Supplementary Table S1. The mutations in the *Slses* mutant

Chr Position	Reference (Micro-Tom)	*slses* mutant	Mutation type	Indel length	DP4 (V,W,X,Y)	Locus	ITAG number	Annotation	Mutation	Effect of mutation
62,468,747	T	TC	IN	1	0,0,3,4	IGR				
62,475,310	GT	G	DEL	-1	0,0,17,25	Intragenic	region	Solyc07g06257(	Ubiquitin-conjugating enzyme E2 N	intron	
62,482,892	C	CAAAATGACT	IN	9	0,0,11,2	IGR					
62,485,918	AG	AGG	IN	1	0,0,1,1	IGR					
62,501,963	TC	T	DEL	-1	0,0,1,1	IGR					
62,501,964	CTTTTTTTTT	CTTTTTTTTTT	IN	1	0,0,5,4	IGR					
62,525,634	GAAAAAAAAAA	GAAAAAAAAAA	DEL	-1	0,0,7,13	IGR					
62,613,928	AT	ATCT	IN	2	0,0,1,2	IGR					
62,614,410	TAAAAAAAAAAA	TAAAAAAAAAAAAA	IN	2	0,0,0,10	IGR					
62,618,272	CAAAAAAAAAA	CAAAAAAAAAAA	IN	1	0,0,9,8	IGR					
62,621,533	CTTTTTTTTTT	CTTTTTTTTTTTT	IN	2	0,0,9,19	IGR					
62,664,178	CTTTTTTTT	CTTTTTTTTT	IN	1	0,0,5,12	IGR					
63,002,908	CAAAAAAAAAA	CAAAAAAAAA	DEL	-1	0,0,23,15	IGR					
63,008,548	T	C	SNP		13,21,168,247	IGR					
63,020,867	GAAAA	GAAA	DEL	-1	0,0,0,4	Intragenic	region	Solyc07g06329(	Unknown Protein	intron	
63,033,736	G	GATGT	IN	4	1,0,8,15	Intragenic	region	Solyc07g06332(	LanC-like protein 2	intron	
63,035,794	C	G	SNP		0,0,2,1	IGR					
63,037,848	GGAG	GAGAG	IN	9	0,0,2,1	IGR					
63,045,924	AGTG	AGAATTAACGGTG	IN	9	0,0,11,14	IGR					
63,053,924	A	AAAAC	IN	4	0,0,4,2	IGR					
63,058,609	TT	TTCAT	IN	3	0,0,3,1	IGR					
63,070,286	CA	CAGA	IN	2	0,0,3,0	IGR					
63,070,690	T	TAAA	IN	3	0,0,1,2	IGR					
63,080,600	G	A	SNP		0,0,1,2	IGR					
63,088,782	CAAGAAGCGAAAAG	CAAG	DEL	-10	0,0,2,0	Intragenic	region	Solyc07g06339(	Beta-glucosidase	intron	
63,091,155	CAAAAAAAA	CAAAAAAAAAAAAAAA	IN	7	0,0,2,1	IGR					
63,091,163	AGG	A	DEL	-2	0,0,1,1	IGR					
63,091,165	GAAAAAAA	GAAAAAAAAA	IN	2	0,0,3,4	IGR					
63,091,769	C	CT	IN	1	0,0,1,2	IGR					
63,091,881	C	T	SNP		0,0,2,0	IGR					
63,092,103	A	C	SNP		0,0,4,0	IGR					
63,102,932	AGG	AGGG	IN	1	0,0,2,2	IGR					
63,104,712	TG	TTAATTCAG	IN	7	0,0,17,13	IGR					
63,105,333	CAAAAAAAAA	CAAAAAAAAAAAAA	IN	4	0,0,2,3	IGR					
63,105,358	AG	A	DEL	-1	0,0,1,1	IGR					
63,108,880	AAA	AAAACAA	IN	4	0,0,14,14	IGR					
63,113,058	GAAAAAAAAA	GAAAAAAAAAA	IN	1	0,0,8,11	IGR					
63,126,005	TAAAAA	TTAAAAAA	IN	2	0,0,22,18	Intragenic	region	Solyc07g06342(	NAC domain transcription factor	intron	
63,129,991	TAAAAAAAAA	TAAAAAAAA	DEL	-1	0,0,6,7	IGR					
63,137,609	GTTT	GTT	DEL	-1	0,0,0,3	IGR					
63,182,669	A	ATATTTTC	IN	7	0,0,5,8	IGR					
63,183,264	TAAAAAAAAA	TAAAAAAAAAAAAAAAAA	IN	8	0,0,2,5	IGR					
63,196,959	AAAA	AAAAGAAA	IN	4	0,0,6,4	IGR					
63,197,263	T	TCAAAAAACA	IN	9	0,0,3,0	IGR					
63,197,574	AATA	AA	DEL	-2	0,0,0,2	IGR					
63,198,726	AC	A	DEL	-1	0,0,14,20	IGR					
63,207,057	AATTT	AATTTAAAGAGCATATGATTAAGGATATTT	IN	25	0,0,3,1	IGR					
63,211,620	GAAA	GAAAA	IN	1	0,0,1,2	Intragenic	region	Solyc07g06352(	Transmembrane protein 34	intron	
63,213,768	TTGT	TT	DEL	-2	0,0,2,2	Intragenic	region	Solyc07g06353(	Unknown Protein	intron	
63,217,639	T	TG	IN	1	0,0,3,1	Intragenic	region	Solyc07g06353(	Unknown Protein	3'UTR	
63,218,656	CT	CTT	IN	1	0,0,0,4	IGR					
63,224,093	CTTT	C	DEL	-3	0,2,12,6	Intragenic	region	Solyc07g06355(	Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 1	intron	
63,224,569	CTATGGAATA	C	DEL	-9	0,0,7,1	Intragenic	region	Solyc07g06355(	Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 1	intron	
63,230,602	ATTTTTT	ATTTTTTTTT	IN	3	0,0,0,4	IGR					
63,233,770	C	T	SNP		0,0,3,1	Intragenic	region	Solyc07g06356(	Cotton fiber expressed protein 1	3'UTR	
63,255,279	T	TA	IN	1	0,0,0,4	Intragenic	region	Solyc07g06359(	Myosin-like protein	intron	
63,263,762	C	CG	IN	1	0,0,1,1	Intragenic	region	Solyc07g06360(	Chlorophyll a-b binding protein 13, chloroplast	intron	
63,264,622	A	T	SNP		0,0,2,2	IGR					
63,271,176	TCCC	TCC	DEL	-1	0,0,1,1	IGR					
63,276,145	TAAAAAAA	TAAAAAA	DEL	-1	0,0,5,3	IGR					
63,276,316	TTTTT	TTTTTTGTTTT	IN	6	0,0,13,6	IGR					
63,279,307	GT	GTAT	IN	2	0,0,0,4	IGR					
63,285,846	T	TA	IN	1	0,0,1,1	Intragenic	region	Solyc07g06365(	Ubiquitin carboxyl-terminal hydrolase	intron	
63,286,441	AC	ACACTC	IN	4	0,0,3,0	Intragenic	region	Solyc07g06365(	Ubiquitin carboxyl-terminal hydrolase	intron	
63,286,442	CTC	CACTCTCAGAAAGCCAAGGCGTC	IN	20	0,0,11,11	Intragenic	region	Solyc07g06365(	Ubiquitin carboxyl-terminal hydrolase	intron	
63,297,255	CAAAAA	CAAAAAA	IN	1	0,0,9,3	IGR					
63,299,377	T	C	SNP		0,0,0,6	IGR					
63,301,438	G	GTATTT	IN	5	0,0,2,1	IGR					
63,302,667	ATT	A	DEL	-2	0,0,3,0	IGR					
63,303,142	GAAGAAGCAACCACAA	GAA	DEL	-13	0,0,12,13	Intragenic	region	Solyc07g06367(	Unknown Protein	exon	Frame shift
63,304,222	T	A	SNP		0,0,1,3	Intragenic	region	Solyc07g06367(	Unknown Protein	exon	Missense
63,309,151	T	TCCTC	IN	4	0,0,25,14	Intragenic	region	Solyc07g06368(	CHP-rich zinc finger protein-like	intron	
63,311,339	ATTTCACT	A	DEL	-7	0,0,4,0	IGR					
63,313,247	CTTTTTTTTT	CTTTTTTTTTT	IN	1	0,0,4,4	IGR					
63,437,474	ATTTTTTTTT	ATTTTTTTTTTT	IN	2	0,0,5,12	IGR					
63,444,260	CAAAAAAAAA	CAAAAAAAAAA	IN	1	0,0,4,18	IGR					
63,473,474	CTTTTTTTTT	CTTTTTTTTTT	IN	1	0,0,12,8	IGR					
63,508,655	TAAAAAAAAAAAA	TAAAAAAAAAAAAAAA	IN	3	0,0,2,7	IGR					
63,862,271	TAAAAAAAAAAA	TAAAAAAAAAAAAA	IN	2	0,0,10,9	Intragenic	region	Solyc07g06455(	Genomic DNA chromosome 5 P1 clone MBG(	intron	
63,948,376	CATATATATATATATATATATAT	CATATATATATATATATATATAT	IN	2	0,0,3,2	IGR					
63,977,710	CTTTTTTTTTTT	CTTTTTTTTTTTT	IN	1	0,2,13,17	Intragenic	region	Solyc07g06472(	GDSL esterase/lipase At5g55050	intron	
64,027,233	A	AAG	IN	2	0,0,4,1	IGR					
64,036,652	ACT	AAACCT	IN	3	0,0,2,0	IGR					
64,036,653	CTA	CA	DEL	-1	0,0,3,1	IGR					
64,069,862	CAAAAAAAAAAA	CAAAAAAAAAAAA	IN	1	0,0,8,6	IGR					
64,079,800	ACCCCCCCCCCCC	ACCCCCCCCCCCCCCCCCC	IN	6	0,0,1,2	IGR					
64,082,904	TAAAAAA	TAAAAA	DEL	-1	0,0,4,1	Intragenic	region	Solyc07g06488(	Small ubiquitin-related modifier	intron	
64,094,485	TA	TCAAAA	IN	4	0,0,3,5	IGR					
64,136,178	ATTTTTTTTTT	ATTTTTTTTTTT	IN	1	0,1,5,9	IGR					
64,265,168	TTATATATATATATATATATATATAT	TTATATATATATATATATATATATAT	IN	41	0,0,3,0	IGR					
64,298,439	CTTTTTTTTT	CTTTTTTTTTT	IN	1	0,0,13,9	IGR					
64,421,532	GATATATATATATATATATATATAT	GATATATATATATATATATATATAT	IN	38	0,0,5,3	IGR					
64,593,337	CA	CAA	IN	1	0,0,4,2	Intragenic	region	Solyc07g06570(	SEC14-like protein 1	exon	Frame shift
64,611,647	CTTTTTTTTTT	CTTTTTTTTTTT	IN	1	0,2,15,15	IGR					

Chr Position; physical position of mutation on the tomato reference genome (SL2.40). Reference (Micro-Tom); Sequence of WT tomato Micro-Tom genome (SL2.40). DP4; Four numbers correspond to numberd of forward ref alleles, reverse ref, forward non-ref, and reverse non-ref alleles, used in variant calling. Locus, mapped position for *slses* mutation. Mutation position; Exon indicates that homozygous indel or SNPs found in *slses* mutant are located within the exon region, while intron indicates that the indel or SNPs are located within the intron region. IGR, intergenic region. ITAG name, ITAG gene number definced in SL2.40. Effect of mutation; Missense mutation causes non-synonymous mutation. Frame shift indicates the gap of amino acid transration.

Supplementary Table S2. List of primers

Primer name	Purpose	Forward Primer Sequence	Reverse Primer Sequence	Restriction Enzyme
SlSES marker-1	DNA marker (*SES* mutation)	CGAGTAAAAATGGACAGAAGAAGAA	TGATGAAACAGGAGTTAATTTAGGG	-
SlSES marker-2	DNA marker (*SES* mutation)	ACACCATAGCTAGCCAGACCATGT	ACAATGAGCCACCAGTTGAAGCTC	*Bsl* I
NPT II marker	DNA marker (*NPT* II)	ATGATTGAACAAGATGGATTGCAC	TCAGAAGAACTCGTCAAGAAGGCG	-
Whole *SlSES* gene	In-Fusion	GATTACGCCAAGCTTCAATTAGCGATGGACGAAGTTCTAGGACGCGTCGACCTCACTTCTAGACTGCCATAAAGC		-

Supplementary Table S3. Homology with SlSES

Protein		Identity	Similarity	Gaps
SPL/NZZ	AT4G27330	26.4%	39.2%	33.7%
TIE1	AT4G28840	12.6%	21.3%	60.0%
TIE2	AT2G20080	12.9%	18.4%	67.9%
TIE3	AT1G29010	21.1%	31.8%	36.3%
TIE4	AT2G34010	17.1%	28.3%	38.0%

Each Homology was calculated with The European Bioinformatics Institute.
SPL/NZZ, SPOROCYTELESS/NOZZLE
TIE, TCP INTERACTOR CONTAINING EAR MOTIF PROTEIN

Supplementary Table S4. *t* -butyl alcohol series

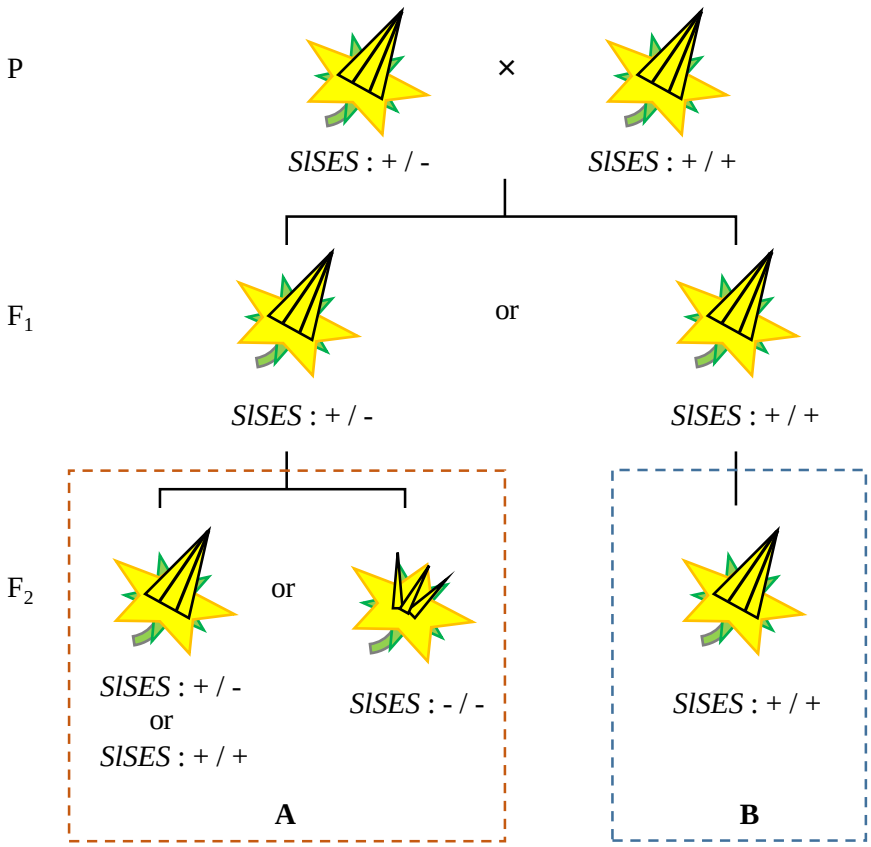
	t -butyl alcohol	Ethanol	DW
1	10 mL	40 mL	50 mL
2	20 mL	50 mL	30 mL
3	35 mL	50 mL	15 mL
4	55 mL	45 mL	0 mL
5	75 mL	25 mL	0 mL
6	100 mL	0 mL	0 mL

Each solution are composed with t-butyl alcohol, ethanol and distilled water (DW).

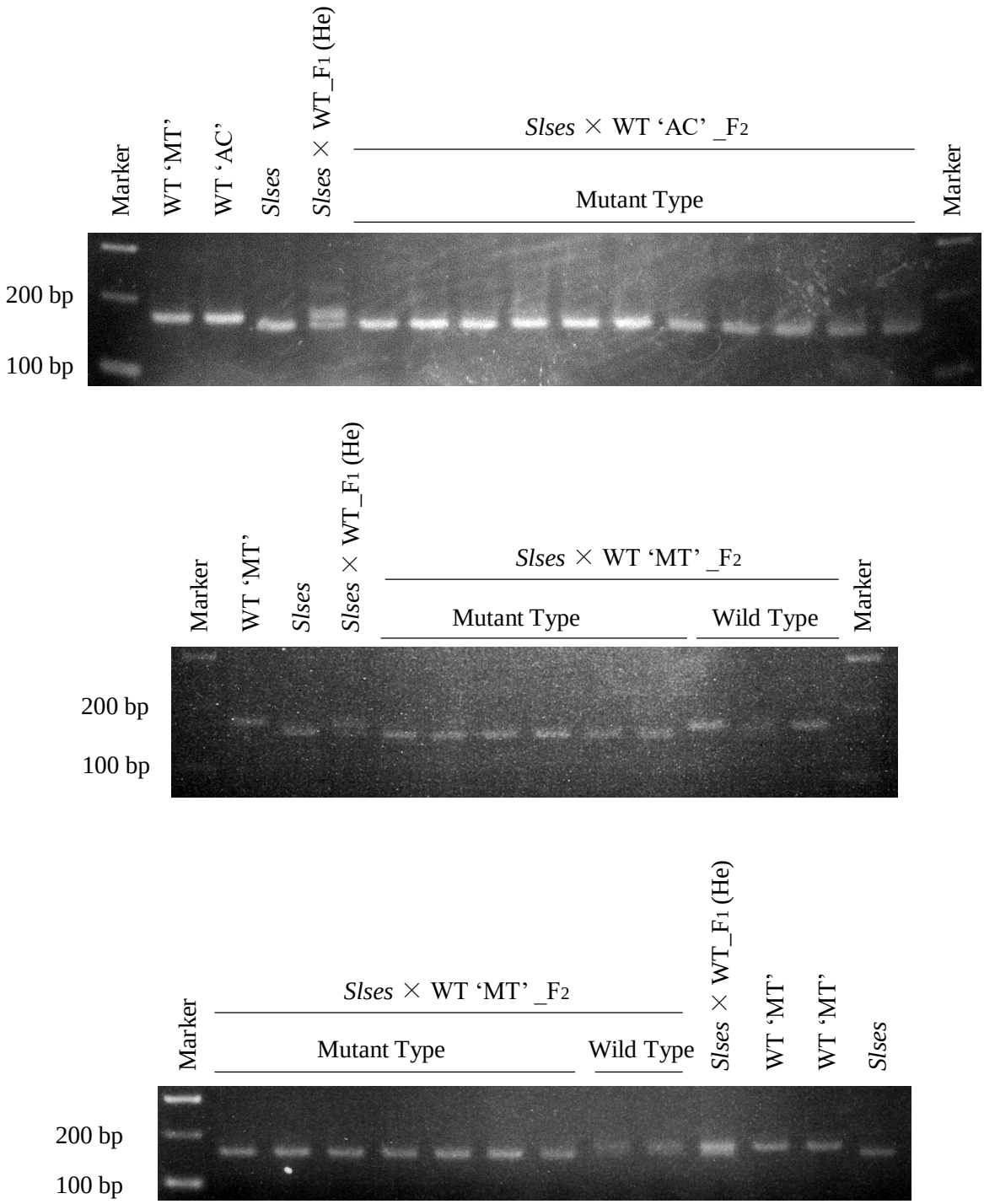
Supplementary Table S5. List of primmers for qRT-PCR

Gene	Solyc ID	Forward Primer Sequence (5'→3')	Reverse Primer Sequence (5'→3')
SlSES	*Solyc07g063670*	AGCCTTTGCTTCACTCATACAGTT	ACTCATCATCGTTGCTTCATTCTC
MS10^{35}	*Solyc02g079810*	AAATGACACCAGTGCCACTG	AGTAGATTCCGTGGATGATCTCC
BAM1/2-like	*Solyc02g091840*	AATTCCCGGGGACACAAAAG	ATAAACCCCCGAGCCTAGAAAG
EMS1/EXS-like	*Solyc09g098420*	TTTCGCGAACTGTTCAAGCC	ATTGTTGCCGAGTGAGATCCC
TAG1	*Solyc02g071730*	GCAGAAGAGGGAAGTTGATTTACAC	GTCTAGGGTAATGGTTGTTGGTTTG
SlWUS	*Solyc02g083950*	AAGAAGAGGCTCATTGCTGCTG	ACCCCATGTGAAGATGGTGATG
SlINO	*Solyc05g005240*	TACCCCAACATGACTCACAAGC	TTGCTATCTCTTGGGACCATGG
ANT-like	*Solyc04g077490*	CTGCTGCCTCATTAGTCTTTGC	AAAGACTGGTAGGTGAGCCATG
PIN1-like	*Solyc03g118740*	CCCACAACCCCATAAACCAAAAC	GCACAACAGCAGTCATAACATGG
BEL1-like	*Solyc08g081400*	TGATGGAGACTCATCCTTGGAG	CCAGTTTGGCGAGCTAAAATG
SlREV	*Solyc11g069470*	ACTCGACATGCTGGAGACAAC	AGATACCACCAGGCAAACACG
CNA-like	*Solyc03g120910*	GTCTAGTGCCGTTTCAGTTTGG	ACCAGCTCTGTTACTCTGCTTC
PHB/PHV-like	*Solyc02g024070*	GCTCTCGTTCTCTTGGAGGAG	TCTCCTCTCTGTAAACACAAGGC
GOB	*Solyc07g062840*	TGCATGAATATCGCCTTGATGG	AGTAGCGGCACCATTAGAACC

SlSES, SEXUAL STERILITY; MS10^{35}*, MALE STERILE 10*^{35}*; BAM1/2, BARELY ANY MERISTEM1 and 2; EMS1/EXS, EXCESS MICROSPOROCYTES1/EXTRA SPOROGENEOUS CELLS; TAG1, TOMATO AGAMOUS1; SlWUS, WUSCHEL; SlINO, INNER NO OUTER; ANT, AINTEGUMENTA; PIN1, PIN-FORMED1; BEL1, BELL1; SlREV, REVOLUTA; CNA, CORONA; PHB/PHV, PHABULOSA/PHAVOLUTA; GOB, GOBLET*



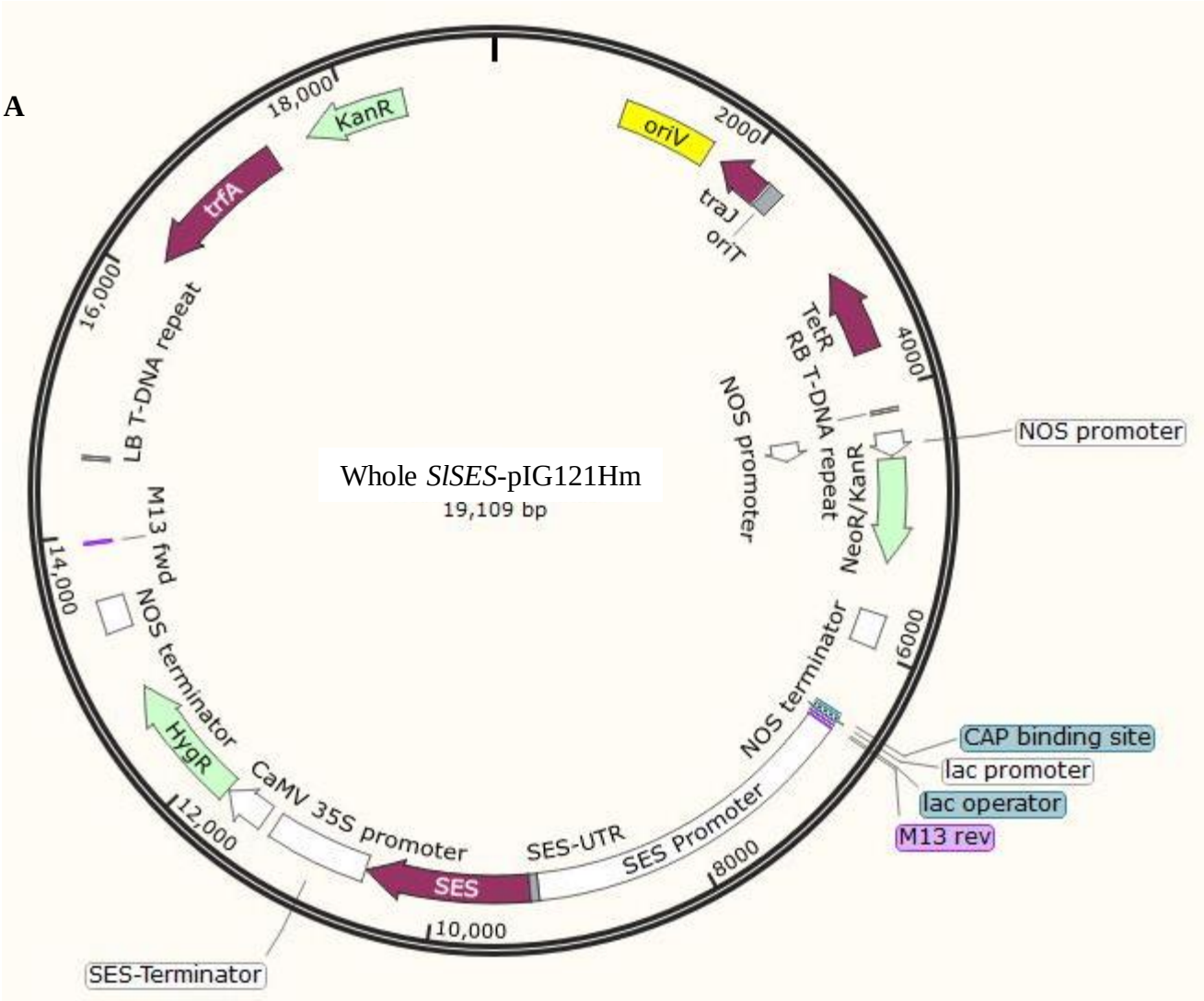
Supplementary Fig. S1. Schematic diagram of crossing analysis.
The *SlSES* homozygous mutant plants showed sexual sterility, and therefore the *SlSES* heterozygous mutant plants were used for crossing. All of F_1 plants showed wild type phenotype, but there were two types of genotypes. One type was the *SlSES* heterozygous genotype, and F_2 plants from this genotype were segregated to WT phenotype〈left image〉 and mutant phenotype〈right image〉(A). Another type was WT genotype, and F_2 plants from this genotype showed WT phenotype (B). + indicates wild type *SlSES* and - indicates mutated *SlSES*.



Supplementary Fig. S2. Linkage analysis of the 13-bp deletion on *Solyc07g063670* by *SlSES* marker-1.

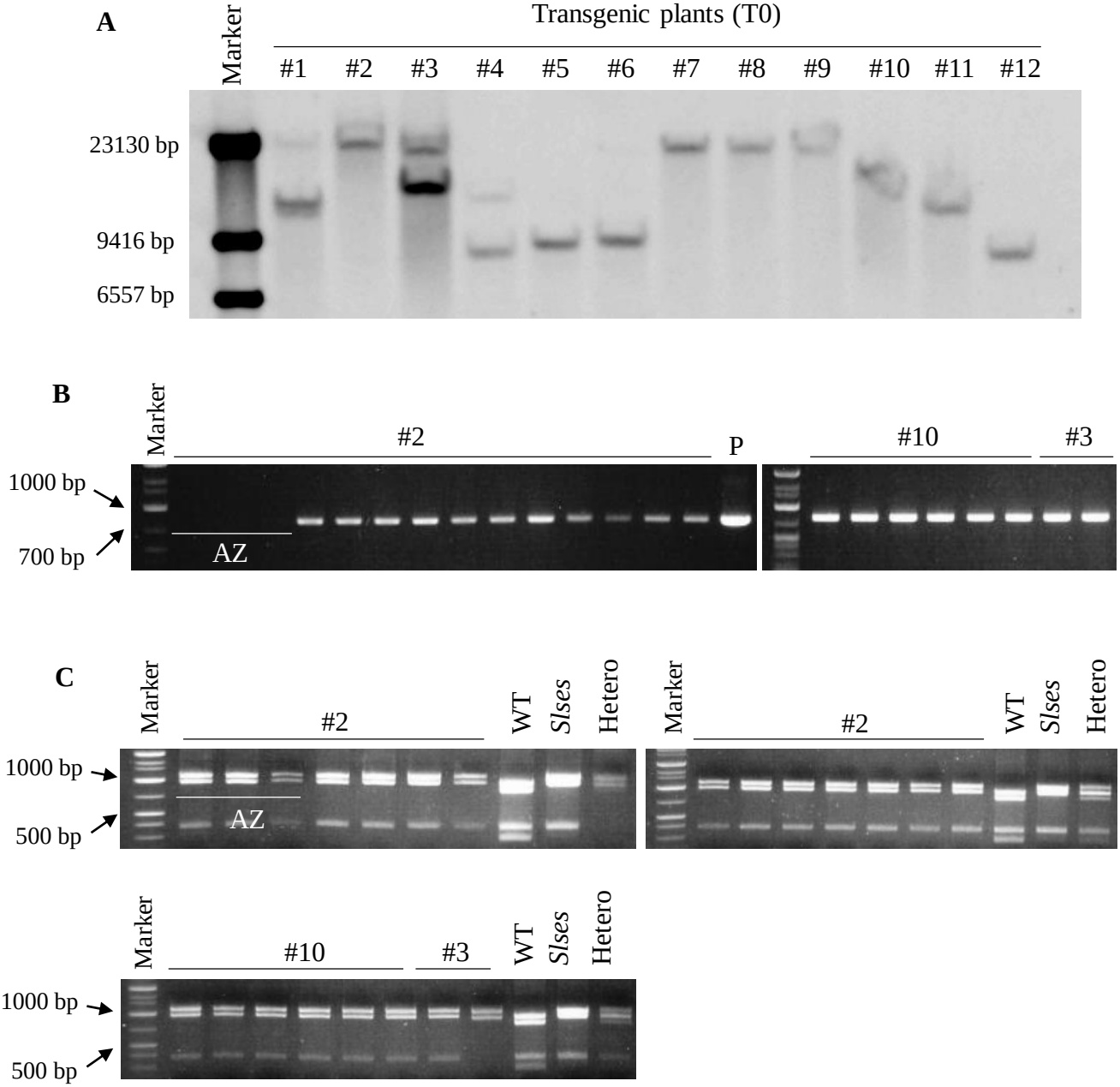
Micro-Tom WT and Ailsa Craig showed upper band (173-bp), the *slses* mutant showed lower band (160-bp) and the heterozygous showed both bands. All of F_2 plants which showed mutant phenotype had the 13-bp deletion. The F_2 population were constructed from crossed with 'Micro-Tom (MT)' WT or 'Ailsa Craig (AC)'. He, heterozygous.

A



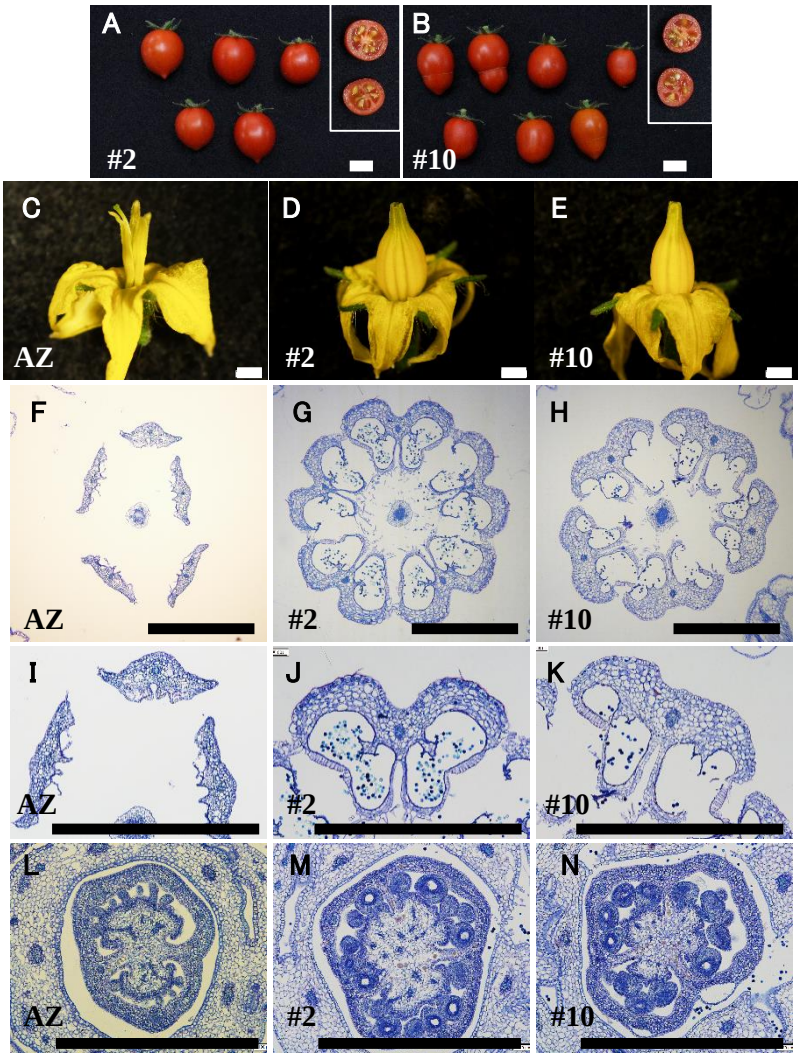
B

Supplementary Fig. S3. The vector map for the whole *SlSES* gene transgenic plant.
(A) Entire vector map constructed from pIG121Hm vector. (B) The transferred region to the plant, from right border (RB) to left border (LB). *NPTII* indicates kanamycin resistance gene. *HPT* indicates hygromycin resistance gene.

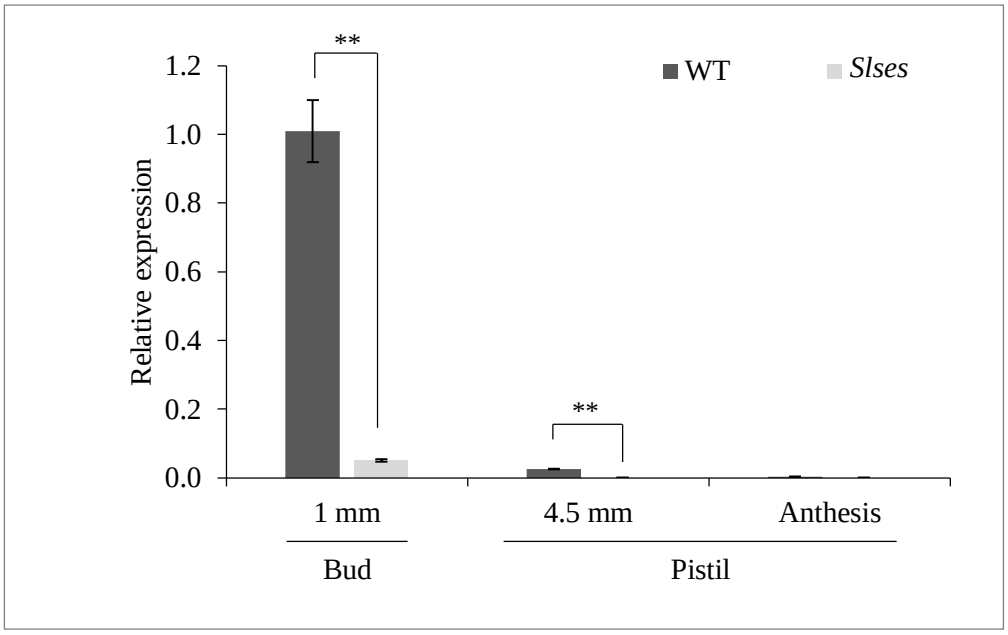


Supplementary Fig. S4. Selection of the plants which not only have transgene but also be the *Slses* homozygous genotype.

(A) Confirmation of copy numbers of transgene in the T0 plants by southern blotting analysis. The probe recognized *NPTII*. (B) *NPTII* existence confirmation in the T1 plants by *NPTII* marker (See supplementary Table S2). (C) The genotype analysis of the T1 plants by *SlSES* marker-2 (See supplementary Table S2). #2, #3, #10 indicate line number and P indicates used vector as a positive control. AZ, azygous; Hetero, heterozygous.



Supplementary Fig. S5. Complementation experiment verified *Solyc07g063670* was responsible for the *Slses* phenotypes. (A, B) The red ripe fruits of the transgenic *Slses* mutant in which *SlSES* whole gene was induced. Bar = 1 cm. (C-E) The anthesis flower. (F-N) The cross section of the flower at anthesis flower, (F-K) the anther and pollen, (L-N) the ovary and ovules. Bar = 1 mm. (A, D, G, J, M) The transgenic line #2, (B, E, H, K, N) the transgenic line #10, (C, F, I, L) azygous (AZ). AZ plant doesn't have transgenes.



Supplementary Fig. S6. The expression analysis of *SlSES* in WT and the *Slses* mutant by qRT-PCR.

The *SlSES* expression of the *Slses* mutant at 1 mm bud and 2 stages of pistils from 4.5 mm bud and anthesis stages. n = 3, error bar = SE, statistical analysis was realized using the Student's *t*-test, **P<0.01; *P<0.05.