTTTTCACAAAACAAACATTTCTGTTAATCACAACCTTTCTAT 127
Ghu6-1 : ATTATTATTAATAATAAATTAAGTTTGCATTAAGTTATTTTATATAAAAAABAACTATCAIAGAACTCTTTTTCGGAAAATGATTIATGTTTTTCAAATGGIAGTCAATTTIACA 127
Ghu6-4 : ATAGCCATTAATAGTGGTTAATTTTTGAAAACIATTAATATGRTTATTATCATTACTTAAAGGCTCTGGATTTTIATTTATTTTAAAGCTTATGGATGTTAATCTTGTACATTTTAT 127

AtU6-26: -----*-----840-----*-----800-----*-----760-----
Ghu6-9 : TTTAAAAATTTCAGACGCTCAATGCCATTTGGATCAAGCAATCCCFCGAGATTGGTTATTTGAAAGCTTCGGAAAATGGGAAAAGGATGGTGAGCTCGAGAATAAGATCAAGGCTAAGCAAAAAGGA 254
Ghu6-7 : TTTCAGGAACCAIAACTTATACACTTTTACACTAGCTTTIATACCCAGAAACAAACATTTAATGGTACAAATTTIAATTTCCATTAATCAGATGAGTATACGCAAAAACCCCAAAATCTTTAA 254
Ghu6-1 : GCAAAAAGCTTTTTTTCATGACCTAATAATCATTTTCTGTTACCTAATTTATTTCTGTGAAAACAAACAGGAGAATTCGAAAATAATTTCCGTAAGTCAATTTCCATGAAAACAAACACC 254
Ghu6-4 : TTTGCATTGTTTTGAACAATCTCATIACAAGTTIAGTCAGAAITATTAATAATTTCTTCAACAIAATAAATAGGATGACAATTCGGCTTGTAGTGCATTTGAACTCAGGCCCTCCTACATTGACA 254

AtU6-26: -----*-----720-----*-----680-----*-----640-----*
Ghu6-9 : ACTTGCCAAAGTGAGCAATAAGCTCGAGGAGGCAGAAACTCATGGCAGACCCGGGAAACAAAGATGAGCAAAAACAGGAACTTCTGCGTGAGAGGTGTTGACTACGATTGCTCGGTGAGTGT 381
Ghu6-7 : ATCACAATCTCAGCAGGATTAACCAACTATCTTATGCGAGCTTTTCTCAIAGACAAAGAAAGACGGATGATCAAAAACAIATAGTTGACATTTGGCCCAAAAIACTTGAIA 381
Ghu6-1 : CTAATCAATTCATGATATTGATTCCGAGATCAATTCATTAATCTTTCTCAAAAACCAATTTGCAATTAATTCGATTAAATCAATTTGACTGATTGGTCTGATTCCAAIAACCTIATAA 381
Ghu6-4 : AGAATGTTCAATGCCAATCGAGCAATTCATCGGCCTTTTATGTGAATTTACTTCCCTCGTCAIAGTTTTIATAIATATTCATTAAAAATTTTGAACCTTGAGATGAIATTAATGGG 381

AtU6-26: -----*-----600-----*-----560-----*-----520-----*
Ghu6-9 : CTCATCGACCTAGCGAATGGATGCTCTTATGCTATTAGTIACCATTIATATTTCAATTAGAATGCATCACAIATTTGAACIATGTTIATATGATTAATCTCTGTIAAGGAATATCATCAA 508
Ghu6-7 : AGTTGCCATTTGACAACATACATCCACATCTCCATGATCGTTIATTCATTCGTTTACAAIACCTTTTIAATGTTCCAGTCTIAAAAATGAAAAAATAATGAAATGGATGAAATGCTTATA 508
Ghu6-1 : AGCTATAGCTAAAATCTAIACTIATAAATTTCCATAAAGCTAAGAGTTAATTTATTAATAAGTAAAGTATTTGATTAATAAATTTTCTGTTAAATTTTAAATTTTAAATTTTAA 508
Ghu6-4 : AGAATTTIAAACCTTGAATATGAATGTAAAAAGGAACATGAGAATTAATAAATAAATTTAATTAAGATCTTIAATAATCAACAATCAIATAATCGIAGTTCAAATTAATTTAATTTGATCA 508

AtU6-26: -----*-----480-----*-----440-----*-----400-----*
Ghu6-9 : AGGGTATCTGGAACTAACAATCTTTGCTTCCAGATAACGGTTCCAAACATTCGCTACGACCGACTGCCGTAGCAAAAAGAGGCCAATGAATGAAATGAGACCGCTGTAGTTGACGAT 635
Ghu6-7 : GTCCATGAATTTAAAGGAATGCGGTTGAATATTTCCATCGATAACAIACAIATCTGAGIATGTTCCBAIAATAATCAIATTTGGGATTTACCTTTTAAAGCAATTTGATTTGAT 635
Ghu6-1 : ATTATACCTTATGGACACTIATTTACTTCTTCCACCTGGTGTGAAGTTTACTCATTGACGAAATAATTTCTTTIATTTGTTATTTTTTAAATTTIATAAATTAATAAAGATTIACATTTGAT 635
Ghu6-4 : ATAAATTCATCTCATTTGATTTGAATTTAAAACAATAAATTTGAACATAACTACTTGAATGATTTGAGCTGACTATCATTTGAAATGAAAACATGACAGCCAAATTTAACCACTTGA 635

AtU6-26: -----*-----360-----*-----320-----*-----280-----*-----240-----
Ghu6-9 : ATACAGTTTTTTTGGTTATCAGCTTACATTTCTTGAACCGTAGCTTTGTTTTCTTCTTTTAACTTTCCATTCGGAGTTTGTGAICTGTTTCAATAGTTTGTCCAGGATAGAAATGATTAG 210
Ghu6-7 : CTGGCGTTTGTCTTCTGTTCTTTTCATTAATACCAGAAIACCAATATGCATCCCTGTCAATGAAATTTGATAAATGAAATCTTGTGCAIACCTTCCATAAGCTGCAATAGTTTCCAAACA 762
Ghu6-1 : GGTAAIACAATAATTTCCAAGGCAACCCAAATATTTTAAATTTAACCTIACACTGTGGTAAATCAAACTAATAGTAAACCCGATTTGTAATGTGAAGCAATAAGAAAGTACATTTGGTTATA 762
Ghu6-4 : AAAGTTTCAACCAAAAACATCATGAATTTAAACCATTATTTTATTTTAAATGATTTTAAAATAAATGTTGAATTAATAATTTATTAATAAATTTIAGCAATCATATTAACATAAIAA 762
Ghu6-4 : CACAATAACAATTAATAATGACTCAATATGAAGTTGAATAAACACAATTAATAAATTTTTTAGTTAATAAATAAATTTIACCTTTAATTTGATTTGATTTTCTTTATTT 762

AtU6-26: -----*-----200-----*-----160-----*-----120-----
Ghu6-9 : GCAATCGAACCTTCAAGAAATTTGATTAATAAACAATCTTCAATCTTAAAGATATGAAATATCTTCAAAGGCCCTGGGAATCTGAAAGAAGAGAAGCAGGCCATTIATAAGGAAAAGCAATA 337
Ghu6-7 : TTTACTCTGTGCTIACGATTAATCTCTGTIAAGGAATATCGTTCCAAAGAGTCAATCGCGAAATGTAACATCTTTCTCATCCAGGCTGATGAAIATGIAATGGAACCTGCCACTGACCCAGAGT 889
Ghu6-1 : TAATAATTTTTCTTAATAATCTAAATATCAGTTGGGAAAGTATAAACACTGAGCTTGGCCGCTGTGTIAACCTGTTTTTCAATGTGCCACTCCAAGACATCAGGCCCTIATTCAGGCTGGC 889
Ghu6-4 : AAATTAACAAGTIAATGTTTCAATAATTTAGCAATGCAATCTTGGATAGTCAACAAAAGGCAACATTTGATTTACAGACCAATAGCCCATAGCCCTCGTTTTGAGCCCATACATTTGGGACT 889
Ghu6-4 : AAATTTCTACACTTTTCAATTCAAAAGGATTTAGAGCTGGGTTAATAATAAACGCAATTTTTTGGGTCTAATAAATAAATAAATTTGCTAGCCACTGTTTTTGGTGCTTCAACCAAGACATAA 889

AtU6-26: -----*-----80-----*-----40-----*-----0-----*
Ghu6-9 : GIATTTCTIATATAGGCCATTTAAGTTGAAAACAATCTTCAAAACTCCACATCGCTTAGATAGAAAGCGAACCTGACTTTIATAIACAGCTAGAGTCCFAGTAGTATGTGCCCTTCGGGGACAT 464
Ghu6-7 : AGGTTTGTCTTCGGGGACATCTTCAGGCCATGGTCAAAAATCTTCCCACATTTGCTAAGAAACCTTAAAGGAAAGGCTTTTATAIATAGCGAAAGAGCAGCACAATCTGCCCTTCGGGGACAT 1016
Ghu6-1 : ATGGTCAGGACGTGGTAGCATACTTCAGGATCTGGTTAGAAAATTTCCCATATCGCTAAGAACTATACACACAGGCTTTIATAIATAGCGAAAGAGCATCAGATGGTTGTCCCTTCGGGGACAT 1016
Ghu6-4 : CAGAGTCCGGGAGGCTGGCTCATGATTIACCTGGIATCCACTAAATATCCACATCCCTIAGCGGACAAATAAGCTAACCTTTIATATAGCTGAAAGCAGCACCAGGATTTGCCCTTCGGGGACAT 1016
Ghu6-4 : ACTGCTACTGGGCTTGTAGTCAAGTTCTIATTTGAAAAGCAGCCAAATATCCCGCATCGCTAAGAGTTTGGAAATTTIATTTGTTIATATAGCFAATACAGGAACCTIATGTGCCCTTCGGGGACAT 1016

AtU6-26: -----*-----40-----*-----80-----*-----120-----*
Ghu6-9 : CCGATAAAATTTGGAACGATACAGAGAAGATTAGCATGGCCCCGCGCAAGGATGACACGCACAATTCGAGAATGGTCCAAATTTTTTTTGCAAAATTTTCAGATCGATTTCTTCTCTCTCTGTTTC 591
Ghu6-7 : CCGATAAAATTTGGAACGATACAGAGAAGATTAGCATGGCCCCGCGCAAGGATGACACGCACAATTCGAGAATGGTCCAAATTTTTTTTGCAAAATTTTCCACATTTTAAAGCTCTCTCTCTTTT 1143
Ghu6-1 : CCGATAAAATTTGGAACGATACAGAGAAGATTAGCATGGCCCCGCGCAAGGATGACACGCACAATTCGAGAATGGTCCAAATTTTTTTTGCAAAATTTTCCACATTTIACAGCTCTCTCTTTT 1143
Ghu6-4 : CCGATAAAATTTGGAACGATACAGAGAAGATTAGCATGGCCCCGCGCAAGGATGACACGCACAATTCGAGAATGGTCCAAATTTTTTTTGCAAAATTTTCCCTCTCTCTCTTTGAAATTTTCGA 1143
Ghu6-4 : CCGATAAAATTTGGAACGATACAGAGAAGATTAGCATGGCCCCGCGCAAGGATGACACGCACAATTCGAGAATGGTCCAAATTTTTTTTCTTGATTTTTTTGGCAATTTTACAGCTCTCTTTCCA 1143

```

Figure S1. Cloning of *AtU6-26* homologous genes and their promoters in cotton. The conserved coding regions are in black background and underlined with a red line. Two conserved elements in the promoter region are indicated in red boxes with annotation.

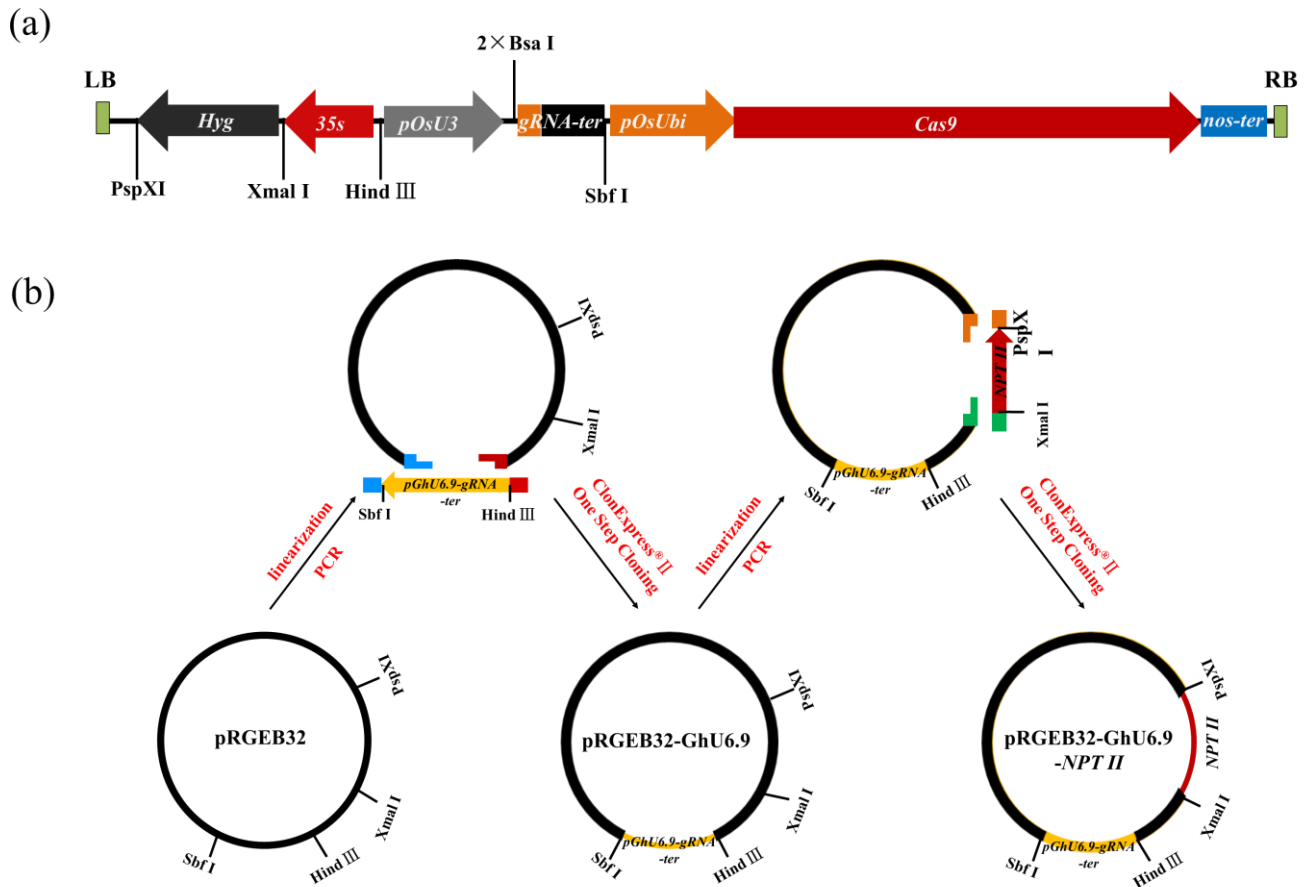


Figure S2. Modification of pRGE32 vector for cotton gene transformation. (a) Schematic of the T-DNA region of vector pRGE32. Restriction enzyme sites near the selection marker *Hyg* and *pOsU3* are labeled below. Two reverse *Bsa* I sites are the cloning sites to insert sgRNAs. (b) Detailed procedure of vector modification is illustrated. PCR adaptors that are homologous to the linearized vector are shown in same color.

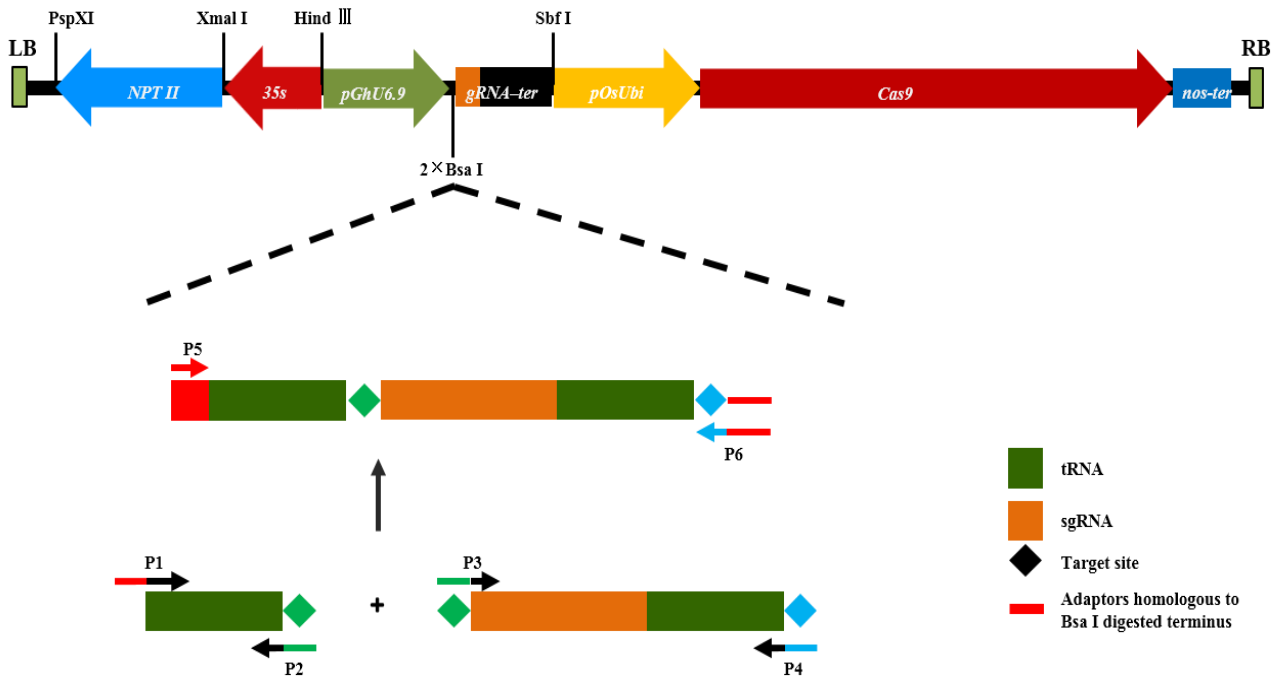


Figure S3. The procedure for pPTG vectors construction with one step cloning method. Above diagram shows the T-DNA region of expression vector pRGEB32-GhU6.9-NPT II. To combine two sgRNAs in one vector, two separate PCR products are obtained with primer pairs P1-P2 and P3-P4, respectively. These two fragments are assembled with overlapping extension PCR with primer pair P5-P6. The final PCR product is designed to be inserted into the Bsa I linearized expression vector using one step cloning method.

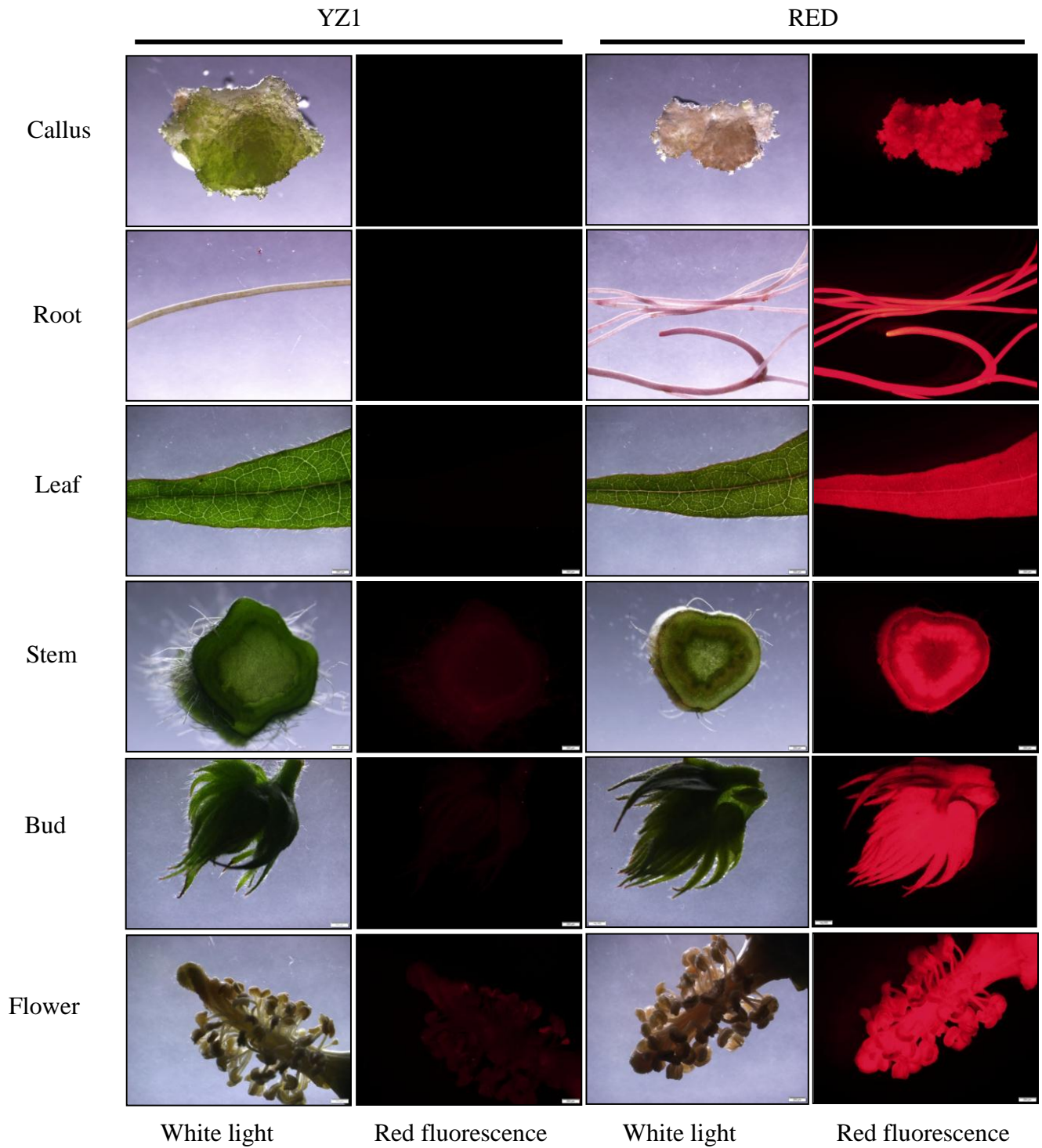


Figure S4. The *DsRed2* transgenic cotton line RED has red fluorescence in all tissues. Samples were observed under a stereomicroscope in the bright field and the red fluorescence field at an excitation wavelength of 530nm to 550nm.

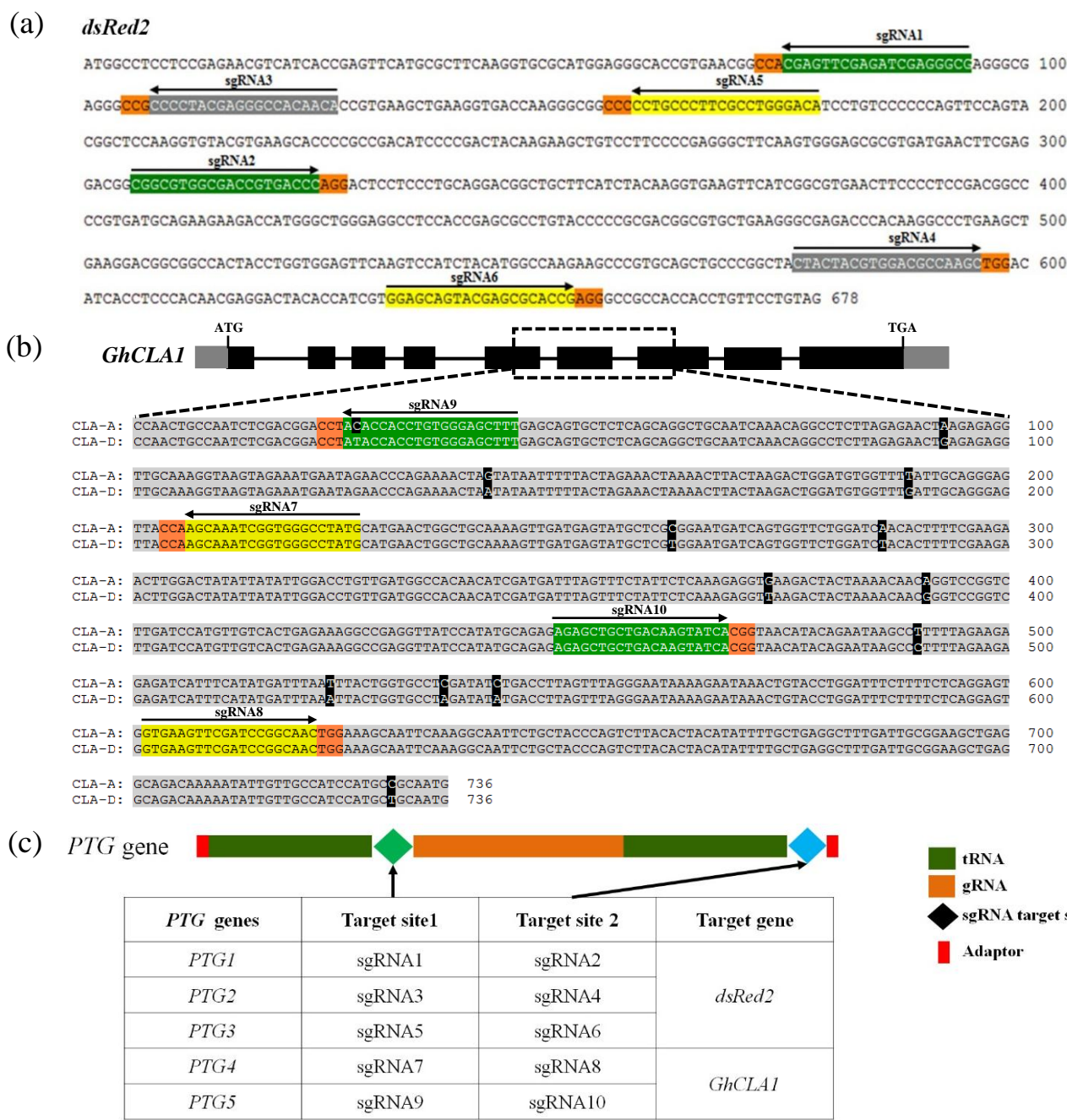


Figure S5. Designed *PTG* genes for *DsRed2* and *GhCLA1* editing. (a) The designed sgRNA target sites to *DsRed2*. (b) The designed sgRNA target sites to *GhCLA1*. The sgRNA target sites are highlighted in yellow or green, with the recognition direction indicated with arrows. sgRNAs chosen to be combined in one vector are illustrated in the same color. The PAM regions are highlighted in orange. Different SNPs in *GhCLA1* DNA sequences are highlighted in black. (c) The illustration of a *PTG* gene. Compositions of different *PTG* gene for the target genes are listed.

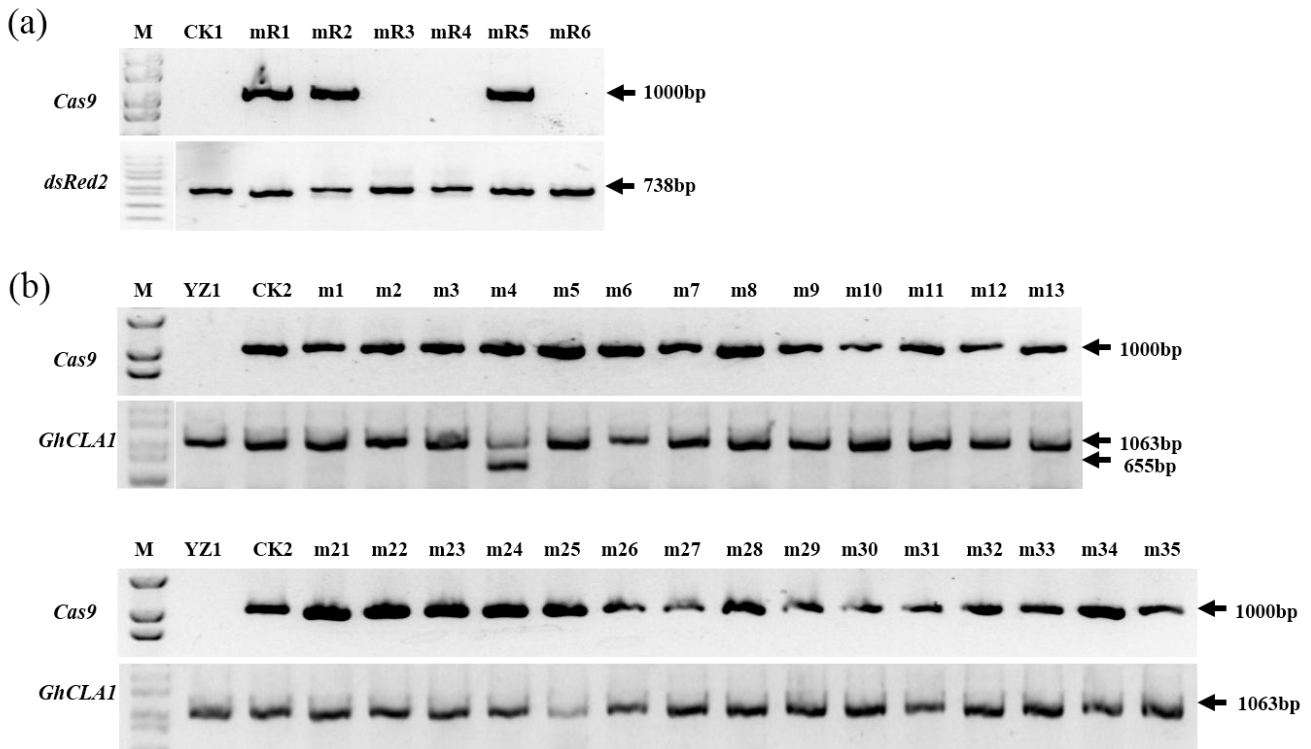
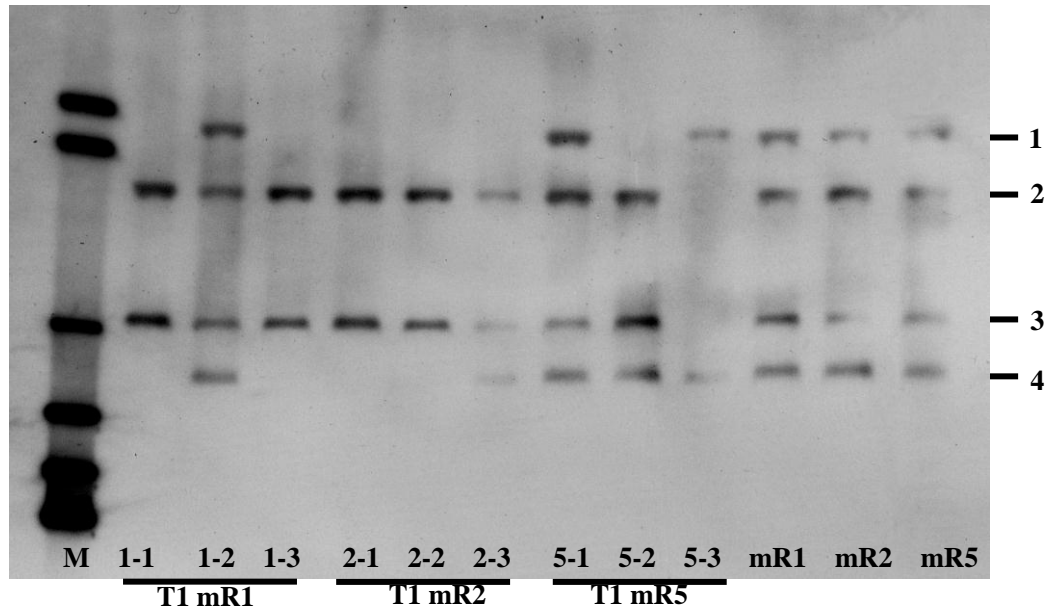


Figure S6. Transgenic positivity check in the regenerated T0 plants with Cas9 specific primers. (a) PCR analysis of *Cas9* positivity and *DsRed2*. (b) PCR analysis of *Cas9* positivity and *GhCLA1*. M, marker. CK1, a Cas9 positive control without sgRNA targeting in *DsRed2* transgenic background. CK2, a Cas9 positive control without sgRNA targeting in YZ1 background.



T0 Lines	<i>DsRed2</i> copies	Mutation type at sgRNA5	T1 progenies	<i>DsRed2</i> copies	Mutation type at sgRNA5
mR1	1, 2, 3, 4	+G , -G	1-1	2, 3	+G
			1-2	1, 2, 3, 4	+G , -G
			1-3	2, 3	+G
mR2	1, 2, 3, 4	+G , -G	2-1	2, 3	+G
			2-2	2, 3	+G
			3-3	2, 3, 4	+G , -G
mR5	1, 2, 3, 4	+G , -G	5-1	1, 2, 3, 4	+G , -G
			5-2	2, 3, 4	+G , -G
			5-3	1, 4	+G , -G

Figure S7. Southern blotting analysis of *DsRed2* gene copies in T0 plants and their T1 progenies. M, marker. mR1, mR2 and mR5 represents the three T0 cotton lines. Three independent T1 progenies for each T0 lines were analyzed. Number 1 to 4 represents the independent gene copies of *DsRed2*. A summary of the Southern result and mutation genotype of T0 and T1 plants is listed. The T1 progenies inherited *DsRed2* mutations from corresponding T0 plants. *DsRed2* copies of 1, 2 and 3 have +G mutation type. The copy 4 carries -G mutation type.

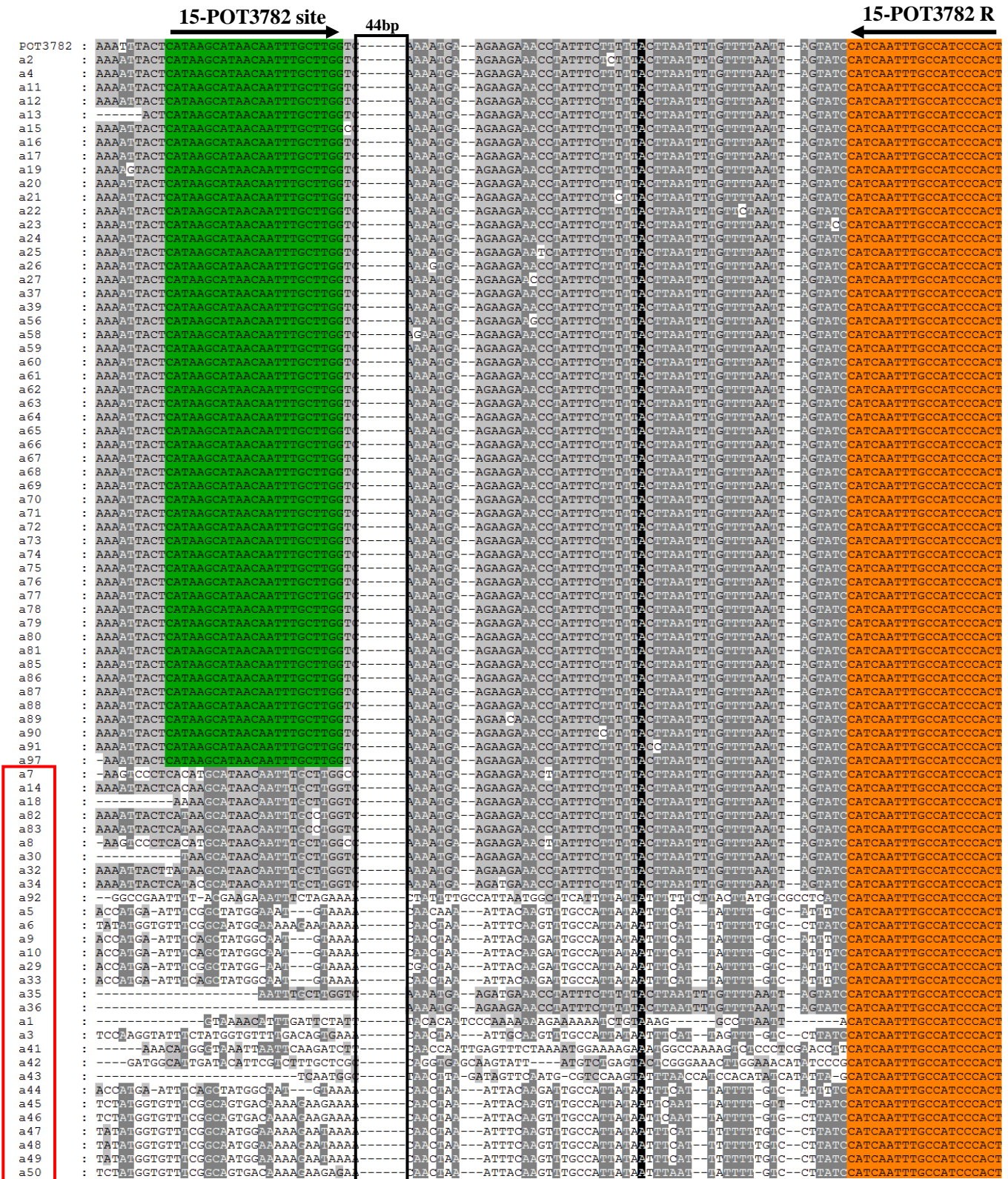


Figure S8 An example of off-target effect analysis at one potential off-target site 15_POT3782. The potential off-target site and the reverse primer for PCR process are highlighted in green and orange background, respectively. The gap of omitted nucleotides is labeled above. The reads in red box were unpredicted sequences that might be generated because of mismatch of primers.

Table S1. Barcoded-primers for *GhCLA1* mutation genotyping in independent T0 transgenic lines with high-throughput sequencing method

Lines	Forward primer	Reverse primer
PTG3	m1 cgactg TAAGACTGGATGTGGTGTATTGC	gctagt AAGATGTAGTGTAAGACTGGGTAGC
	m2 cgactg TAAGACTGGATGTGGTGTATTGC	atgcta AAGATGTAGTGTAAGACTGGGTAGC
	m3 cgactg TAAGACTGGATGTGGTGTATTGC	ctgcga AAGATGTAGTGTAAGACTGGGTAGC
	m4 cgactg TAAGACTGGATGTGGTGTATTGC	gtactc AAGATGTAGTGTAAGACTGGGTAGC
	m5 cgactg TAAGACTGGATGTGGTGTATTGC	tctagc AAGATGTAGTGTAAGACTGGGTAGC
	m6 cgactg TAAGACTGGATGTGGTGTATTGC	gagtca AAGATGTAGTGTAAGACTGGGTAGC
	m7 tgatag TAAGACTGGATGTGGTGTATTGC	gctagt AAGATGTAGTGTAAGACTGGGTAGC
	m8 tgatag TAAGACTGGATGTGGTGTATTGC	atgcta AAGATGTAGTGTAAGACTGGGTAGC
	m9 tgatag TAAGACTGGATGTGGTGTATTGC	ctgcga AAGATGTAGTGTAAGACTGGGTAGC
	m10 tgatag TAAGACTGGATGTGGTGTATTGC	gtactc AAGATGTAGTGTAAGACTGGGTAGC
	m11 tgatag TAAGACTGGATGTGGTGTATTGC	tctagc AAGATGTAGTGTAAGACTGGGTAGC
	m12 tgatag TAAGACTGGATGTGGTGTATTGC	gagtca AAGATGTAGTGTAAGACTGGGTAGC
	m13 gtcacg TAAGACTGGATGTGGTGTATTGC	gtactc AAGATGTAGTGTAAGACTGGGTAGC
yz1-1 gtcacg TAAGACTGGATGTGGTGTATTGC	tctagc AAGATGTAGTGTAAGACTGGGTAGC	
PTG4	m21 gtcacg TCTCTGCCAACTGCCAATCTCG	gagtca TCTCTTCTAAAAAGGCTTATTCTGT
	m22 atgatg TCTCTGCCAACTGCCAATCTCG	gctagt TCTCTTCTAAAAAGGCTTATTCTGT
	m23 atgatg TCTCTGCCAACTGCCAATCTCG	atgcta TCTCTTCTAAAAAGGCTTATTCTGT
	m24 atgatg TCTCTGCCAACTGCCAATCTCG	ctgcga TCTCTTCTAAAAAGGCTTATTCTGT
	m25 atgatg TCTCTGCCAACTGCCAATCTCG	gtactc TCTCTTCTAAAAAGGCTTATTCTGT
	m26 atgatg TCTCTGCCAACTGCCAATCTCG	tctagc TCTCTTCTAAAAAGGCTTATTCTGT
	m27 atgatg TCTCTGCCAACTGCCAATCTCG	gagtca TCTCTTCTAAAAAGGCTTATTCTGT
	m28 cagtca TCTCTGCCAACTGCCAATCTCG	gctagt TCTCTTCTAAAAAGGCTTATTCTGT
	m29 cagtca TCTCTGCCAACTGCCAATCTCG	atgcta TCTCTTCTAAAAAGGCTTATTCTGT
	m30 acgtca TCTCTGCCAACTGCCAATCTCG	ctgcga TCTCTTCTAAAAAGGCTTATTCTGT
	m31 acgtca TCTCTGCCAACTGCCAATCTCG	gtactc TCTCTTCTAAAAAGGCTTATTCTGT
	m32 acgtca TCTCTGCCAACTGCCAATCTCG	tctagc TCTCTTCTAAAAAGGCTTATTCTGT
	m33 acgtca TCTCTGCCAACTGCCAATCTCG	gagtca TCTCTTCTAAAAAGGCTTATTCTGT
	m34 gtcacg TCTCTGCCAACTGCCAATCTCG	tgcgac TCTCTTCTAAAAAGGCTTATTCTGT
	m35 gtcacg TCTCTGCCAACTGCCAATCTCG	gtcacg TCTCTTCTAAAAAGGCTTATTCTGT
	yz1-2 acgtca TCTCTGCCAACTGCCAATCTCG	acgtca TCTCTTCTAAAAAGGCTTATTCTGT

Note: The 6-nucleotide barcodes were in colors and they were chosen as specific combinations to mark independent plantlets.

Table S2. Statistics of the sequencing reads generated from barcode-based sequencing

Lines	Barcode-sorted unique reads	Lines	Barcode-sorted unique reads	Lines	Barcode-sorted unique reads
m1	162	m11	181	m27	675
m2	622	m12	645	m28	61
m3	891	m13	552	m29	179
m4	817	yz1-1	329	m30	316
m5	497	m21	320	m31	257
m6	269	m22	164	m32	175
m7	56	m23	571	m33	262
m8	192	m24	724	m34	181
m9	329	m25	556	m35	93
m10	257	m26	434	yz1-2	78
Total barcode-sorted unique reads				10845	
Unique reads				137545	
Unknown reads				99054	
Total reads				200687	

Table S3. Statistics of sequencing reads generated for off-target analysis

Off-target site	Primers-sorted unique reads	Off-target site	Primers-sorted unique reads
15_POT1500	258	21_POT7274	414
15_POT2941	340	21_POT7350	224
15_POT3515	415	21_POT9661	244
15_POT3782	108	21_POT10018	447
15_POT9381	185	28_POT25	370
15_POT12615	171	28_POT26	124
36_POT585	385	28_POT198	116
36_POT4307	122	28_POT456	189
36_POT8435	141	28_POT1542	235
36_POT11074	178	28_POT4528	123
21_POT1840	289	28_POT4625	276
21_POT3811	244	28_POT6578	569
21_POT6973	444	28_POT7818	361
Total primers-sorted unique reads		6972	
Unique reads		337594	
Unknown reads		330622	
Total reads		953687	

Table S4 Primers used for vectors construction, genotyping at on-targets and off-target sites

Primers	Sequences (5' to 3')	Purpose
pGhU6.9 F	TGATTGCTAGAATTTGCAGTAGGCTT	pGhU6.9 promoter amplification
pGhU6.9 R	AGTTATGTGCTGCTTCTTTTCGCTTAT	
midU6-9 R	TAGCCGTCTCATTTCACATTCATTG	pGhU6.9 mutation to destroy the Bsa I site
midU6-9 F	CAATGAATGTGAAATGAGACGGCTA	
infU6-9 F	TGATTACGCCAAGCTT TGATTGCTAGAATTTGCA GTAGGCTT	Overlap-extension amplification of pGhU6.9-gRNA-ter for ligation to pRGEB32
infU6-9 R	AAACCGAGACCTCGGTCTCCTGCC AGTTATGTG CTGCTTCTTTTCGCTTAT	
gRNA-ter F	GGCAGGAGACCGAGGTCTCGGTTT	
gRNA-ter R	CCGAATTTGTGGACCTGCAGGCATG	
inf32B-Kan F	TTTCGCAGATCCCGGG ATGATTGAACAAGATGG ATTG	<i>NPT II</i> change at the <i>Hpt</i> site
inf32B-Kan R	TATGGAGAAACTCGAGC TCAGAAGAACTCGTC AAGAAG	
PTG-RED1-1 R	CCTGCCCTTCGCCTGGGACA tgcaccagccgggaat	<i>PTG1</i> construction for <i>DsRed2</i> targeting
PTG-RED1-1 F	TGTCCCAGGCGAAGGGCAGG gttttagagctagaaata	
PTG-RED1-2 R	CGGTGCGCTCGTACTGCTCC tgcaccagccgggaat	
PTG-RED1-2 F	GGAGCAGTACGAGCGCACCG gttttagagctagaaata	
infRED1 R	ttctagctctaaaac CGGTGCGCTCGTACTGCTCC	<i>PTG2</i> construction for <i>DsRed2</i> targeting
PTG-RED2-1 R	CGAGTTCGAGATCGAGGGCG tgcaccagccgggaat	
PTG-RED2-1 F	CGCCCTCGATCTCGAACTCG gttttagagctagaaata	
PTG-RED2-2 R	GGGTCACGGTCGCCACGCCG tgcaccagccgggaat	
PTG-RED2-2 F	CGGCGTGCGGACCGTGACCC gttttagagctagaaata	<i>PTG3</i> construction for <i>DsRed2</i> targeting
infRED2 R	ttctagctctaaaac GGGTCACGGTCGCCACGCCG	
PTG-RED3-1 R	CCCCTACGAGGGCCACAACA tgcaccagccgggaat	
PTG-RED3-1 F	TGTTGTGGCCCTCGTAGGGG gttttagagctagaaata	
PTG-RED3-2 R	GCTTGCGTCCACGTAGTAG tgcaccagccgggaat	<i>PTG4</i> construction for <i>GhCLA1</i> targeting
PTG-RED3-2 F	CTACTACGTGGACGCCAAGC gttttagagctagaaata	
infRED3 R	ttctagctctaaaac GCTTGCGTCCACGTAGTAG	
PTG-CLA1-1 R	AGCAAATCGGTGGGCCTATG tgcaccagccgggaat	
PTG-CLA1-1 F	CATAGGCCACCGATTTGCT gttttagagctagaaata	<i>PTG5</i> construction for <i>GhCLA1</i> targeting
PTG-CLA1-2 R	GTTGCCGATCGAACTTCAC tgcaccagccgggaat	
nPTG-CLA1-2 F	GTGAAGTTCGATCCGGCAAC gttttagagctagaaata	
infCLA1 R	ttctagctctaaaac GTTGCCGATCGAACTTCAC	
PTG-CLA2-1 R	ATACCACCTGTGGGAGCTTT tgcaccagccgggaat	<i>PTG5</i> construction for <i>GhCLA1</i> targeting
PTG-CLA2-1 F	AAAGCTCCCACAGGTGGTAT gttttagagctagaaata	
PTG-CLA2-2 R	TGATACTTGTGACGAGCTCT tgcaccagccgggaat	
PTG-CLA2-2 F	AGAGCTGCTGACAAGTATCA gttttagagctagaaata	
infCLA2 R	ttctagctctaaaac TGATACTTGTGACGAGCTCT	

Table S4 continued		
pG32-9 F	CAGCACATAACTGGCA aa caaaagcaccagtggctag	Infusion ligation of <i>PTG</i> genes to expression vector
infpG32-9 F	CAGCACATAACTGGCAAACAAA	
u6-9 F	GTCAAAAACATATCCACATTGCTAA	Clone verification with PCR and sequencing
ubi2 R	CTGGCTTCCGCCTTGACCCG	
gtCas9 F	GCTTGTGCGTTTCGATTTGA	Transgenic <i>Cas9</i> positivity verification
gtCas9 R	CCGCTCGTGCTTCTTATCCT	
35S F	GTGGAAAAGGAAGGTGGCT	<i>DsRed2</i> positivity check
RED R	CTACAGGAACAGGTGGTGGCGGCC	
CLA1 F	GGATGGCTGTGGGAAGGGATCTGAAAGGTG	Full length <i>GhCLA1</i> , TA cloning for sgRNA9-sgRNA10 editing check
CLA1 R	CATAAGCCCTTTGCATGAATGATGAGTAGAT	
sCLA-1 F	CTCGACGGACCTATAACCACCTGTGG	TA cloning for sgRNA7-sgRNA8 editing check with primer 'CLA1 R'
sgR9 R	GCCTTTCTCAGTGACAACATGGATC	T7E1 assay for target sgRNA9 with primer 'CLA1 F'
sgR7 F	GGTAAGTAGAAATGAATAGAACCCAGAAAA	T7E1 assay for target sgRNA7 with primer 'sgR9 R'
sgR8 F	TTTAGTTTCTATTCTCAAAGAGGTTAAGACT	T7E1 assay for target sgRNA8
sgR8 R	GTTTAATCCGGTTCACCTCCCATTGCAGCA	
sgR10 F	TTTAGTTTCTATTCTCAAAGAGGTTAAGACT	T7E1 assay for target sgRNA10
sgR10 R	GACTGGGTAGCAGAATTGCCTTTGA	
28_POT25 F	GACTTCGCTTCATTGCCTGA	Off-target site amplification
28_POT25 R	TCTTATGGTCGAGTCTGACGAA	
28_POT26 F	TGCATGTGGTAGAGCTTCTGA	
28_POT26 R	TTTTACACAGATTCAATCAAACACC	
28_POT198 F	GGGTCGCCAGTTAGAAGAAA	
28_POT198 R	TTGTGAACCTGGTTGGCAAG	
28_POT456 F	TTTGTTTTATTGCCCGAGGA	
28_POT456 R	ATCCGGATGTTATGGTCGAG	
28_POT1542 F	GCCTGAGGATTCAAGCTAACA	
28_POT1542 R	CGATCTTTTTCTTCATATCTGGTTG	
28_POT4528 F	GCATAACTGGCAGCAAGGAT	
28_POT4528 R	TGGTCACACCCTGGAGCTAT	
28_POT4625 F	TGGCTTTTCTACACTGCTCAA	
28_POT4625 R	CGGATGTGCCAGGATTAGAT	
28_POT6578 F	TTCAATCATCTCGCCAAACA	
28_POT6578 R	AGCAATATGCCCAAAGATGG	
28_POT7818 F	TGCAAGAGCTGTCAAGGATG	
28_POT7818 R	TCAAAAGCAACAACGTTTCA	
36_POT585 F	CAACTACTGCACAGGCCAAA	
36_POT585 R	AAAATAAAATTCTCGTCTGACATGAT	

36_POT585 R	AAAATAAAATTCTCGTCTGACATGAT	Table S4 continued
36_POT4307 F	TGGTTGCAAACAAAGAGGACT	
36_POT4307 R	CCTTTGGCTGCTCTGTTGAC	
36_POT8435 F	GTTTCAAATAAAAAGGAGGTTTGC	
36_POT8435 R	ACAAATTTAACTCTTAACCTTACACG	
36_POT11074 F	TCACCACATGAACCAAATCA	
36_POT11074 R	CTTACTCTGTTTCTTTTCCCATGTT	
21_POT1840 F	TTGTGCTGCTGTTTCTTTGC	
21_POT1840 R	CCAAATGGCCCAAAAATAA	
21_POT3811 F	TTTTGTCTTGCAACACTTTTGG	
21_POT3811 R	CTGAGCTTCCCAGTTTGTTTG	
21_POT6973 F	TCAAACGAGGATCTTTTACAG	
21_POT6973 R	TGGCCTCTTTATGTTTCTAGCAT	
21_POT7274 F	GCATTACAATGCTCCCTGGT	
21_POT7274 R	CAACAACAAGTGAGTTTATCACACA	
21_POT7350 F	CAAGCATCAGGTAGGGCATT	
21_POT7350 R	CCTACCTTGACACGCCTTCT	
21_POT9661 F	TTCATGAACAACAGGAATGATTG	
21_POT9661 R	CCGACTGTTTTGAACCCATT	
21_POT9729 F	AGAGGCCTGTTTGATTGCAG	
21_POT9729 R	TGGTGCTATGACTGCAGGAC	
21_POT10018 F	TTCACAAGGGATTTTAGTTGTTC	
21_POT10018 R	CAACAAGTTTCTTCAAGGCTCA	
15_POT1500 F	CACGAGTTTCCCAAACCTCA	
15_POT1500 R	CAGACAGGATCCCAATTTCAA	
15_POT2941 F	CATGATTAATTGTCATGAACTGCT	
15_POT2941 R	TGAAAATTGGGCTGTTACAAAA	
15_POT3515 F	ACGGCCGTGACATTTTATTG	
15_POT3515 R	AGGCAACCCGAGCACTAACT	
15_POT3782 F	TCAATGGCAACTTCCAAAACCT	
15_POT3782 R	AGTGGGATGGCAAATTGATG	
15_POT9381 F	AACAACCTAATTGGTCCAAAATCA	
15_POT9381 R	GGGTAAATGGATCCCTCCTC	
15_POT12615 F	CTAGGGGCTAGCCGTTTGAT	
15_POT12615 R	TCGCAGAGCACTTCAATAGC	

Notes: The nucleotide in red capital is a mutation to destroy Bsa I site of original pGhU6.9. The nucleotides highlighted in yellow background represent its overlap with terminus of the digested expression vector. Nucleotides in blue or red lower case represent its match with gRNA and tRNA, respectively.

Appendix S1 DNA sequence of promoter *pGhU6.9*

>pGhU6.9

TGATTGCTAGAATTTGCAGTAGGCTTTGCAATTAATACATTATTCGAAACCATTAGATGA
TGCTTAGTATTTAATATTTATCCTCAGCCGATGATGGCTGAGGCCCTCGAGATCATAAACC
AGTGTA AAAAATTTTGAGACGCTCAATGCCATTTGGATCAAGCAATCCCTCGAGATTGGTT
ATTTGAAAGCTTCGGAAAATGCGGAAAGGATGGTGAGCTCGAGAATAAGATCAAGGCTA
AGGAAAAGGAACTTGCCAAAGTGAGCAATAAGCTCGAGGAGGCAGATAACTCATTGGC
AGACCGGGAGAACAAAGATGCAGAAAAAACTAGGAACCTTCTGCGTGAGAGGTGTTGAC
TACGATTGCTCGGTGATGTCTCTCATCGACCTAGCGAATGGATGCTACTTTATGCATTAGT
TACCATTTATATTTCAATTAGAAATGCATCACATAATTGAACTATTGTGTTATATGATTAAT
TCTCTGTTAAGGAATATCATTCAAAGGGTTATCTGGAACTAACATATCTTTGTCTTCCAG
AATACGGTTCCAAACAATTCGCTACGACCGACTGCCGTAGAGCAAAGAAGGCCAATGA
ATGTGAAAT **GAGACC** GCTAGTAGTTGACGATCTGGAGGTTTGTTCCTTCGTGTTCTTTTCA
TTAATACCACAATACCATATGCATACCCTGTCATGAATATTGTATAATAGAATGTTAGTTTG
CATAACCTTCCAATATGCTGCAAATAGTTTCCAACATTTTACTCTGTGCTACGATTTAATTC
TCTGTTAAGGAATATCGTTCAAAGAGTCATCGCGAAAGTAACATCTTTTCTCATCCAGGC
TGATGAATATGTAATGGAAGTCCAGTGACCGAAGATTCGGAGGTTTGTTCCTTCGGGGAC
ATACTTCAGGGCCATGGTCAAAAACCTATCCACATTGCTAAAGAACCATAAGGAAGAAG
CATTTATATAAGCGAAAGAAGCAGCACATAACT

Note: The highlighted “GAGACC”, which was a Bsa I recognition site, is mutated to “GAGACG” to destroy the recognition site to avoid more than two specific Bsa I sites in the final expression vector.

Appendix S2 Genome DNA Sequences of each potential off-target site

>CLA_A_15_POT1500

ATTTTTCAATAACCGGAGACAAGGATAACACGAGTTTCCCAAACCTCATAGCCTCTCAACAAATCTTA
AAAATTTTCATGCAAAATAATATATATATATAAAAAGGACCATTGATTTGCTTGGATGGAGACACCCCTAT
GCTGATGTTGGAGTCTCTTAAATCTCCACTTGCTTCTATGTATAAATTGACTTGTGTTGAGCATCAAATA
TCTTGAAATTGGGATCCTGTCTGTATTTATATTCTTTGGACT

>CLA_A_15_POT2941

TACCTATCAAAATATGTACAATTAATATAAAACATTAATGTCATGATTAATTGTCATGAACTGCTAACTAT
CAAAATTCATAAGATCTCCAATTTGCTTGGAAAGGTCCTTTTACACCAAAAAAAGGTTAAAATATGTT
ATAAGTCCTTGTAGTCTTTGTAAATTTAAAGTTTAGCCTCTATACTTTTGTAACAGCCCAATTTTCAGTA
GTGTCAGAACAGTGATTTGAGATCACTAAATTCGATGAAGA

>CLA_A_15_POT3515

GACCGTGGCCATGTCGCACGGCCGTGACATTTTATTGTAGCTCGAGTTTGGGAAAATAGTTTCCCTATT
TTCACGTGGCCCTAAGCACGCCATTTGCTTGGCCGTGTCTCTGTGGAAAACCTGTATTCAAGAGCTC
CATTAGTAAGTTAGGTGTTGAAGACTAAATTTTAAAGAAGTTAATACAGTTAGTGCTCGGGTTGCCTGC
CGAGAAGCGCTTATTTGTAGTCTAAGCTCGACTTACCTCTCCATTG

>CLA_A_15_POT3782

TTCATAAAAAATATCTAATATCCATCAATGGCAACTTCCAAAACCTTAAAAATTACAAGAAACAGGTAAA
AAAATTTACTCATAAGCATAACAATTTGCTTGGTCGACTTTCCTAGCTTGAAAAACCATGAATTCGGC
TATGGAATGTAAAATGAAGAAGAAACCTATTTCTTTTTACTTAATTTTGTTTTAATTAGTATCCATCAATT
TGCCATCCCCTATACTATTTAGGGCCTAATTATCACTTAAGT

>CLA_A_15_POT9381

CTAATATTATAGTATGTGATATAGTAATACATAATGTAATAATATATTTTAAAACCTATTAATACATATATATA
ACAACCTAATTGGTCCAAAATCATAACTAAATTTACCAACCGATTTGCTTGGATTGGCTCGGTTTGGTTG
GAATCGGTTTTAATTGCTAATTATAATAGATTATATACAATTGCATAATATGTACTATTACATAATTTATTA
AATAGTATATGAGGAGGGATCCATTTACCCCTGTGTA

>CLA_A_15_POT12615

ATTTTGCAACTGAGTTAAATGATAAATTGTTGTAAAATCTTATTCTAGGGGCTAGCCGTTTGATTGAACA
TTTGCATGCAAAGGAGTACCGATTTGCTTGGCAACAGGGTAAGCATTGTCATTTCCAGTTCTTATTCC
CTTTAGTTGCTTTACTCAAACTAAACATGGAGTGCATACACTAGTGTGAATGAGTTTTGGGTTCCCTTA
ACCTTAATGGAATTGTTTAAGCTATTGAAGTGCTCTGCGAGCAT

>CLA_A_21_POT1840

TCGAAGCAAATACAACCATTGTACTTTTCGTTTTTGTCTTTTGTGCTGCTGTTTCTTTGCCCTTGTCTC
GTGTCTGTGCAGGTACAGAGGCCAGATGGCGTGGAGGCTCGCAGTGGTGGTATAGGGAGTATGGCGG
TGACGTGGCACTAGAGGCTGGAGGTTGCGGCGCACCTAGGGCTAGGGTTCCCTAGGTTGGCTGAAAT
TGTTTTAGTTTTTGGGCCATTTGGGCCTTGTATTTTTAGGCTAGGGTTTACTTCATTTTGGGCCAT

>CLA_A_21_POT3811

AAAATCTAAACCATCAAATGAGGACAACTAACTTGTAAGTTTTGTCTTGCAACACTTTTGGTTAGG
TTACTTGCTACACTTCTGGTGGAGATACTTAGGGAAAAGCTCCCACAGGTTCTTTAAGAGGGAAACCA
GGTGGTAGGCCTCCCAGTACTCCTTTTCCTTTGTTCATAGCAGTAGCATTGTTGGAGGACACAAGGTG
CCCAAATACTATTCAAACAACTGGGAAGCTCAGATCTAACTCCCCCTTAACTCTTCCTTAAAC
>CLA_A_21_POT6973

ATCTCGCCTTATCTCACCTCTATTTCAAACGAGGATCTTTTCACGGTCATGGCATAGGTCTCAGAGATTT
CATCTATTGAGCAAAGTCTTTGGGTGGGGATTTTAGAAGTGCCAGCAGGTGGTATAGGAATAAACTATT
TGACTIONAAAAAGGCAGTGAAAGTTGGCGAAGACTCATTAGCTAACTATGCTAGAAACATAAAGAG
GCCAATATCTTTGTCTAGAAAATGGACACATAACTCTCAATCATAAGAAGGAAACACAAAGAGGT
>CLA_A_21_POT7274

CGATTAGGATACGATTTGCATGCCAATAAGGTTAGAACGTGCGCCTGTATGGGATTTGCACTTCAGTGC
CCCTGTTAGCATTACAATGCTCCCTGGTGTGGTATAGGTAACCATGTGTTTGAGTTATGTTTGGTATAGT
TCATCGGGCTCCTAATATTCTTACTATGAAATTGTTTGAATGATGTTGAATACCGATTCTGAATTAGATAA
ATGAGAGTGGAATGACATAAATGTTATATGATTCATGTGTGATAAACTCACTTGTGTTGT
>CLA_A_21_POT7350

GTAATGCGCCGGTCAAGCATCAGGTAGGGCATTTCATGCACTAGTTGACGGACTCATGCAGCACCTT
CGGCACTCAAAGAAATCAAAGCTTCCAAAGGTGGGATGGGATGGCTAGGAAAGAACCAACATAAA
GAAAACAGGAAGGTGAAGCAATTACATTGGTGGCAGATGTTTCAGCGTCAAGGTGGAGTAAAATTAC
CCAATAGAAGGCGTGTCAAGGTAGGGTTAATGAGTAAAAAAAAGCAGCTTAGGGTACCTAAGTTGAA
ATA

>CLA_A_21_POT9661
CAGTCGCATATGCCCTGGTGCCATCTTGAACCTATCTGATGCTTAAGAGAAACATAAAATTCATGAACAA
CAGGAATGATTGTGTTTTCTTATGGAATGATACAAAATCGCTCCCAATGGTGGTATTGGACTAAAGTCT
ATATTTCTTGCAGTGGGCCATACAAGGTTCAAATCCTCATTCTTGTATAATAGGTCTCCCTTATGATTTG
AGAAAATATTTTTCAACATTCAAATGATGAAATATTAATGGGTTCAAACAGTCGGGGTTTC

>CLA_A_21_POT9729
TTCTATTCAATTTCTACTTACCTTTGCAACCTCTCTTAGTTCTCTAAGAGGCCTGTTTGATTGCAGCCTGC
TGAGAGCACTGCTCAAAGCTCCCACAGGTGGTGTAGGTCCGTCGAGATTGGCAGTTGGCAGAGAAAC
TTGTTTATTGTCATTAAGAATAACAATCATATCAGAATCAAGATATCCGGCATTGTTTCATTGCTTCGTAA
GCTTGTCTGTCAGTCATAGCACCATCACCTATGACAGCAACAACATGATTCCTTTACCTTTTCAG

>CLA_A_21_POT10018

TTTCACAAGGGATTTTAGTTGTTTCATTTATCATGTCTCATTATTTTCACATTAGTTAATATGCATAACATTT
ATTCAATTTATATCAAAATATAAAATTCAAGAATAAAATTATCACATGTGGTATAGGAGATTATAGACTTT
TACTACTTTAGTTTCCTTGAGCCTTGAAGAACTTGTTGATCAAATTCCTAAGAATGACATACGTAGTTT
ACAAGTCTGATGGTGATCTTCTTCATTCTTCCTTCTTGGCGCCATGTTTCCTTACAAT

>CLA_S_28_POT25

AGTGGATTATAATACGGTTGTCTAAATATGATCCAAGTGAGCACATGAAAGAAGACTGATAGCCCGTG
AAGAAATACAAGACTTCGCTTCATTGCCTGAAGACAGAACTGACAAAGATTATTCGAGAGCCGTCA
CATCTTGACCTTCTTAAAGGAGCTGACAAGTATCACAGTAATAAGTGAGCAACGAGTCGCAGCCTGGA
TCGAGCAAAAAAAGGAGTTAATATAGACATCTCTTGGAGAATTCGTCAGACTCGACCATAAGATCATG
ATATGAAGAGGAAGATAGGTGTCTTCTCTT

>CLA_S_28_POT26

ATACTAAAATAAAAAATACATACCTCCTTAGAAGATCAATAGAATACTACAAAATTTAAAAGTAATAAA
AAATTAATAAAAAACAATATTTATATGTTTTCTTAAAAGGTCACTAACATGCATGTGGTAGAGCTTCTGA
CAAGAATAAGGGTCTGTTTGATTGCTAGTAAAATGTTTTTCGTAAAATGATTTCTGGAAAATGTTTTAC
TTTTTTGTAAAATAATTTACTGAAAATATTTTTCTGGTGTGTTGATTGAATCTGTGTAAAATATTTTTCTACT
GTTTGACNGTAAAATATTTTTCT

>CLA_S_28_POT198

AAGGTGGGAATTGAAAGAGTGGGTACTATGGGGTTGCATTGTGGGTATTAGTTCTTCAAGGAAAATAG
GAGATTAGGAAGAGATTGTATTATGGTATGGACCCATAGTTACGACAATCAATTGAGTAAATGCGAAGG
GTCGCCAGTTAGAAGAAATGGATACAAGTATCACGGATGTGAAATATCGATAATCAGGGGTGAAACCT
ATGAAAGAACATGGTTTGGGCCAGACCAGGGTCAATGTCTGCAAATGAATGGCTCAGAGAGCATGAG
GCATTAGCCTTGCCAACCAAGTTCACAAA

>CLA_S_28_POT456

GTGGATTATAACGCGGTTGTCTAAATATGGTCCAAGTAAACACGAAGAAAGAAGGCTGATAGCCCATG
AAGAAATACATGACTTTGTTTTATTGCCCGAGGATTAATCAATAAAGATTATTCAAGAGCCGTCACG
TCTTGACTTTCTTAAAGGAGCTGACAAGTATCATGGGGATAAGTGAACAACGAGTCGCAGCCTGGATC
AAGCAAAAAGGAGTTCATGGGGATGTCTTTTGGAAAATTCACAAGACTCGACCATAACATCCGGATAT
GAAGAGGAAGATAGGTGTCTTCACTTGA

>CLA_S_28_POT1542

CTTGATAAAGTGGATTATAACACGGTTGTCTAAATATGTTCCAAGTAAACACAATGAAGGAAGATTGAT
ATTCCATGAAGAAATACAGGACTTTGCTTTATAGCCTGAGGATTCAAGCTAACAAAGATTATTCGAGAG

CTGTCATGTCTTAAAGAAGCTAACGAGTATCACGGGGATAAGTGGGCAATGGGCCGCGATCCAGATCG
AGCAGAAAGAAAATAATAGAGATATCTTTTGGAAAATTCGTAAGATTTGACCATAACAACCAGATATG
AAGAAAAAGATCGATATCTTCGCTTGG

>CLA_S_28_POT4528

ATATGTTAGGATGCACATTGTAAAGGCTACAATAGAAGACAAACAACAAAAGATCTGCCAAGATCAAA
GGCATAACTGGCAGCAAGGATCAAGGGATTAAGAAGGCAAGATATGCAAAAATTAAGGGCAGAACTG
GAAACAAGTATCAAGGGATTA AAAAGACAAGATTTGACCTAACCTCTAGAAGAGTTTTGTCTAGAAGA
GTTATCCAATCAAATCTAAAAAATTCTACTTCAAAGTAGCAATAGCTCCAGGGTGTGACCACAAGGTTA
TGAAGCAGTCAGCACCAATTGTCCCCGTGAA

>CLA_S_28_POT4625

TGTCCAATTTTGAACCCTGCCTACAGCTGCTTCACTTTTAGGGAAGTTGATTTGGTACCTACCGTAGA
AGAGTATGTGGCTTTTCTACACTGCTCAAGGGTTAAAGTTGACAAGATCTATTCCAGAGTTGCCAACG
TCCCGCCCTTTGTAAAGAGACTGACGAGTATCACGGGGATGAGCGAGCAATGGATTGCGGCTAGGATT
AAGTAAAAGTGAGACAGAAGTTGTATTCCTTGAAGAACCTAAGAGATCTAATCCTGGCACATCCGGA
TATGAAAAAGAGGGTTGATATTTTTGCT

>CLA_S_28_POT6578

CTTGTTTTTTAGTGTTGATCATTGACGCTTTCCCCTGCATCTATCTTCTCACTTCTGATTGTATTTCAA
TCATCTCGCCAAACATACTATATCTGAGAACTCTTCGTAGCGCTTCCCAACATCTGGTTAATGAATAG
GGCTTTCAGAGTGTTGATGAAAAGTATCATGGTTTCTTTCTCCAGAAGAGGTGGCTCGACTTGTGTCA
CTACCTCTCTCCATCTTTGGGCATATTGCTTGAAGCTCTCATTTTGCTTCTTTTTCATATTCTGCAGTGTA
ATTCTATCAGGTGTCATGTTT

>CLA_S_28_POT7818

ACATAACAATTTTTGGGGACGAAACTGGGGACAGAACTGCTTTCTTAAACAATTTTAGTAGTTTTTTTTTC
TATAATCTTTGCAAGAGCTGTCAAGGATGACAAGGTTACGAAATCTCCGTGCAGGAGGCAGAGTTGTT
GACAAATATCACAGAACATATGTTTGTGACAAGGTTACGAAATCTCCATGCTGACAGTATTTTGTTAA
TTTTGCTGAAAGATCCAGATCTTGTTGAATTTCTTACATATAGACTTATGAAACGTTGTTGCTTTTTGATA
TTTTAGGGTACACATGGTTTTCATGA

>CLA_S_36_POT585

ATGCTGAGAGAACCGGCCAGCAATCTGATCTGAACAACACTACTGCACAGGCCAAATAAAAATTCCGAAA
GTGGAGCAATATTGTTAAAAGGAAAGTGATGTTAGAACCGGCAACTAGCCATAAACAGATGCTCCAAT
CATATCATTAATAAACAATTGGAGAAAAAAAAGAAGAAGAGATAAAAAGATGCTTCAAGTCACTT

AGATAATCATGTCAGACGAGAATTTTATTTTTCTTTTATTTTCAGTTTTTTCATAGAGATGGAAC TAAGC
AGATGGCATCTGATCAT

>CLA_S_36_POT4307

GGGTCTAAAAC TGTTCATGGTTGCAAACAAAGAGGACTCCACTTTGGCCTTTCCTAGGTGCTGGTGG
AGGGGTACCCTTAACAATCAATTTGATCCCCAGCAACCTGTAATTGTATCGAGCAATTCGCTCCGGCAA
CGGGATGTTGGTGTAGACCCTGAGTAGGGAGAGGATGAAGCCTATAGGAAGCCATAGGAAGGTCAAC
AGAGCAGCCAAAGGGGTTGGCCTTTGGACTAGGCGGCCCTCATGAAATATAACATGGCTTAGAAGCTT
GTTCCCTTGGCAATGGTTCG

>CLA_S_36_POT8435

TGAAAACCTTACTTAGAATATATTTTAATTTTCAATTTTTTAATAACCAATCCCAGTCAAAGTGTGACTA
GACCATACTAGTTTCAAATAAAAAGGAGGTTTGC GTGCCAGAGGTAGTGGGAAGTTCGTGACGGCAA
CTGGGCAA AATTGAAGGGCATCGAGCACGGTTAATTAGAAGACAAAATAGGATAAATTAAGTAATGTG
TAAACATTTAGGACTATTTTTTTTTTAAATTAATACTAAACTGACAAAACGTGTAAAGGTTAAGAGTTAA
ATTTGTTATTATGCTAA

>CLA_S_36_POT11074

AGCCAAATCACATGGCTTAGACTTATCACCACATGAACCAA AATCACCATCTCAAGTGAACATAACTAT
CATCTTTATAACTAGCCTATACATGCCATATTTACATATATCCACAAGTTCAGAAGTTCCAAACGGCAAC
TGGATAGTGTGATGCGTAACTCCGACTTGTCCAAAATGAGCGAGCTATCGAACCTCTATAAAACATGG
GAAAAGAAACAGAGTAAGCTTTCTAGCTTAGTAAGCCCGTATAGTTCAGAATTA AACTGACCATTTATA
CAATTAAGGCAA