

CRISPR/Cas9-mediated efficient and heritable targeted mutagenesis in tomato plants in the first and later generations

Changtian Pan^{1,2}, Lei Ye^{1,2}, Li Qin², Xue Liu², Yanjun He², Jie Wang², Lifei Chen², Gang Lu^{1,2*}

Supplementary Information

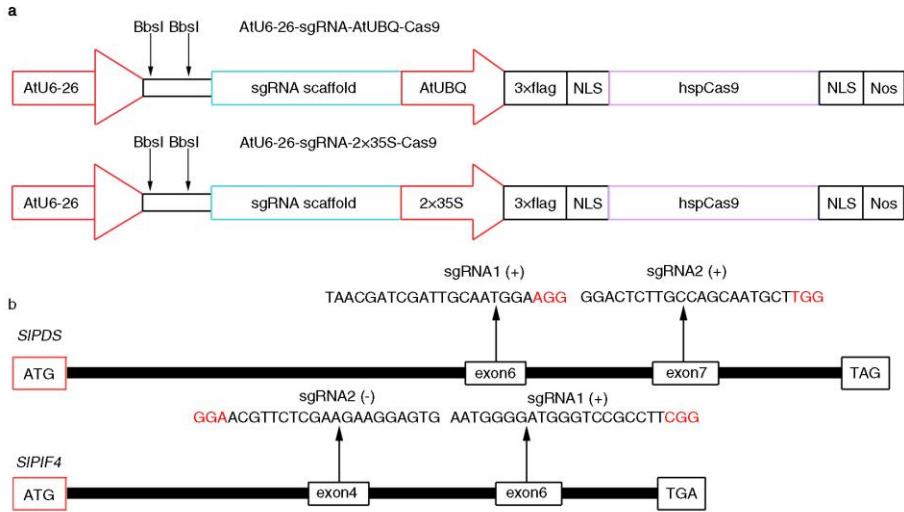


Figure S1. Schematic diagrams for binary vectors used in this study and selected target sites in *SIPDS* and *SIPF4*. (a) Schematic view of the expression cassettes. Cas9 fused with a flag tag (3xflag) and two nuclear localization signal (NLS) is expressed by either *Cauliflower mosaic virus* 35S promoter or *Arabidopsis* UBQ promoter. The scaffold sequence of sgRNA is derived using U6 promoters of *Arabidopsis*. Two *Bbs* I sites are located among the U6 promoter and sgRNA scaffold. (b) Schematic illustrating the target sites of *SIPDS* and *SIPF4*. All the 20-bp sequence are followed by a PAM sequence (NGG; red). +: plus strand; -: minus strand. ATG: initiation codon; TAG or TGA: termination codon.

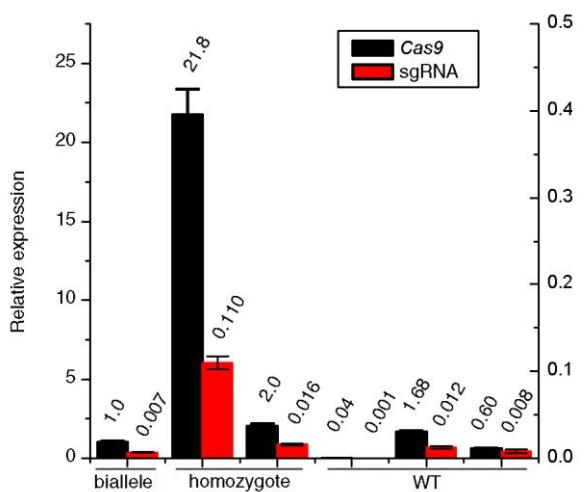


Figure S2. Expression analysis of Cas9 and sgRNA by RT-qPCR. #WT, wild-type sequence with no mutation detected. \$The zygosity of homozygote, biallele and WT in T0 lines are putative. The *SlUbi3* was used as the internal control. The RT-qPCR products were verified by sequencing.

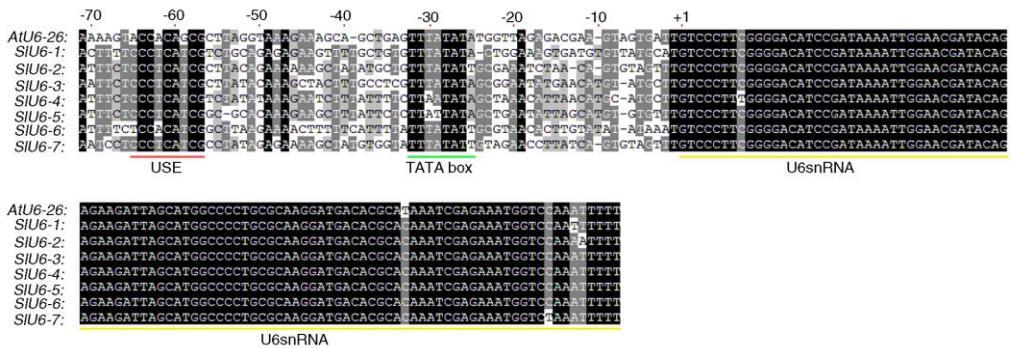


Figure S3. Alignment of 7 tomato *U6* small nuclear RNA genes with *Arabidopsis U6-26* genes.

Tomato *U6* and *Arabidopsis U6-26* are highly-conserved. +1; transcription start site of *U6* snRNA. Upstream sequence element (USE), TATA-like elements and *U6* small nuclear RNA (snRNA) sequence regions are underlined.

Supplementary Table S1. Genotyping of T0 independent transgenic lines of sgRNA1-*SlPDS*

Target	Lines [#]	Zygosity ^{\$}	Genotypes	Total	Ratio
sgRNA1- <i>SlPDS</i>	T0-1	Chimera	1d1,6i1,2WT		
	T0-2	Chimera	8d1,1d8,1d28,1i1,2WT		
	T0-4	Chimera	1d28,1c14,3WT		
	T0-5	Chimera	1d2,6i1,3WT		
	T0-6	Chimera	1d6,1i1,1c8,7WT		
	T0-10	Chimera	2d1,1d65,3i1,4WT		
	T0-11	Chimera	1d1,1d1a,2i1,3WT		
	T0-12	Chimera	1d2,3d72,3WT	15	71.4%
	T0-14	Chimera	1d55,2i1,2i1b,3WT		
	T0-15	Chimera	1d1,1i1,4WT		
	T0-16	Chimera	3d1,6i1,1i1a,		
	T0-19	Chimera	5d5,2d11,1i1,3WT		
	T0-20	Chimera	2d5,1d12,1c102,6WT		
	T0-21	Chimera	1d2,1d4,2i1		
	T0-22	Chimera	1d2,7i1,2WT		
	T0-3	WT*			
	T0-7	WT			
	T0-8	WT		6	28.6%
	T0-9	WT			
	T0-13	WT			
	T0-18	WT			

[#]Line name is in the format of T0-#. ^{\$}The zygosity of T0 lines is putative. *WT, no mutation detected at target sites. d#, # of bp deleted at the target sites; i#, # of bases insertion at target sites; i#a, the same number of insertions at one site; i#b, the same number of insertions at other sites; c#, combined mutation.

Supplementary Table S2. Genotyping of T0 independent transgenic lines of sgRNA2-*SIPDS*

Target	Lines	Zygosity	Genotypes	Total	Ratio
sgRNA2- <i>SIPDS</i>	T0-5	Biallele	14d3,5d5	1	14.3%
	T0-1	Chimera	1d2,1d4,1d23,1i2,1WT		
	T0-2	Chimera	1d2,3d5,1i1		
	T0-3	Chimera	3d1,1d5,1WT		
	T0-4	Chimera	2d1,1d3,1d4,1d102	6	85.8%
	T0-6	Chimera	1d1,2d3,3WT		
	T0-7	Chimera	6d3,1d5,4d14		

See Supplementary Table S1 for lines naming and genotype denotation.

Supplementary Table S3. Genotyping of T0 independent transgenic lines of sgRNA1-*SIPIF4*.

Target	Lines	Zygosity	Genotypes	Total	Ratio
	T0-22	Homozygote	d1		
	T0-23	Homozygote	d1	2	8.0%
	T0-7	Biallele	7c2,7c14		
	T0-15	Biallele	8d1,4d3	3	18.8%
	T0-19	Biallele	9d1,1d19		
	T0-1	Chimera	1d1,1d6,2WT		
	T0-2	Chimera	2d4,2d18,5WT		
	T0-3	Chimera	3d3,1d4,5i1		
	T0-4	Chimera	2d1,1d20,1d61		
	T0-5	Chimera	1d3,1d30,2WT		
	T0-8	Chimera	1d1,1d3,1d7,1WT		
	T0-9	Chimera	2d1,2d18,1c5		
sgRNA1- <i>SIPIF4</i>	T0-10	Chimera	2c51,1c126,1WT		
	T0-11	Chimera	4d8,1c51,1c52,3WT	16	64.0%
	T0-13	Chimera	2d1,1d4,1d7		
	T0-14	Chimera	2d1,2d4,1WT		
	T0-16	Chimera	2d1,5d3,1d5,1i1		
	T0-20	Chimera	1d1,1d5,2WT		
	T0-21	Chimera	4d1,1d4,1d50,3i1		
	T0-24	Chimera	2d1,1d4,1WT		
	T0-25	Chimera	5d1,1d4,1d5		
	T0-6	WT			
	T0-12	WT			
	T0-17	WT		4	16.0%
	T0-18	WT			

See Supplementary Table S1 for lines naming and genotype denotation.

Supplementary Table S4. Genotyping of T0 independent transgenic lines of sgRNA2-*SlPIF4*.

Target	Lines	Zygosity	Genotypes	Total	Ratio
sgRNA2- <i>SlPIF4</i>	T0-13	Homozygote	d1		
	T0-17	Homozygote	d1	3	15.8%
	T0-19	Homozygote	d1		
	T0-2	Biallele	13d1,2d3		
	T0-7	Biallele	9d2,4d9		
	T0-8	Biallele	6d2,6d9	5	26.3%
	T0-10	Biallele	6d3,7i1		
	T0-18	Biallele	7i1,6c43		
	T0-1	Chimera	1d127,5i1,1WT		
	T0-4	Chimera	1d1,4d6,3d17		
	T0-6	Chimera	3d2,2d2a,2d3,1d4,2d9		
	T0-9	Chimera	3d1,5d3,2d6		
	T0-11	Chimera	3d2,1d3,2i1	9	47.4%
	T0-12	Chimera	3d2,1d6,1d17,4d6a		
	T0-14	Chimera	2d1,3d6,1d17,2i1		
	T0-15	Chimera	5d1,4d2,1d2a		
	T0-16	Chimera	3d1,1d2,1d3		
	T0-3	WT		2	10.5%
	T0-5	WT			

See Supplementary Table S1 for lines naming and genotype denotation. d#a, the same number bases of deletion at one site.

Supplementary Table S5. Compare the genotypes of leaves and mixed tissues.

Target	Lines	Zygosity	Genotypes of leaf	Genotypes of mixed tissues*
sgRNA1- <i>SIPIF4</i>	T0-22	Homozygote	d1	d1
sgRNA1- <i>SIPIF4</i>	T0-23	Homozygote	d1	d1
sgRNA2- <i>SIPIF4</i>	T0-13	Homozygote	d1	d1
sgRNA2- <i>SIPIF4</i>	T0-17	Homozygote	d1	d1
sgRNA2- <i>SIPIF4</i>	T0-19	Homozygote	d1	d1
sgRNA1- <i>SIPIF4</i>	T0-7	Biallele	7c2,7c14	4c2,6c14
sgRNA1- <i>SIPIF4</i>	T0-15	Biallele	8d1,4d3	5d1,4d3
sgRNA2- <i>SIPIF4</i>	T0-7	Biallele	9d2,4d9	5d2,2d9
sgRNA2- <i>SIPIF4</i>	T0-8	Biallele	6d2,6d9	6d2,2d9
sgRNA2- <i>SIPIF4</i>	T0-9	Chimera	3d1,5d3,2d6	2d1,5d3,3d6
sgRNA1- <i>SIPDS</i>	T0-22	Chimera	1d2,7i1,2WT	<u>1d6,1d13,2i1,6WT</u>
sgRNA2- <i>SIPIF4</i>	T0-15	Chimera	5d1,4d2,1c3	8d1,8d2
sgRNA1- <i>SIPIF4</i>	T0-6	WT	N [#]	N
sgRNA2- <i>SIPIF4</i>	T0-5	WT	N	N
sgRNA1- <i>SIPDS</i>	T0-13	WT	N	N
sgRNA1- <i>SIPDS</i>	T0-18	WT	N	N

See Supplementary Table S1 for lines naming and genotype denotation. *Mixed tissues included leaves, shoots and flowers; [#]N, no mutation detected. Underline means new mutation were detected.

Supplementary Table S6. Genotyping the regeneration plantlets in T0 generation.

Target	Lines [#]	Zygosity	Genotypes
sgRNA2- <i>SIPIF4</i>	T0-13	Homozygote	d1
sgRNA2- <i>SIPIF4</i>	T0-13(1)	Homozygote	d1
sgRNA2- <i>SIPIF4</i>	T0-13(2)	Homozygote	d1
sgRNA2- <i>SIPIF4</i>	T0-17	Homozygote	d1
sgRNA2- <i>SIPIF4</i>	T0-17(1)	Homozygote	d1
sgRNA2- <i>SIPIF4</i>	T0-17(2)	Homozygote	d1
sgRNA1- <i>SIPIF4</i>	T0-22	Homozygote	d1
sgRNA1- <i>SIPIF4</i>	T0-22(1)	Homozygote	d1
sgRNA1- <i>SIPIF4</i>	T0-22(2)	Homozygote	d1
sgRNA1- <i>SIPIF4</i>	T0-7	Biallele	7c2,5c14
sgRNA1- <i>SIPIF4</i>	T0-7(1)	Biallele	8c2,3c14
sgRNA2- <i>SIPIF4</i>	T0-7	Biallele	9d2,4d9
sgRNA2- <i>SIPIF4</i>	T0-7(1)	Biallele	6d2,3d9
sgRNA2- <i>SIPIF4</i>	T0-7(2)	Biallele	4d2,4d9
sgRNA1- <i>SIPIF4</i>	T0-1	Chimera	1d1,1d6,2WT
sgRNA1- <i>SIPIF4</i>	T0-1(1)	Chimera	2d1,4 <u>d</u> 10,3WT
sgRNA1- <i>SIPIF4</i>	T0-1(2)	Chimera	1d1,6 <u>d</u> 10,3WT
sgRNA2- <i>SIPIF4</i>	T0-9	Chimera	3d1,5d3,2d6
sgRNA2- <i>SIPIF4</i>	T0-9(1)	Chimera	<u>1d</u> 2,2d3,5 <u>i</u> 1,2WT
sgRNA2- <i>SIPIF4</i>	T0-9(2)	Chimera	1d1,1 <i>i</i> 1,7WT
sgRNA1- <i>SIPIF4</i>	T0-6	WT	WT
sgRNA1- <i>SIPIF4</i>	T0-6(1)	WT	WT
sgRNA1- <i>SIPIF4</i>	T0-6(2)	WT	WT
sgRNA2- <i>SIPIF4</i>	T0-5	WT	WT
sgRNA2- <i>SIPIF4</i>	T0-5(1)	WT	WT
sgRNA2- <i>SIPIF4</i>	T0-5(2)	WT	WT

[#]Line name of regeneration plantlets is in the format of T0-M(N), with N designated the plantlets regenerated from the T0 plant T0-M. Underline means new mutation were detected.

Supplementary Table S7. Segregation patterns of CRISPR/Cas9-mediated targeted mutagenesis during the T1 to T2 generation in T-DNA-free plants.

Target gene	sgRNA	Line [#]	T1			T2	
			Zygosity	Genotype	T-DNA	Mutation segregation	T-DNA
<i>SIP1F4</i>	1	T1-22(14)	Homozygote	d1d1	-	15d1d1	15-
<i>SIP1F4</i>	1	T1-8(10)	Homozygote	d1d1	-	17d1d1	17-
<i>SIP1F4</i>	2	T1-16(3)	Homozygote	d2d2	-	10d2d2	10-
<i>SIP1F4</i>	2	T1-12(7)	Homozygote	d2d2	-	12d2d2	12-

[#]Line name is in the format of T1-M(N), with N designated the progeny of T1 plant T1-M. -, T-DNA was not detected.

Supplementary Table S8. Sequencing results of sgRNA1/2-*SIPDS* and sgRNA1/2-*SIPF4* in T0 plants.

Target	Genotypes	The sequences of target sites	Frequency
T0-1			
WT	GGGATT <ins>AACGATCGATTGCAATGGAAGG</ins> AACATT C	2/9	
d1	GGGATT <ins>AACGATCGATTGCAA</ins> - GGAAGG AACATT C	1/9	
i1	GGGATT <ins>AACGATCGATTGCAAT</ins> TGGAAGG AACATT C	6/9	
T0-2			
WT	GGGATT <ins>AACGATCGATTGCAATGGAAGG</ins> AACATT C	2/13	
d1	GGGATT <ins>AACGATCGATTGCAA</ins> - GGAAGG AACATT C	8/13	
d8	GGGATT <ins>AACGATC</ins> ----- TGGAAGG AACATT C	1/13	
d28	GATCGA----- TTGCAA	1/13	
i1	GGGATT <ins>AACGATCGATTGCAAT</ins> TGGAAGG AACATT C	1/13	
T0-3			
WT	GGGATT <ins>AACGATCGATTGCAATGGAAGG</ins> AACATT C		
	GGGATT <ins>AACGATCGATTGCAATGGAAGG</ins> AACATT C		
T0-4			
WT	GGGATT <ins>AACGATCGATTGCAATGGAAGG</ins> AACATT C	3/5	
d28	GGGATT <ins>AACGATCGATTGCAA</ins> ----- TTGCAA	1/5	
c14	GGGATT <ins>AACGATTGGAAGGAA</ins> ----- CATTC	1/5	
T0-5			
WT	GGGATT <ins>AACGATCGATTGCAATGGAAGG</ins> AACATT C	3/10	
d2	GGGATT <ins>AACGATCGATTG</ins> ----- TGGAAGG AACATT C	1/10	
i1	GGGATT <ins>AACGATCGATTGCAAT</ins> TGGAAGG AACATT C	6/10	
T0-6			
WT	GGGATT <ins>AACGATCGATTGCAATGGAAGG</ins> AACATT C	7/10	
d6	GGGATT <ins>AACGATCGAT</ins> ----- GGAAGG AACATT C	1/10	
i1	GGGATT <ins>AACGATCGATTGCAAT</ins> TGGAAGG AACATT C	1/10	
sgRNA1	c5	GGGATT <ins>AACGATCGATTGCAATGAAA</ins> ----- CATTC	1/10
<i>SIPDS-</i>	T0-7		
WT	GGGATT <ins>AACGATCGATTGCAATGGAAGG</ins> AACATT C		
	GGGATT <ins>AACGATCGATTGCAATGGAAGG</ins> AACATT C		
T0-8			
WT	GGGATT <ins>AACGATCGATTGCAATGGAAGG</ins> AACATT C		
	GGGATT <ins>AACGATCGATTGCAATGGAAGG</ins> AACATT C		
T0-9			
WT	GGGATT <ins>AACGATCGATTGCAATGGAAGG</ins> AACATT C		
	GGGATT <ins>AACGATCGATTGCAATGGAAGG</ins> AACATT C		
T0-10			
WT	GGGATT <ins>AACGATCGATTGCAATGGAAGG</ins> AACATT C	4/10	
d2	GGGATT <ins>AACGATCGATTG</ins> ----- TGGAAGG AACATT C	2/10	
d65	ATTAGG----- AATTCA	1/10	
i1	GGGATT <ins>AACGATCGATTGCAAT</ins> TGGAAGG AACATT C	3/10	

	T0-11		
WT	GGGATT <ins>AACGATCGATTGCAATGGA</ins> AGG AACATTC	3/7	
d1	GGGATT <ins>AACGATCGATTGCAA</ins> - GGA AGG AACATTC	1/7	
d1b	GGGATT <ins>AACGATCGATTGCA</ins> - TGGA AGG AACATTC	1/7	
i1	GGGAT <ins>AACGATCGATTGCAAT</ins> TGGA AGG AACATTC	2/7	
T0-12			
WT	GGGATT <ins>AACGATCGATTGCAATGGA</ins> AGG AACATTC	3/7	
d3	GGGATT <ins>AACGATCGATTGC</ins> -- GGA AGG AACATTC	1/7	
d72	GGAGAATT-----CAGCCG	3/7	
T0-13			
WT	GGGATT <ins>AACGATCGATTGCAATGGA</ins> AGG AACATTC		
	GGGATT <ins>AACGATCGATTGCAATGGA</ins> AGG AACATTC		
sgRNA1	T0-13	Mixed tissues	
SIPDS-	WT	GGGATT <ins>AACGATCGATTGCAATGGA</ins> AGG AACATTC	
		GGGATT <ins>AACGATCGATTGCAATGGA</ins> AGG AACATTC	
T0-14			
WT	GGGATT <ins>AACGATCGATTGCAATGGA</ins> AGG AACATTC	3/8	
d55	TATTCA-----ATGATA	1/8	
i1	GGGATT <ins>AACGATCGATTGCAAT</ins> TGGA AGG AACATTC	2/8	
i1b	GGGATT <ins>AACGATCGATTGCAA</ins> ATGGA AGG AACATTC	2/8	
T0-15			
WT	GGGATT <ins>AACGATCGATTGCAATGGA</ins> AGG AACATTC	4/6	
d1	GGGATT <ins>AACGATCGATTGCA</ins> - TGGA AGG AACATTC	1/6	
i1	GGGAT <ins>AACGATCGATTGCAAT</ins> TGGA AGG AACATTC	1/6	
T0-16			
WT	GGGATT <ins>AACGATCGATTGCAATGGA</ins> AGG AACATTC		
d1	GGGATT <ins>AACGATCGATTGCAA</ins> - GGA AGG AACATTC	3/10	
i1	GGGATT <ins>AACGATCGATTGCAAT</ins> TGGA AGG AACATTC	6/10	
i1a	GGGAT <ins>AACGATCGATTGCAAT</ins> AGGA AGG AACATTC	1/10	
T0-18			
WT	GGGATT <ins>AACGATCGATTGCAATGGA</ins> AGG AACATTC		
	GGGATT <ins>AACGATCGATTGCAATGGA</ins> AGG AACATTC		
T0-18		Mixed tissues	
WT	GGGATT <ins>AACGATCGATTGCAATGGA</ins> AGG AACATTC		
	GGGATT <ins>AACGATCGATTGCAATGGA</ins> AGG AACATTC		
T0-19			
WT	GGGATT <ins>AACGATCGATTGCAATGGA</ins> AGG AACATTC	3/11	
i1	GGGAT <ins>AACGATCGATTGCAAT</ins> TGGA AGG AACATTC	1/11	
d5	GGGAT <ins>AACGATCGATTG</ins> ----- GAAGGA AACATTC	5/11	
d12	GGGAT <ins>AACGATCG</ins> ----- GGA AACATTC	2/11	
T0-20			
WT	GGGATT <ins>AACGATCGATTGCAATGGA</ins> AGG AACATTC	6/10	
d5	GGGATT <ins>AACGATCGATT</ins> ----- GGA AGGA AACATTC	2/10	
d12	GGGATT <ins>AACGATCG</ins> ----- GGA AACATTC	1/10	

	c102	GCTTAC-----A-----AGCCGC	1/10
	T0-21		
	WT	GGGATTAA CGATCGATTGCAATGGA AGG AACATT C	
	i1	GGGATTAA CGATCGATTGCAAT TGGA AGG AACATT C	2/4
	d2	GGGATTAA CGATCGATTGCAAT A AGGAACATT C	1/4
	d4	GGGATTAA CGATCGATTG --- GGA AGGAACATT C	1/4
	T0-22		
	WT	GGGATTAA CGATCGATTGCAATGGA AGG AACATT C	2/10
	i1	GGGATTAA CGATCGATTGCAAT TGGA AGG AACATT C	7/10
sgRNA1	d2	GGGATTAA CGATCGATTG --- TGGA AGGAACATT C	1/10
-SIPDS	T0-22	Mixed tissues	
	WT	GGGATTAA CGATCGATTGCAATGGA AGG AACATT C	6/10
	i1	GGGATTAA CGATCGATTGCAAT TGGA AGG AACATT C	2/10
	d6	GGGATTAA CGATCGAT --- GGA AGG AACATT C	1/10
	d13	GGGATTAA CGATC --- GG AACATT C	1/10
	T0-1		
	WT	CAATTGGACTCTTGCCAGCAATGCT TGG AGGGCAA	1/5
	d4	CAATTGGACTCTTGCCA--- TGCT TGG AGGGCAA	1/5
	d23	C----- TG AGGGCAA	1/5
	d2	CAATTGGACTCTTGCCAGC--- TGCT TGG AGGGCAA	1/5
	i2	AATTGGACTCTTGCCAGCAAT TATGCT TGG AGGGCAA	1/5
	T0-2		
	WT	CAATTGGACTCTTGCCAGCAATGCT TGG AGGGCAA	
	d5	CAATTGGACTCTTGCC--- TGCT TGG AGGGCAA	3/5
	d2	CAATTGGACTCTTGCCAGCA--- GCT TGG AGGGCAA	1/5
	i1	CAATTGGACTCTTGCCAGCAAT TGCT TGG AGGGCAA	1/5
	T0-3		
	WT	CAATTGGACTCTTGCCAGCAATGCT TGG AGGGCAA	1/5
	d1	CAATTGGACTCTTGCCAGCA--- TGCT TGG AGGGCAA	3/5
	d5	CAATTGGACTCTTGCC--- TGCT TGG AGGGCAA	1/5
	T0-4		
	WT	CAATTGGACTCTTGCCAGCAATGCT TGG AGGGCAA	
	d1	CAATTGGACTCTTGCCAGCA--- TGCT TGG AGGGCAA	2/5
sgRNA2	d3	CAATTGGACTCTTGCCAG--- TGCT TGG AGGGCAA	1/5
-SIPDS	d4	CAATTGGACTCTTGCCA--- TGCT TGG AGGGCAA	1/5
	d102	CTTA-----AAAG	1/5
	T0-5		
	WT	CAATTGGACTCTTGCCAGCAATGCT TGG AGGGCAA	
	d5	CAATTGGACTCTTGCCAGC--- TTGG AGGGCAA	5/19
	d3	CAATTGGACTCTTGCCAGCAA--- TTGG AGGGCAA	14/19
	T0-6		
	WT	CAATTGGACTCTTGCCAGCAATGCT TGG AGGGCAA	3/6
	d3	CAATTGGACTCTTGCCAGC--- GCT TGG AGGGCAA	2/6
	d1	CAATTGGACTCTTGCCAGCAA--- GCT TGG AGGGCAA	1/6

T0-7				
WT	CAATT GGACTCTGCCAGCAATGCTGGAGGGCAA			
d14	CAATT GG ----- TGCTTGGAGGGCAA	4/11		
d5	CAATT GGACTCTGCCA ----- GCTTGGAGGGCAA	1/11		
d3	CAATT GGACTCTGCCAGC --- GCTTGGAGGGCAA	6/11		
<hr/>				
T0-1				
WT	ATGGG AATGGGGATGGGTCCGCCTTCGGTGCCTTC	2/4		
d6	ATGGG AATGGGGATGG ----- CTTCGGTGCCTTC	1/4		
d1	ATGGG AATGGGGATGGGTCCG - CTTCGGTGCCTTC	1/4		
T0-1(1)				
WT	ATGGG AATGGGGATGGGTCCGCCTTCGGTGCCTTC	3/9		
sgRNA1	ATGGG AATGGGGAT ----- TCGGTGCCTTC	4/9		
-SIPF4	ATGGG AATGGGGATGGGTCCG - CTTCGGTGCCTTC	2/9		
T0-1(2)				
WT	ATGGG AATGGGGATGGGTCCGCCTTCGGTGCCTTC	3/10		
d10	ATGGG AATGGGGAT ----- TCGGTGCCTTC	6/10		
d1	ATGGG AATGGGGATGGGTCCG - CTTCGGTGCCTTC	1/10		
T0-2				
WT	ATGGG AATGGGGATGGGTCCGCCTTCGGTGCCTTC	5/9		
d4	ATGGG AATGGGGATGGGT --- CTTCGGTGCCTTC	2/9		
d18	ATGG----- CTTCGGTGCCTTC	2/9		
T0-3				
WT	ATGGG AATGGGGATGGGTCCGCCTTCGGTGCCTTC			
d4	ATGGG AATGGGGATGGGT --- CTTCGGTGCCTTC	1/9		
i1	ATGGG AATGGGGATGGGTCCGCACCTTCGGTGCCTTC	5/9		
d3	ATGGG AATGGGGATGGGT --- CTTCGGTGCCTTC	3/9		
T0-4				
WT	ATGGG AATGGGGATGGGTCCGCCTTCGGTGCCTTC			
d1	ATGGG AATGGGGATGGGTCC - CCTTCGGTGCCTTC	2/4		
d20	ATGGG AA ----- G TGCCTTC	1/4		
d61	CATT----- GCTA	1/4		
T0-5				
WT	ATGGG AATGGGGATGGGTCCGCCTTCGGTGCCTTC	2/4		
d3	ATGGG AATGGGGATGGGTCCGCC --- GGTGCCTTC	1/4		
d30	C----- GGTGCCTTC	1/4		
T0-6				
WT	ATGGG AATGGGGATGGGTCCGCCTTCGGTGCCTTC			
	ATGGG AATGGGGATGGGTCCGCCTTCGGTGCCTTC			
T0-6	Mixed tissues			
WT	ATGGG AATGGGGATGGGTCCGCCTTCGGTGCCTTC			
	ATGGG AATGGGGATGGGTCCGCCTTCGGTGCCTTC			
T0-6(1)				
WT	ATGGG AATGGGGATGGGTCCGCCTTCGGTGCCTTC			
	ATGGG AATGGGGATGGGTCCGCCTTCGGTGCCTTC			

	T0-6(2)		
	WT	ATGGG AATGGGGATGGGTCCGCCTT CGG TGCCTTC	
		ATGGG AATGGGGATGGGTCCGCCTT CGG TGCCTTC	
	T0-7		
	WT	ATGGG AATGGGGATGGGTCCGCCTT CGG TGCCTTC	
	c2	ATGGG AATGGGGATGGGTCCG-CTT CGG TGCC CTC	7/12
	c14	GGG AATGGGGATGGTGTCAA-CACTACATT-TC	5/12
	T0-7	Mixed tissues	
sgRNA1	WT	ATGGG AATGGGGATGGGTCCGCCTT CGG TGCCTTC	
- <i>SIPF4</i>	c2	ATGGG AATGGGGATGGGTCCG-CTT CGG TGCC CTC	4/10
	c14	GGG AATGGGGATGGTGTCAA-CACTACATT-TC	6/10
	T0-7(1)		
	WT	ATGGG AATGGGGATGGGTCCGCCTT CGG TGCCTTC	
	c2	ATGGG AATGGGGATGGGTCCG-CTT CGG TGCC CTC	8/11
	c14	GGG AATGGGGATGGTGTCAA-CACTACATT-TC	3/11
	T0-8		
	WT	ATGGG AATGGGGATGGGTCCGCCTT CGG TGCCTTC	1/4
	d7	ATGGG AATGGGGATG-----CTT CGG TGCCTTC	1/4
	d1	ATGGG AATGGGGATGGGTCCG-CTT CGG TGCCTTC	1/4
	d3	ATGGG AATGGGGATGGGTC---CTT CGG TGCCTTC	1/4
	T0-9		
	WT	ATGGG AATGGGGATGGGTCCGCCTT CGG TGCCTTC	
	d1	ATGGG AATGGGGATGGGTCCG-CTT CGG TGCCTTC	2/5
	d18	ATGGG AATGGGGATGGGTCC-----GCAC	2/5
	c62	GT TTCCAACACTACATGTCCA---AATATATGATTC	1/5
	T0-10		
	WT	ATGGG AATGGGGATGGGTCCGCCTT CGG TGCCTTC	1/4
	c51	TGGTGATATT CAGATGATGTGGATGGGAAGTG--G	2/4
	c126	ATATT CAGATGATGTGGATGGGAAGTG--GCATT	1/4
	T0-11		
	WT	ATGGG AATGGGGATGGGTCCGCCTT CGG TGCCTTC	3/9
	d8	ATGGG AATGGGGAT-----CTT CGG TGCCTTC	4/9
	c52	TTCCA----- TGCACAATGCTAT-----GCATT	1/9
	c51	TGATATT CAGATGATGTGGATGGGAAGTG-GCATT	1/9
	T0-12		
	WT	ATGGG AATGGGGATGGGTCCGCCTT CGG TGCCTTC	
		ATGGG AATGGGGATGGGTCCGCCTT CGG TGCCTTC	
sgRNA1	T0-13		
- <i>SIPF4</i>	WT	ATGGG AATGGGGATGGGTCCGCCTT CGG TGCCTTC	
	d1	ATGGG AATGGGGATGGGTCCG-CTT CGG TGCCTTC	2/4
	d4	ATGGG AATGGGGATGGGT-----CTT CGG TGCCTTC	1/4
	d7	ATGGG AATGGGGATG-----CTT CGG TGCCTTC	1/4
	T0-14		
	WT	ATGGG AATGGGGATGGGTCCGCCTT CGG TGCCTTC	1/5

	d1	ATGGG AATGGGGATGGGTCCG-CTTCGG TGCCTTC	2/5
	d4	ATGGG AATGGGGATGGGT---CTTCGG TGCCTTC	2/5
T0-15			
	WT	ATGGG AATGGGGATGGGTCCGCCCTCGG TGCCTTC	
	d3	ATGGG AATGGGGATGGGTCCGC---CGG TGCCTTC	4/12
	d1	ATGGG AATGGGGATGGGTCCG-CTTCGG TGCCTTC	8/12
T0-15		Mixed tissues	
	WT	ATGGG AATGGGGATGGGTCCGCCCTCGG TGCCTTC	
	d3	ATGGG AATGGGGATGGGTCCGC---CGG TGCCTTC	4/9
	d1	ATGGG AATGGGGATGGGTCCG-CTTCGG TGCCTTC	5/9
T0-16			
	WT	ATGGG AATGGGGATGGGTCCGCCCTCGG TGCCTTC	
	d3	ATGGG AATGGGGATGGGTCCGC---CGG TGCCTTC	5/9
	d5	ATGGG AATGGGGATGGGTC---TTCGG TGCCTTC	1/9
	d1	ATGGG AATGGGGATGGGTCCG-CTTCGG TGCCTTC	2/9
	i1	ATGGG AATGGGGATGGTCCGCACCTTCGG TGCCTTC	1/9
T0-17			
	WT	ATGGG AATGGGGATGGGTCCGCCCTCGG TGCCTTC	
		ATGGG AATGGGGATGGGTCCGCCCTCGG TGCCTTC	
T0-18			
	WT	ATGGG AATGGGGATGGGTCCGCCCTCGG TGCCTTC	
		ATGGG AATGGGGATGGGTCCGCCCTCGG TGCCTTC	
T0-19			
		ATGGG AATGGGGATGGGTCCGCCCTCGG TGCCTTC	
	d1	ATGGG AATGGGGATGGGTCCG-CTTCGG TGCCTTC	9/10
sgRNA1	d19	ATGG----- TTCGG TGCCTTC	1/10
-SIPIF4	T0-20		
	WT	ATGGG AATGGGGATGGGTCCGCCCTCGG TGCCTTC	2/4
	d1	ATGGG AATGGGGATGGGTCCG-CTTCGG TGCCTTC	1/4
	d5	ATGGG AATGGGGATGGG---CTTCGG TGCCTTC	1/4
T0-21			
	WT	ATGGG AATGGGGATGGGTCCGCCCTCGG TGCCTTC	
	i1	ATGGG AATGGGGATGGTCCGCACCTTCGG TGCCTTC	3/9
	d1	ATGGG AATGGGGATGGGTCCG-CTTCGG TGCCTTC	4/9
	d4	ATGGG AATGGGGATGGGT---CTTCGG TGCCTTC	1/9
	d50	GGTGTC-----TTCC	1/9
T0-22			
	WT	ATGGG AATGGGGATGGGTCCGCCCTCGG TGCCTTC	
	d1	ATGGG AATGGGGATGGGTCCG-CTTCGG TGCCTTC	
T0-22		Mixed tissues	
	WT	ATGGG AATGGGGATGGGTCCGCCCTCGG TGCCTTC	
	d1	ATGGG AATGGGGATGGGTCCG-CTTCGG TGCCTTC	
T0-22(1)			
	WT	ATGGG AATGGGGATGGGTCCGCCCTCGG TGCCTTC	
	d1	ATGGG AATGGGGATGGGTCCG-CTTCGG TGCCTTC	

T0-22(2)			
WT	ATGGG AATGGGGATGGGTCCGCCTT CGG TGCCTTC		
d1	ATGGG AATGGGGATGGGTCCG --- CTTC CGG TGCCTTC		
T0-23			
WT	ATGGG AATGGGGATGGGTCCGCCTT CGG TGCCTTC		
d1	ATGGG AATGGGGATGGGTCCG --- CTTC CGG TGCCTTC		
T0-23	Mixed tissues		
WT	ATGGG AATGGGGATGGGTCCGCCTT CGG TGCCTTC		
d1	ATGGG AATGGGGATGGGTCCG --- CTTC CGG TGCCTTC		
T0-24			
WT	ATGGG AATGGGGATGGGTCCGCCTT CGG TGCCTTC	1/4	
d1	ATGGG AATGGGGATGGGTCCG --- CTTC CGG TGCCTTC	2/4	
d4	ATGGG AATGGGGATGGGT --- CTTC CGG TGCCTTC	1/4	
T0-25			
WT	ATGGG AATGGGGATGGGTCCGCCTT CGG TGCCTTC		
d1	ATGGG AATGGGGATGGGTCCG --- CTTC CGG TGCCTTC	5/7	
sgRNA1	d5	ATGGG AATGGGGATGGG --- CTTC CGG TGCCTTC	1/7
-SIPF4	d4	ATGGG AATGGGGATGGGT --- CTTC CGG TGCCTTC	1/7
<hr/>			
T0-1			
WT	GTAGA GTGAGGAAGAAGCTCTTGCA AGG CCTTCAT	3/9	
i1	GTAGA GTGAGGAAGAAGCTCTTGCA AGG CCTTCAT	5/9	
d128	CATGA-----TTAAGGTG	1/9	
T0-2			
WT	GTAGA GTGAGGAAGAAGCTCTTGCA AGG CCTTCAT		
d3	GTAGA GTGAGGAAGAAGCT --- GCA AGG CCTTCAT	2/15	
sgRNA2	d1	GTAGA GTGAGGAAGAAGCTCT --- GCA AGG CCTTCAT	13/15
-SIPF4	T0-3		
WT	GTAGA GTGAGGAAGAAGCTCTTGCA AGG CCTTCAT		
	GTAGA GTGAGGAAGAAGCTCTTGCA AGG CCTTCAT		
T0-4			
WT	GTAGA GTGAGGAAGAAGCTCTTGCA AGG CCTTCAT		
d6	GTAGA GTGAGGAAGAA ----- GCA AGG CCTTCAT	4/8	
d1	GTAGA GTGAGGAAGAAGCTCT --- GCA AGG CCTTCAT	1/8	
d17	GTAGA GTGAGG -----CCTTCAT	3/8	
T0-5			
WT	GTAGA GTGAGGAAGAAGCTCTTGCA AGG CCTTCAT		
	GTAGA GTGAGGAAGAAGCTCTTGCA AGG CCTTCAT		
T0-5	Mixed tissues		
WT	GTAGA GTGAGGAAGAAGCTCTTGCA AGG CCTTCAT		
	GTAGA GTGAGGAAGAAGCTCTTGCA AGG CCTTCAT		
T0-5(1)			
WT	GTAGA GTGAGGAAGAAGCTCTTGCA AGG CCTTCAT		
	GTAGA GTGAGGAAGAAGCTCTTGCA AGG CCTTCAT		
T0-5(2)			

	WT	GTAGA GTGAGGAAGAAGCTCTTGCAAGG CCTTCAT GTAGA GTGAGGAAGAAGCTCTTGCAAGG CCTTCAT	
T0-6			
	WT	GTAGA GTGAGGAAGAAGCTCTTGCAAGG CCTTCAT	
	d2	GTAGA GTGAGGAAGAAGCT--TGCAAGG CCTTCAT	3/10
	d3	GTAGA GTGAGGAAGAAGCT---GCAAGG CCTTCAT	2/10
	d9	GTAGA GTGAGGAA-----GCAAGG CCTTCAT	2/10
	d2a	GTAGA GTGAGGAAGAAGCTC--GCAAGG CCTTCAT	2/10
	d4	GTAGA GTGAGGAAGAAGC---GCAAGG CCTTCAT	1/10
T0-7			
	WT	GTAGA GTGAGGAAGAAGCTCTTGCAAGG CCTTCAT	
	d9	GTAGA GTGAGGAA-----GCAAGG CCTTCAT	4/13
	d2	GTAGA GTGAGGAAGAAGCTC--GCAAGG CCTTCAT	9/13
T0-7		Mixed tissues	
	WT	GTAGA GTGAGGAAGAAGCTCTTGCAAGG CCTTCAT	
	d9	GTAGA GTGAGGAA-----GCAAGG CCTTCAT	2/7
	d2	GTAGA GTGAGGAAGAAGCTC--GCAAGG CCTTCAT	5/7
T0-7(1)			
	WT	GTAGA GTGAGGAAGAAGCTCTTGCAAGG CCTTCAT	
	d9	GTAGA GTGAGGAA-----GCAAGG CCTTCAT	3/9
	d2	GTAGA GTGAGGAAGAAGCTC--GCAAGG CCTTCAT	6/9
T0-7(2)			
	WT	GTAGA GTGAGGAAGAAGCTCTTGCAAGG CCTTCAT	
	d9	GTAGA GTGAGGAA-----GCAAGG CCTTCAT	4/8
	d2	GTAGA GTGAGGAAGAAGCTC--GCAAGG CCTTCAT	4/8
T0-8			
	WT	GTAGA GTGAGGAAGAAGCTCTTGCAAGG CCTTCAT	
	d2	GTAGA GTGAGGAAGAAGCTC--GCAAGG CCTTCAT	6/12
	d9	GTAGA GTGAGGAA-----GCAAGG CCTTCAT	6/12
T0-9			
	WT	GTAGA GTGAGGAAGAAGCTCTTGCAAGG CCTTCAT	
	d6	GTAGA GTGAGGAAGA-----TGCAAGG CCTTCAT	2/10
	d3	GTAGA GTGAGGAAGAAGC---TGCAAGG CCTTCAT	5/10
	d1	GTAGA GTGAGGAAGAAGCTC-TGCAAGG CCTTCAT	3/10
T0-9		Mixed tissues	
	WT	GTAGA GTGAGGAAGAAGCTCTTGCAAGG CCTTCAT	
	d6	GTAGA GTGAGGAAGA-----TGCAAGG CCTTCAT	3/10
sgRNA2	d3	GTAGA GTGAGGAAGAAGC---TGCAAGG CCTTCAT	5/10
-SIP1F4	d1	GTAGA GTGAGGAAGAAGCTC-TGCAAGG CCTTCAT	2/10
T0-9(1)			
	WT	GTAGA GTGAGGAAGAAGCTCTTGCAAGG CCTTCAT	2/10
	d3	GTAGA GTGAGGAAGAAG---TTGCAAGG CCTTCAT	2/10
	d2	GTAGA GTGAGGAAGAAGC---TTGCAAGG CCTTCAT	1/10
	i1	GTAGA GTGAGGAAGAAGCTCTTGCAAGG CCTTCAT	5/10

T0-9(2)			
WT	GTAGA GTGAGGAAGAAGCTCTGCAAGG CCTTCAT	7/9	
i1	GTAGA GTGAGGAAGAAGCTCTTGCAAGG CCTTCAT	1/9	
d1	GTAGA GTGAGGAAGAAGCTCT-GCAAGG CCTTCAT	1/9	
T0-10			
WT	GTAGA GTGAGGAAGAAGCTCTGCAAGG CCTTCAT		
d3	GTAGA GTGAGGAAGAAGCT---GCAAGG CCTTCAT	6/13	
i1	GTAGA GTGAGGAAGAAGCTCTTGCAAGG CCTTCAT	7/13	
T0-11			
WT	GTAGA GTGAGGAAGAAGCTCTGCAAGG CCTTCAT		
d3	GTAGA GTGAGGAAGAAGCT---GCAAGG CCTTCAT	1/6	
i1	GTAGA GTGAGGAAGAAGCTCTTGCAAGG CCTTCAT	2/6	
d2	GTAGA GTGAGGAAGAAGCT---TGCAAGG CCTTCAT	3/6	
T0-12			
WT	GTAGA GTGAGGAAGAAGCTCTGCAAGG CCTTCAT		
d17	GTAGA GTGAGG-----CCTTCAT	1/9	
d6	GTAGA GTGAGGAAGAA-----GCAAGG CCTTCAT	1/9	
d2	GTAGA GTGAGGAAGAAGCTC---GCAAGG CCTTCAT	3/9	
sgRNA2	d6a	GTAGA GTGAGGAAGA-----TGCAAGG CCTTCAT	4/9
- <i>SIP1F4</i>	T0-13		
WT	GTAGA GTGAGGAAGAAGCTCTGCAAGG CCTTCAT		
d1	GTAGA GTGAGGAAGAAGCTCT-GCAAGG CCTTCAT		
T0-13	Mixed tissues		
WT	GTAGA GTGAGGAAGAAGCTCTGCAAGG CCTTCAT		
d1	GTAGA GTGAGGAAGAAGCTCT-GCAAGG CCTTCAT		
T0-13(1)			
WT	GTAGA GTGAGGAAGAAGCTCTGCAAGG CCTTCAT		
d1	GTAGA GTGAGGAAGAAGCTCT-GCAAGG CCTTCAT		
T0-13(2)			
WT	GTAGA GTGAGGAAGAAGCTCTGCAAGG CCTTCAT		
d1	GTAGA GTGAGGAAGAAGCTCT-GCAAGG CCTTCAT		
T0-14			
WT	GTAGA GTGAGGAAGAAGCTCTGCAAGG CCTTCAT		
d17	GTAGA GTGAGG-----CCTTCAT	1/8	
d6	GTAGA GTGAGGAAGAA-----GCAAGG CCTTCAT	3/8	
d1	GTAGA GTGAGGAAGAAGCTCT-GCAAGG CCTTCAT	2/8	
i1	GTAGA GTGAGGAAGAAGCTCTTGCAAGG CCTTCAT	2/8	
T0-15			
WT	GTAGA GTGAGGAAGAAGCTCTGCAAGG CCTTCAT		
d1	GTAGA GTGAGGAAGAAGCTCT-GCAAGG CCTTCAT	5/10	
d2	GTAGA GTGAGGAAGAAGCT---TGCAAGG CCTTCAT	4/10	
d2a	GTAGA GTGAGGAAGAAGCTC---GCAAGG CCTTCAT	1/10	
T0-15	Mixed tissues		
WT	GTAGA GTGAGGAAGAAGCTCTGCAAGG CCTTCAT		

	d1	GTAGA GTGAGGAAGAAGCTCT-GCAAGG CCTTCAT	8/16
	d2	GTAGA GTGAGGAAGAAGCT--TGCAAGG CCTTCAT	8/16
T0-16			
	WT	GTAGA GTGAGGAAGAAGCTTGCAGG CCTTCAT	
	d1	GTAGA GTGAGGAAGAAGCTCT-GCAAGG CCTTCAT	3/5
	d3	GTAGA GTGAGGAAGAAGCT---GCAAGG CCTTCAT	1/5
	d2	GTAGA GTGAGGAAGAAGCTC-GCAAGG CCTTCAT	1/5
T0-17			
	WT	GTAGA GTGAGGAAGAAGCTTGCAGG CCTTCAT	
	d1	GTAGA GTGAGGAAGAAGCTCT-GCAAGG CCTTCAT	
T0-17		Mixed tissues	
	WT	GTAGA GTGAGGAAGAAGCTTGCAGG CCTTCAT	
	d1	GTAGA GTGAGGAAGAAGCTCT-GCAAGG CCTTCAT	
T0-17(1)			
	WT	GTAGA GTGAGGAAGAAGCTTGCAGG CCTTCAT	
	d1	GTAGA GTGAGGAAGAAGCTCT-GCAAGG CCTTCAT	
T0-17(2)			
	WT	GTAGA GTGAGGAAGAAGCTTGCAGG CCTTCAT	
	d1	GTAGA GTGAGGAAGAAGCTCT-GCAAGG CCTTCAT	
sgRNA2	T0-18		
- <i>SIP1F4</i>	WT	GTAGA GTGAGGAAGAAGCTTGCAGG CCTTCAT	
	i1	GTAGA GTGAGGAAGAAGCTTTGCAGG CCTTCAT	7/13
	c43	AA-- GATCGTGTATACTTCCGTGCAGG CCTTCAT	6/13
T0-19			
	WT	GTAGA GTGAGGAAGAAGCTTGCAGG CCTTCAT	
	d1	GTAGA GTGAGGAAGAAGCTCT-GCAAGG CCTTCAT	
T0-19		Mixed tissues	
	WT	GTAGA GTGAGGAAGAAGCTTGCAGG CCTTCAT	
	d1	GTAGA GTGAGGAAGAAGCTCT-GCAAGG CCTTCAT	

DNA was extracted from the leaves or mixed tissues of T0 plants, then amplified by PCR and sequenced. On the first round, homozygote and WT were identified, with PCR product was one type. For others, DNA were cloned and a number of clones were sequenced. In X/Y, Y is the number clones sequenced, and X is the number of clones which showed a specific sequence. #WT, no mutations were detected at target sites. ^{\$} Mixed tissues included leaves, shoots and flowers. d#, # of bp deleted at the target sites; d#a, same number base of deletion at one site; i#, # number of bases insertion at target sites; i#a, same number base of deletion at one site; i#b, same number base of deletion at other sites ; c#: combined mutation. PAM (NGG) is indicated in orange; The 20 bp target sequence is marked in green; the bases colored red and blue mean insertion and substitution respectively.

Supplementary Table S9. Chromosomal locations of tomato U6 genes.

Gene	Chromosome	Strand	Location
<i>SIU6-1</i>	ch01	-	5813051-5813153
<i>SIU6-2</i>	ch01	+	92151263-92151365
<i>SIU6-3</i>	ch07	-	292992-293094
<i>SIU6-4</i>	ch07	+	327864-327966
<i>SIU6-5</i>	ch07	+	329337-329439
<i>SIU6-6</i>	ch07	-	2045653-2045755
<i>SIU6-7</i>	ch09	-	5169327-5169429

Supplementary Table S10. Primers used in the study.

Primer names	Sequence of primers	Aims
sgRNA1-SIPDS-F	5' TCTCCTATCCTCGTTGTCGT 3'	
sgRNA1-SIPDS-R	5' TTGCTTCTCATCCAGTCCTT 3'	
sgRNA2-SIPDS-F	5' ATGGTGAGCTAATCACGAGTAA 3'	
sgRNA2-SIPDS-R	5' AAAGAGAGGCAGGTAGACAATC 3'	
sgRNA1-SIPIF4-F	5' ATACGGGTGAGTTAGCGA 3'	Genotyping
sgRNA1-SIPIF4-R	5' AGTGGCAGGTGCATTACTATTA 3'	
sgRNA2-SIPIF4-F	5' GAGGAAACAAGTCAGCCCCA 3'	
sgRNA2-SIPIF4-R	5' TCGCTAACTCACCCGTAT 3'	
OFF1-F	5' ACGATTGATGGATTGAG 3'	
OFF1-R	5' TTCAGGGACGAATGTTGAG 3'	
OFF2-F	5' GTGCCCTGCCTATCTACTGG 3'	
OFF2-R	5' CATTGCGTCAACATCACCT 3'	
OFF3-F	5' CATGATTAGGCCAGGATTTC 3'	
OFF3-R	5' GAAGTGTAAACCCCCCTGAAT 3'	
OFF4-F	5' ACAATGGATTCACGACTCTC 3'	
OFF4-R	5' AAACCCGTTCCGTCTGTAG 3'	
OFF5-F	5' AGCTGAATATCATAGGTTTCCT 3'	
OFF5-R	5' CTCTATCACCGAAGTGGCTAG 3'	Off-target analysis
OFF6-F	5' AAGAAATCTGTTGTCAGTATCAGT 3'	
OFF6-R	5' AGTTGTAACGGTTAAAGGGC 3'	
OFF7-F	5' CACCTCAGTTTCACATCAGC 3'	
OFF7-R	5' CTCGCTCTACGATAGCACATT 3'	
OFF8-F	5' ATGGGACGATAATGAACACTG 3'	
OFF8-R	5' GCATCTCTTAGGTCAGCATC 3'	
OFF9-F	5' GCCTCCTTACATTACAAGAAACTA 3'	
OFF9-R	5' AGACGCACAAATCGGACTAT 3'	
SIUbi-1F	5' TCCATCTCGTGCTCCGTCT 3'	
SIUbi-1R	5' CTGAACCTTCCAGTGTCA 3'	
Cas9-F	5' GACGCTAACCTGGACAAAGTG 3'	
Cas9-R	5' TCAGGGTAAACAGGTGGATG 3'	
sgRNA1-SIPDS-F	5' CGATTGCAATGGAGTTTAGAG 3'	
sgRNA1-SIPDS-R	5' GTGCCACTTTCAAGTTGAT 3'	qRT-PCR of Cas9
sgRNA1-SIPIF4-F	5' GGGTCCGCCTGTTAGA 3'	and sgRNA
sgRNA1-SIPIF4-R	5' CCGACTCGGTGCCACTT 3'	
sgRNA2-SIPIF4-R	5' GAAGCTCTGCAGTTAGAGC 3'	
sgRNA2-SIPIF4-R	5' CGGTGCCACTTTCAAGT 3'	
Cas9-pCAMBIA1301-F	5' ATAAGCCCATCAGAGAGCAG 3'	Detect the T-DNA
Cas9-pCAMBIA1301-R	5' TAGCATTGCCATTCAAGG 3'	region