Supplementary Information for the mauscript

Gene duplication and genetic exchange drive the evolution of S-RNase based self-incompatibility

Ken-ichi Kubo, Timothy Paape, Masaomi Hatakeyama, Tetsuyuki Entani, Akie Takara, Kie Kajihara, Mai Tsukahara, Rie Shimizu-Inatsugi, Kentaro K. Shimizu & Seiji Takayama

This supplementary pdf file contains the following information:
Supplementary Methods
Supplementary Material
Supplementary Figures 1–13
Supplementary Tables 1–14
Supplementary Reference

Supplementary Methods

Plant materials. Lines of S_5-, S_7-, S_9- and S_{11}-haplotypes from *Petunia hybrida*[9,51] and the lines of S_{17}-, S_{19}- and S_{C2}-haplotypes from *P. axillaris*[21,52] were described previously. In this research, we used additional lines of S_{10}-, S_{22}-, S_{0m}-, S_m-, and S_{22m}-haplotypes from *P. hybrida.* Homozygous self-compatible lines of S_m- and S_{0m}-haplotypes were the doubled-haploid line "Mitchell" and the inbred line W138, respectively[53]. *S-RNase* sequences were identified by degenerate PCR using primer sequences listed in Supplementary Table 3. *S-RNase* sequence from Mitchell (S_m-*RNase*) was novel, but *S-RNase* from W138 was identical with previously identified S_0-*RNase* from commercial SC *P. hybrida* cv. Strawberry Daddy[54]. Because we cannot judge the identity of *S*-haplotype only from *S-RNase* sequence, we named *S*-haplotype from W138 as S_{0m} in this work. Homozygous lines of S_{10}-, S_{22}- and S_{22m}-haplotypes were established in this work from three commercial lines of *P. hybrida*. We determined S_{22m}- and S_{C2}-haplotypes as pollen-side SC haplotypes by reciprocal pollination with S_{22}- and S_{17}-homozygous plants, respectively (Supplementary Fig. 10a,b; see main text). We confirmed that SC phenotypes were genetically linked to the *S*-locus in all SC lines.

The interspecific crosses between the lines from *P. hybrida* and *P. axillaris* were compatible, and all the resulting progenies were fertile. Therefore, we do not distinguish them, and simply refer to them as '*Petunia*' in this article.

Expression profiling. Template preparations and reaction conditions were described previously[9]. We conducted RT-PCR using *SLF* genes-specific primers (listed in Supplementary table 2) with 32 cycles for all of *SLF*s except for S_5-*SLF18*, for which reaction was conducted with 28 cycles.

Vector construction. Fragments containing open reading frames (ORFs) of S_5-*SLF3*, S_7-*SLF3*, S_{11}-*SLF3B*, S_7-*SLF9A* and S_{11}-*SLF9* were amplified with forward primers containing *Bam*HI sites and reverse primers containing *Sac*I sites. *pRI909-LAT52-pro:TAP:*S_{11}*-SLF3-35Spro:AtFT-LAT52-pro:Venus* plasmid vector[9] was digested with *Bam*HI and *Sac*I, and the S_{11}-*SLF3* coding region was replaced with these amplified fragments to yield vectors listed in Supplementary Fig. 3.

Plant transformation and *in vivo* function assay. S_7-*SLF1*-expressing plants with S_{22}-haplotype were obtained by crossing with S_7-*SLF1*-transgenic plants previously described[9]. Other transgenic plants were newly obtained by *Agrobacterium*-mediated plant transformations described previously[9]. Breeding histories, genotypes and SI phenotypes of all transgenic lines are listed in Supplementary Table 4.

Genotyping and linkage analysis by genomic PCR. Genotyping of transgenic plants and linkage analysis were performed as described[9]. Progenies segregating for S_5-, S_7-, S_9-, S_{11}-haplotypes were obtained from S_5S_{11} × S_7S_9 and S_5S_9 × S_7S_{11} crosses, and progenies segregating for S_{17}- and S_{19}-haplotypes were obtained from $S_{17}S_{19}$ × S_5S_5 and $S_{11}S_{11}$ × $S_{17}S_{19}$ crosses. Gene-specific primers not described[9] are listed in Supplementary Table 2.

Preparation of cDNA libraries and next generation sequencing. Total RNA was extracted from mature pollen of an S_7-homozygous plant and unopened mature anthers of S_5-, S_9-, S_{11}-, S_{17}-, S_{19}- and S_{0m}-homozygous plants, as described previously[9]. For sequencing of anther transcripts from S_{0m}-homozygous plant, poly $(A)^+$ RNA were enriched using Oligotex-dT30 super (Takara), and the preparation of cDNA library and the sequencing using GS Junior system were performed at Roche Diagnostics Japan (http://www.roche-diagnostics.jp). For sequencing of transcripts from other plants, cDNA libraries were prepared from total RNA using the SMARTer PCR cDNA synthesis kit (Clontech). Sequencings were performed using Roche 454 Genome Sequencer FLX System at Hokkaido System Science (for S_7-homozygous plant), and at the Functional Genomics Center Zurich (for all other plants). The sequenced reads information is summarized in Supplementary Table 14.

Monte-Carlo simulation of S-RNase proportion recognized by SLFs. Monte-Carlo simulation was conducted in order to consider the difference of recognition rates among SLF types. The proportion of S-RNases recognized by n SLF types, $P_S(n)$, was simulated by the following equation (4):

$$P_S(n) = \frac{\sum_{i=1}^{m} P_{Mi}(n)}{m} \tag{4}$$

$$P_{Mi}(n) = 1 - \prod_{j=1}^{n}(1 - P_{Tj})$$

where m is the number of bootstrapping sampling times and the n elements of $\{P_{Tj}\}$ are selected in each bootstrapping sampling time i at random with replacement from the recognition rates of each SLF type,

$$P_T := \left\{\frac{6}{12}, \frac{3}{6}, \frac{1}{6}, \frac{1}{8}, \frac{1}{8}, \frac{1}{8}, \frac{1}{8}, \frac{1}{6}, \frac{0}{6}\right\}. \qquad (5)$$

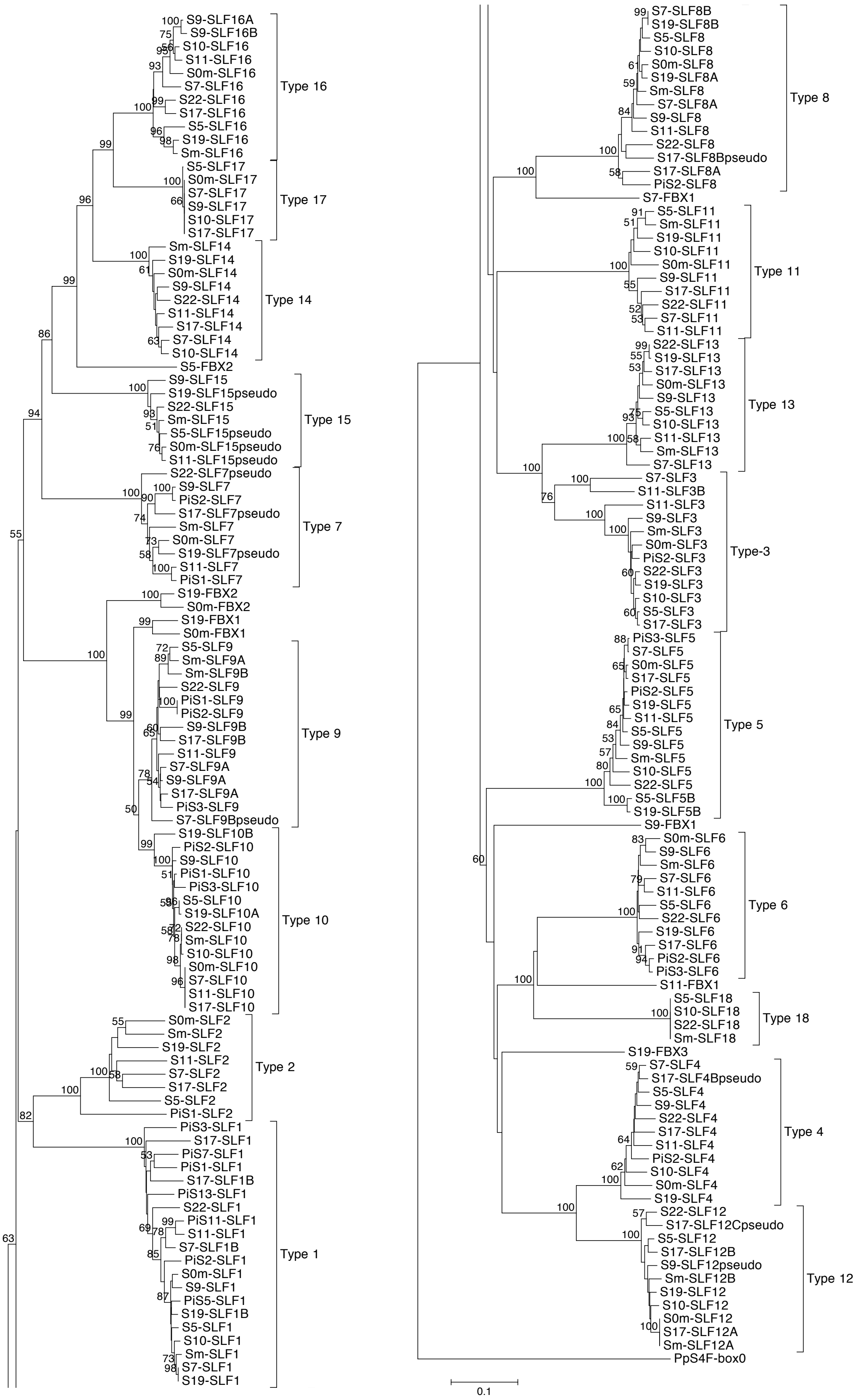
P_{Ti} corresponds to the recognition rate of SLF type i (Supplementary Table 13b). To calculate P_T, the recognition rates of SLF type, the interaction between SLF type and a particular S-RNase allelic variant is considered positive, when one or more allelic variants of the SLF type showed positive interaction experimentally. In this simulation, we used m = 10,000 times as bootstrapping sampling iteration. The Monte-Carlo simulation is implemented and performed in Ruby (ver. 1.9.3) (Supplementary Material). Mersenne Twister[55] was used for the random number generator in the Ruby script.

Supplementary Material Ruby script code that realizes the Monte-Carlo simulation for the estimation of the proportion of S-RNases recognized by *n* SLF types described in the Online Method.

```
#!/usr/bin/env ruby
# encoding: utf-8
# Date: 20140501
# Author: Masaomi Hatakeyama

TRIAL = 10000
N_MAX = 30
PROBS = [0.5, 0.5, 0.166666667, 0.125, 0.125, 0.125, 0.125, 0.166666667, 0.0]
SEED = 1234

srand(SEED)
dat_file = File.basename(__FILE__).gsub(/.rb/,'.dat')
plt_file = File.basename(__FILE__).gsub(/.rb/,'.plt')
png_file = File.basename(__FILE__).gsub(/.rb/,'.png')

class Array
  def sum
    inject(0.0) { |sum, i| sum += i }
  end
  def ave
    inject(0.0) { |sum, i| sum += i } / size
  end
  def var
    average = ave
    inject(0.0) { |sum, i| sum += (i - average)**2 } / (size-1)
  end
  def sd
    Math::sqrt(var)
  end
```

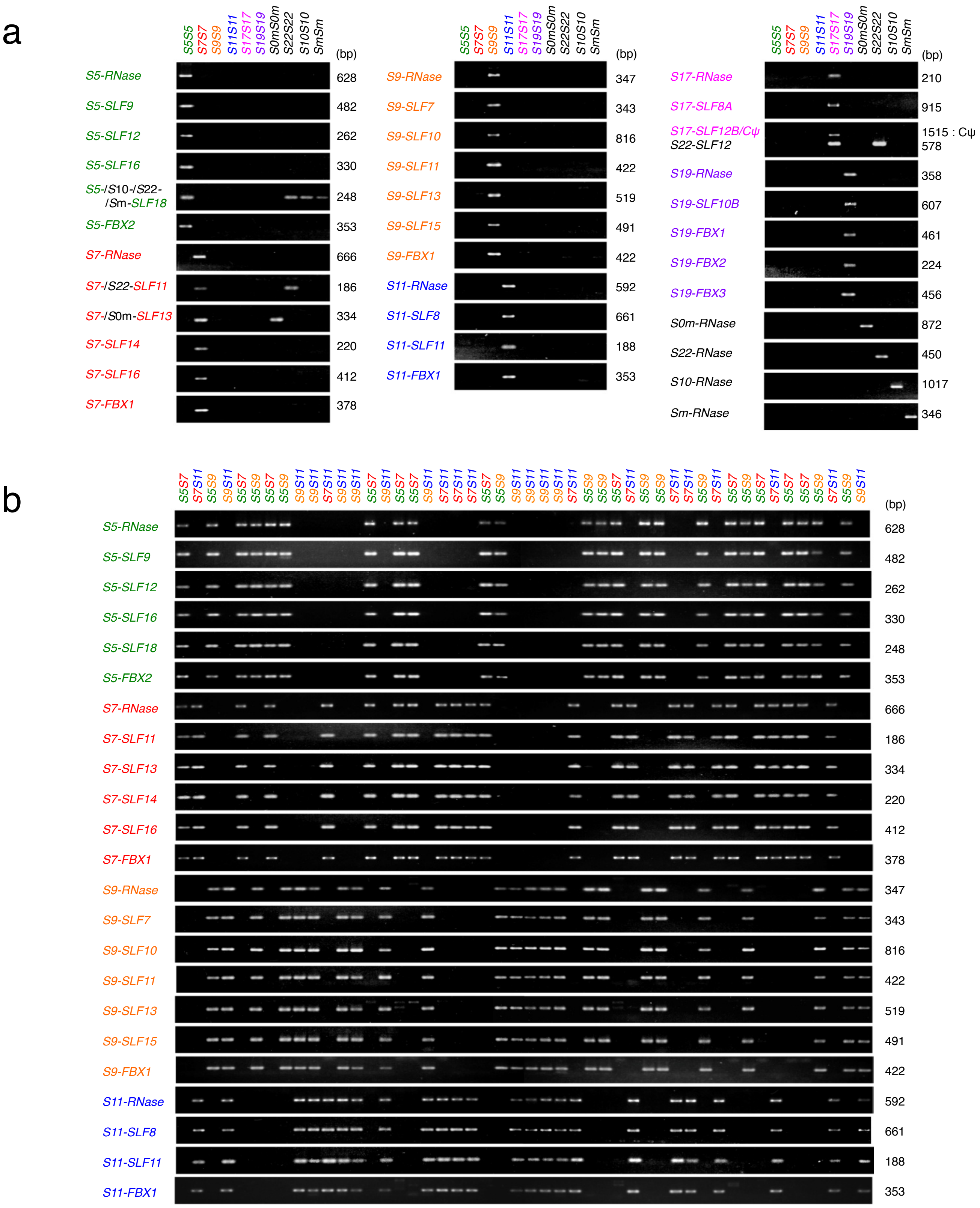
```
  def se
    sd/Math.sqrt(size)
  end
  def ci
    1.96*se
  end
end

def f(n,probs)
  fail_prob = 1.0
  n.times do
    px = probs[rand(probs.length)]
    fail_prob *= (1.0-px)
  end
  1.0-fail_prob
end

open(dat_file, "w") do |out|
  (1..N_MAX).each do |n|
    trials = []
    trials2 = []
    TRIAL.times do
      trials << f(n, PROBS)
    end
    #out.puts [n, trials.ave, trials.sd].join("¥t")
    out.puts [n, trials.ave, trials.ave-trials.sd, trials.ave+trials.sd].join("¥t")
  end
end

open(plt_file, "w") do |out|
  out.print <<-EOF
set xlabel "Number of SLF types"
set ylabel "SRNase recognized probability by SLF types"
```

```
set yrange[0.1:1.0]
set key below
set term png
set out "#{png_file}"
set arrow 1 from 20,0.1 to 20,1 nohead linewidth 0.1
set arrow 2 from 16,0.1 to 16,1 nohead linewidth 0.1
set arrow 3 from 18,0.1 to 18,1 nohead linewidth 0.1
set xtics('0' 0, '5' 5, '10' 10, '15' 15, '16' 16, '18' 18, '20' 20, '25' 25, '30' 30)
p '#{dat_file}' not w l,'#{dat_file}' u 1:2:3:4 not with yerrorbar, 0.95 not, 0.99 not
   EOF
end

command = "gnuplot -persist #{plt_file}"
puts command
system command
```

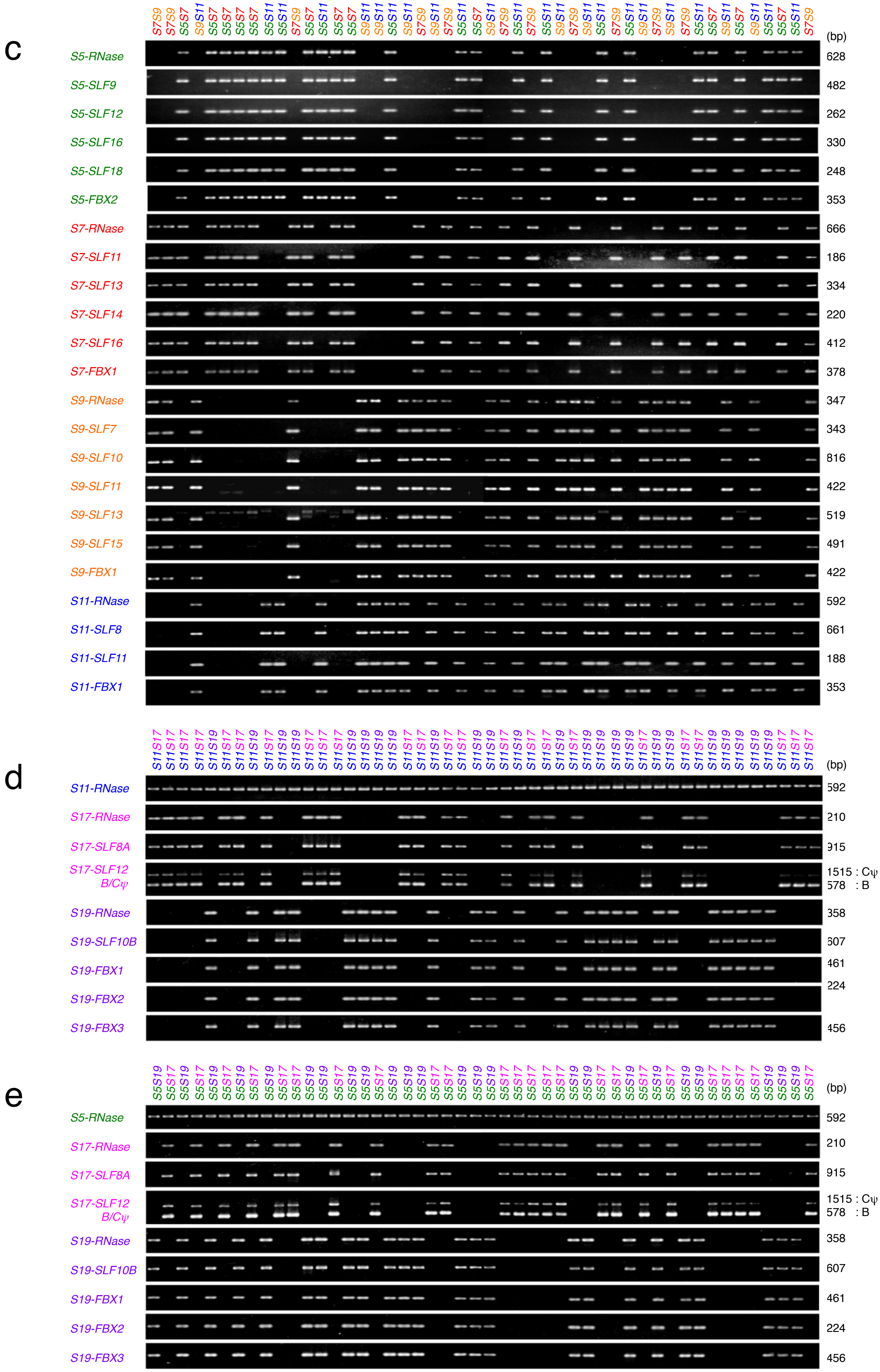

100
S9-SLF16A
75
S9-SLF16B
95
56
S10-SLF16
S11-SLF16
93
S0m-SLF16
S7-SLF16
Type 16
100
99
S22-SLF16
S17-SLF16
96
S5-SLF16
98
S19-SLF16
Sm-SLF16
99
S5-SLF17
100
S0m-SLF17
S7-SLF17
66
S9-SLF17
Type 17
96
S10-SLF17
S17-SLF17
100
Sm-SLF14
S19-SLF14
61
S0m-SLF14
99
S9-SLF14
S22-SLF14
Type 14
S11-SLF14
S17-SLF14
63
S7-SLF14
86
S10-SLF14
S5-FBX2
100
S9-SLF15
S19-SLF15pseudo
94
98
S22-SLF15
Sm-SLF15
Type 15
51
S5-SLF15pseudo
76
S0m-SLF15pseudo
S11-SLF15pseudo
S22-SLF7pseudo
100
S9-SLF7
100
90
PiS2-SLF7
S17-SLF7pseudo
74
Sm-SLF7
Type 7
55
73
S0m-SLF7
58
S19-SLF7pseudo
100
S11-SLF7
PiS1-SLF7
100
S19-FBX2
S0m-FBX2
99
S19-FBX1
S0m-FBX1
100
72
S5-SLF9
89
Sm-SLF9A
Sm-SLF9B
S22-SLF9
100
PiS1-SLF9
PiS2-SLF9
99
60
S9-SLF9B
65
S17-SLF9B
Type 9
S11-SLF9
S7-SLF9A
78
54
S9-SLF9A
S17-SLF9A
PiS3-SLF9
50
S7-SLF9Bpseudo
S19-SLF10B
99
PiS2-SLF10
100
S9-SLF10
51
PiS1-SLF10
PiS3-SLF10
58
96
S5-SLF10
S19-SLF10A
58
82
S22-SLF10
Type 10
78
Sm-SLF10
S10-SLF10
98
S0m-SLF10
96
S7-SLF10
S11-SLF10
S17-SLF10
55
S0m-SLF2
Sm-SLF2
S19-SLF2
S11-SLF2
100
58
S7-SLF2
Type 2
100
S17-SLF2
S5-SLF2
82
PiS1-SLF2
PiS3-SLF1
100
S17-SLF1
53
PiS7-SLF1
PiS1-SLF1
S17-SLF1B
PiS13-SLF1
S22-SLF1
99
PiS11-SLF1
69
78
S11-SLF1
63
S7-SLF1B
85
PiS2-SLF1
Type 1
S0m-SLF1
S9-SLF1
87
PiS5-SLF1
S19-SLF1B
S5-SLF1
S10-SLF1
73
Sm-SLF1
98
S7-SLF1
S19-SLF1
99
S7-SLF8B
S19-SLF8B
S5-SLF8
S10-SLF8
61
S0m-SLF8
S19-SLF8A
59
Sm-SLF8
Type 8
S7-SLF8A
84
S9-SLF8
S11-SLF8
100
S22-SLF8
S17-SLF8Bpseudo
100
58
S17-SLF8A
PiS2-SLF8
S7-FBX1
91
S5-SLF11
51
Sm-SLF11
S19-SLF11
S10-SLF11
100
S0m-SLF11
Type 11
55
S9-SLF11
S17-SLF11
52
S22-SLF11
53
S7-SLF11
S11-SLF11
99
S22-SLF13
55
S19-SLF13
53
S17-SLF13
S0m-SLF13
S9-SLF13
Type 13
93
75
S5-SLF13
S10-SLF13
100
58
S11-SLF13
Sm-SLF13
100
S7-SLF13
100
S7-SLF3
S11-SLF3B
76
S11-SLF3
100
S9-SLF3
100
Sm-SLF3
S0m-SLF3
PiS2-SLF3
Type-3
60
S22-SLF3
S19-SLF3
S10-SLF3
60
S5-SLF3
S17-SLF3
88
PiS3-SLF5
S7-SLF5
65
S0m-SLF5
S17-SLF5
PiS2-SLF5
65
S19-SLF5
84
S11-SLF5
Type 5
S5-SLF5
53
S9-SLF5
57
Sm-SLF5
80
S10-SLF5
100
S22-SLF5
100
S5-SLF5B
S19-SLF5B
S9-FBX1
83
S0m-SLF6
S9-SLF6
60
Sm-SLF6
79
S7-SLF6
S11-SLF6
100
S5-SLF6
Type 6
S22-SLF6
S19-SLF6
91
S17-SLF6
94
PiS2-SLF6
PiS3-SLF6
100
S11-FBX1
S5-SLF18
100
S10-SLF18
Type 18
S22-SLF18
Sm-SLF18
S19-FBX3
59
S7-SLF4
S17-SLF4Bpseudo
S5-SLF4
S9-SLF4
S22-SLF4
Type 4
64
S17-SLF4
S11-SLF4
PiS2-SLF4
62
S10-SLF4
100
S0m-SLF4
S19-SLF4
100
57
S22-SLF12
S17-SLF12Cpseudo
100
S5-SLF12
S17-SLF12B
S9-SLF12pseudo
Sm-SLF12B
Type 12
S19-SLF12
S10-SLF12
S0m-SLF12
100
S17-SLF12A
Sm-SLF12A
PpS4F-box0
0.1

sup. Fig. 1

Supplementary Figure 1 Phylogeny of SLFs from *Petunia*. Phylogenetic tree of deduced amino-acid sequences of SLFs shown in Fig.1 is described without the compressed representation. For details, see METHODS and caption of Fig. 1. Based on this phylogeny, previously identified S_7-*SLF3* (Ref. 9) is now assigned into a clade type-13, and renamed as S_7-*SLF13*. Instead, we newly identified *SLF* that belongs to the type-3 clade from S_7-haplotype, and named it as S_7-*SLF3*. The phylogeny also suggests that the previously identified *SLF*-like genes, *SLFLa*, *SLFLb*, *A113* and *A134*, are alleles of type 7–10 *SLF*s, and renamed as *SLF7*, *SLF8*, *SLF9*, and *SLF10*, respectively[37,56]. Information of accession codes and synonyms of *SLF*s used in this phylogenetic analysis was summarized in Supplementary Tables 1 and 9.

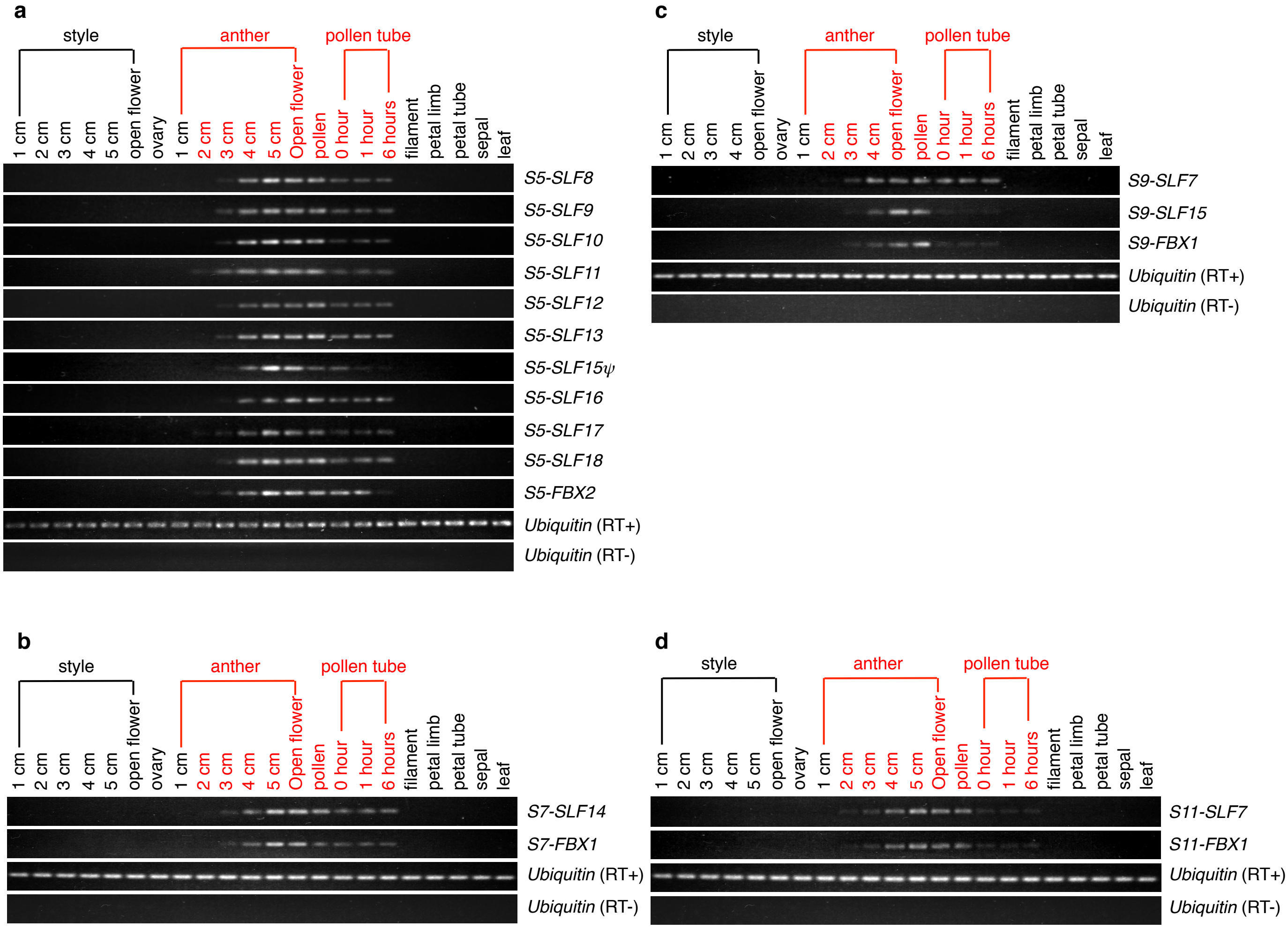

a
S5S5
S7S7
S9S9
S11S11
S17S17
S19S19
S0mS0m
S22S22
S10S10
SmSm
(bp)
S5-RNase 628
S5-SLF9 482
S5-SLF12 262
S5-SLF16 330
S5-/S10-/S22-/Sm-SLF18 248
S5-FBX2 353
S7-RNase 666
S7-/S22-SLF11 186
S7-/S0m-SLF13 334
S7-SLF14 220
S7-SLF16 412
S7-FBX1 378
S9-RNase 347
S9-SLF7 343
S9-SLF10 816
S9-SLF11 422
S9-SLF13 519
S9-SLF15 491
S9-FBX1 422
S11-RNase 592
S11-SLF8 661
S11-SLF11 188
S11-FBX1 353
S17-RNase 210
S17-SLF8A 915
S17-SLF12B/Cψ 1515 : Cψ
S22-SLF12 578
S19-RNase 358
S19-SLF10B 607
S19-FBX1 461
S19-FBX2 224
S19-FBX3 456
S0m-RNase 872
S22-RNase 450
S10-RNase 1017
Sm-RNase 346
b
S5S7 S7S11 S5S9 S9S11 S5S7 S5S9 S5S7 S5S9 S9S11 S9S11 S7S11 S9S11 S9S11 S5S7 S9S11 S5S7 S5S7 S9S11 S7S11 S7S11 S7S11 S5S7 S5S9 S9S11 S9S11 S9S11 S9S11 S7S11 S5S9 S5S9 S5S7 S7S11 S5S9 S5S9 S7S11 S7S11 S5S9 S7S11 S5S7 S5S9 S5S7 S7S11 S5S7 S5S7 S5S9 S7S11 S5S9 S9S11
(bp)
S5-RNase 628
S5-SLF9 482
S5-SLF12 262
S5-SLF16 330
S5-SLF18 248
S5-FBX2 353
S7-RNase 666
S7-SLF11 186
S7-SLF13 334
S7-SLF14 220
S7-SLF16 412
S7-FBX1 378
S9-RNase 347
S9-SLF7 343
S9-SLF10 816
S9-SLF11 422
S9-SLF13 519
S9-SLF15 491
S9-FBX1 422
S11-RNase 592
S11-SLF8 661
S11-SLF11 188
S11-FBX1 353

sup. Fig. 2

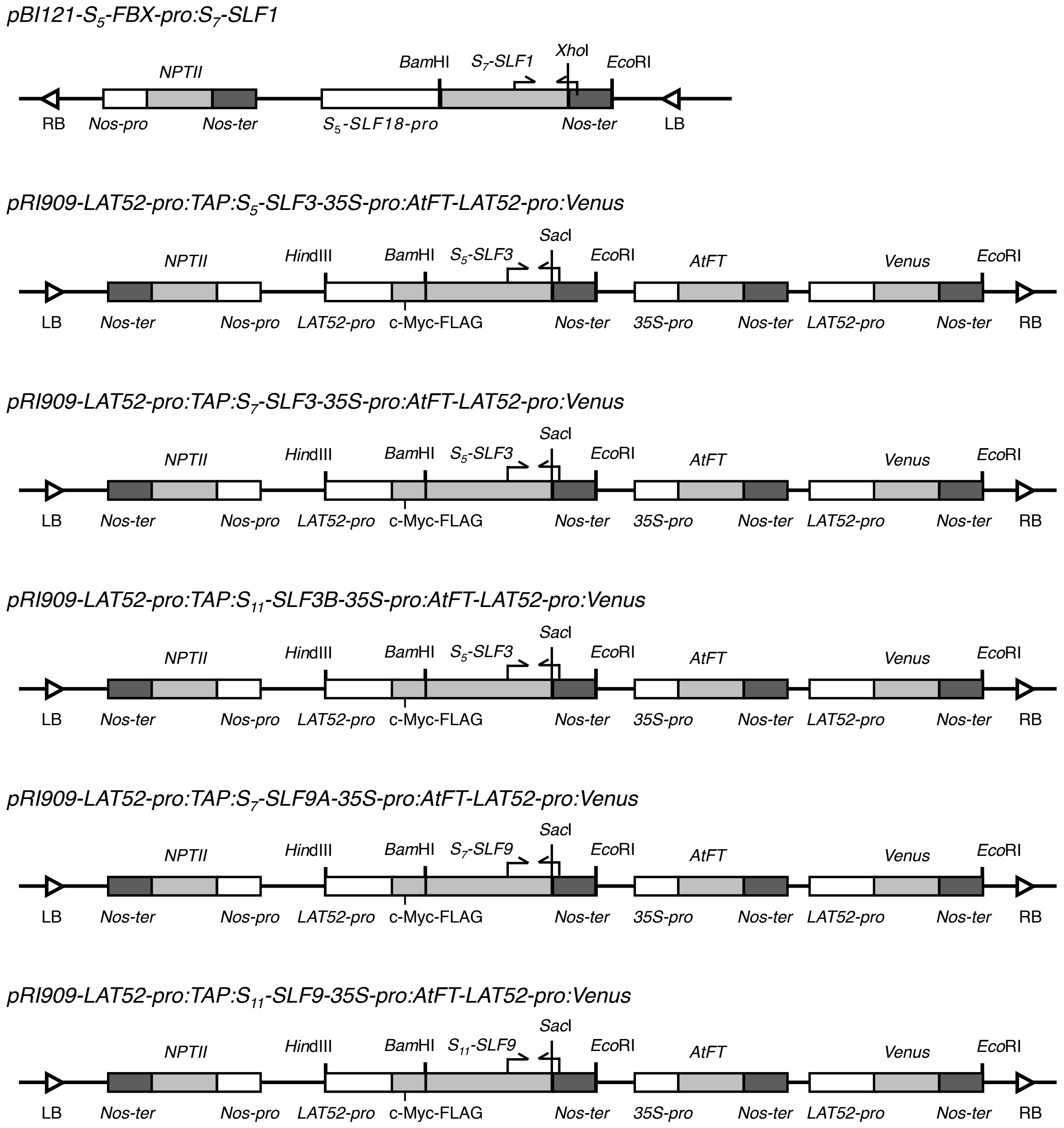

c
S7S9 S7S9 S5S7 S9S11 S5S7 S5S7 S5S7 S5S7 S5S11 S5S11 S7S9 S5S7 S5S11 S5S7 S5S7 S9S11 S9S11 S5S11 S9S11 S7S9 S9S11 S7S9 S5S11 S5S7 S9S11 S7S9 S5S11 S7S9 S5S11 S9S11 S7S9 S9S11 S5S11 S7S9 S5S11 S9S11 S7S9 S9S11 S7S9 S5S11 S5S7 S9S11 S5S7 S9S11 S5S11 S5S7 S5S11 S7S9
(bp)
S5-RNase 628
S5-SLF9 482
S5-SLF12 262
S5-SLF16 330
S5-SLF18 248
S5-FBX2 353
S7-RNase 666
S7-SLF11 186
S7-SLF13 334
S7-SLF14 220
S7-SLF16 412
S7-FBX1 378
S9-RNase 347
S9-SLF7 343
S9-SLF10 816
S9-SLF11 422
S9-SLF13 519
S9-SLF15 491
S9-FBX1 422
S11-RNase 592
S11-SLF8 661
S11-SLF11 188
S11-FBX1 353
d
S11S17 S11S17 S11S17 S11S17 S11S19 S11S17 S11S17 S11S19 S11S17 S11S19 S11S19 S11S17 S11S17 S11S17 S11S19 S11S19 S11S19 S11S19 S11S17 S11S17 S11S19 S11S17 S11S17 S11S19 S11S19 S11S17 S11S19 S11S17 S11S17 S11S19 S11S17 S11S19 S11S19 S11S19 S11S19 S11S17 S11S19 S11S19 S11S17 S11S17 S11S19 S11S19 S11S19 S11S19 S11S19 S11S17 S11S17 S11S17
(bp)
S11-RNase 592
S17-RNase 210
S17-SLF8A 915
S17-SLF12 B/Cψ 1515 : Cψ 578 : B
S19-RNase 358
S19-SLF10B 607
S19-FBX1 461
S19-FBX2 224
S19-FBX3 456
e
S5S19 S5S17 S5S19 S5S17 S5S19 S5S17 S5S19 S5S17 S5S19 S5S17 S5S17 S5S19 S5S19 S5S17 S5S19 S5S19 S5S17 S5S19 S5S19 S5S19 S5S17 S5S17 S5S19 S5S19 S5S19 S5S17 S5S17 S5S17 S5S17 S5S17 S5S19 S5S19 S5S17 S5S17 S5S19 S5S17 S5S19 S5S17 S5S19 S5S19 S5S17 S5S17 S5S17 S5S17 S5S19 S5S19 S5S19 S5S17
(bp)
S5-RNase 592
S17-RNase 210
S17-SLF8A 915
S17-SLF12 B/Cψ 1515 : Cψ 578 : B
S19-RNase 358
S19-SLF10B 607
S19-FBX1 461
S19-FBX2 224
S19-FBX3 456

sup. Fig. 2

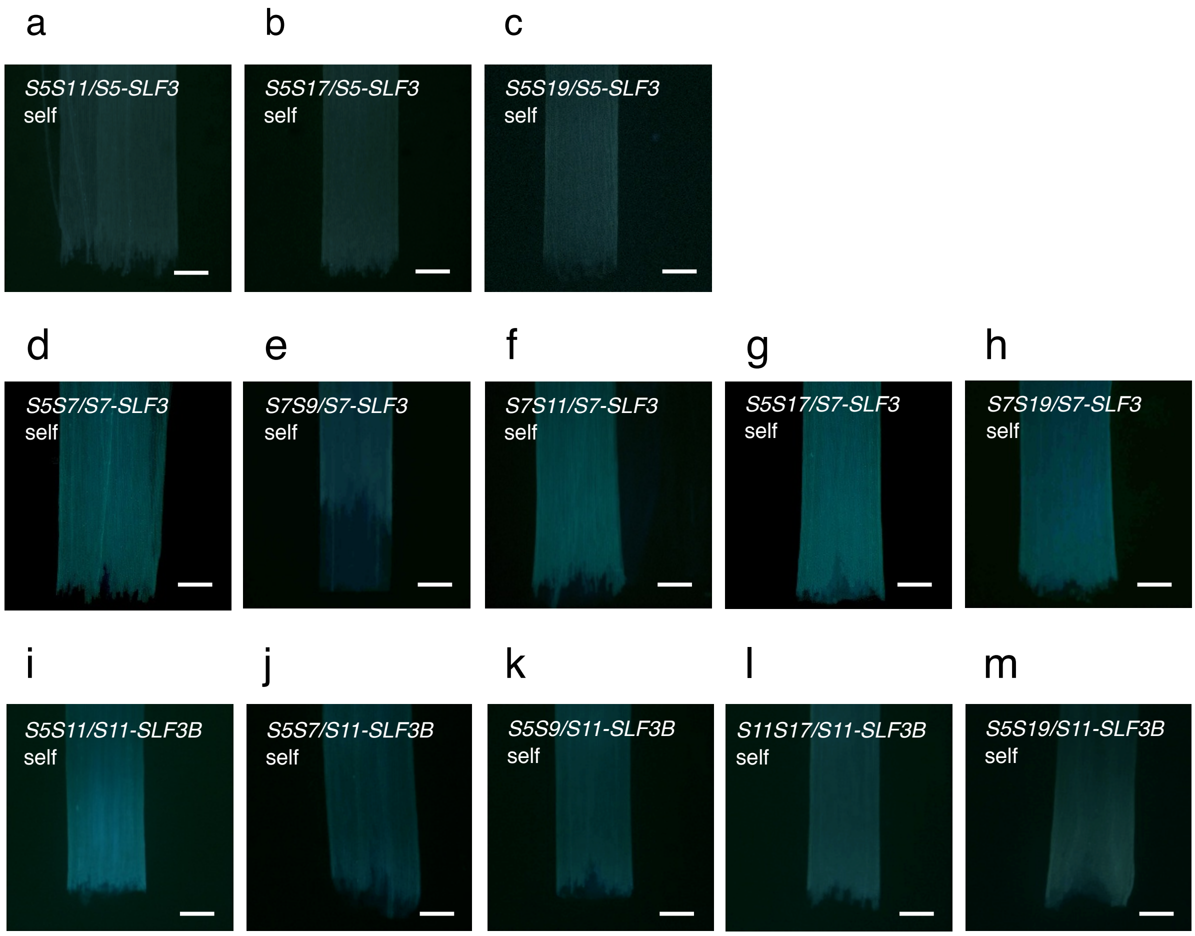
Supplementary Figure 2 Genetic linkage between *SLF*s and *S-RNase*. (**a**) PCR was performed using genomic DNA prepared from *S*-homozygous plants to evaluate the specificity of primer pairs. Primers are listed in Supplementary Table 2. (**b, c**) Genetic linkage analyses between *S-RNase* and *SLF* genes of S_5-, S_7-, S_9- and S_{11}-haplotypes. PCR was performed using genomic DNA prepared from 48 progeny plants of an S_5S_{11} × S_7S_9 cross (b), and from 48 progeny plants of an S_5S_9 × S_7S_{11} cross (c). (**d, e**) Genetic linkage analyses between *S-RNase* and *SLF* genes of S_{17}- and S_{19}-haplotypes. PCR was performed on genomic DNA prepared from 48 progeny plants of an $S_{11}S_{11}$ × $S_{17}S_{19}$ cross (d) and from 48 progeny plants of an $S_{17}S_{19}$ × S_5S_5 cross (e).



Supplementary Figure 3 Newly isolated *SLF* genes show a male reproductive organ-specific expression profile. RT-PCR analyses of the expression profiles of six types of *SLF* genes in (**A**) S_5-, (**B**) S_7-, (**C**) S_9- and (**D**) S_{11}-homozyogotes. cDNA was prepared from each *S*-homozygote, and Type-7 to Type-18 *SLF*s and ungrouped *SLF*-like F-box (*FBX*) genes were amplified by specific primer pairs. The *ubiquitin* gene was also amplified and electrophoresed as a control. All primer sequences are shown in Supplementary Table 2.

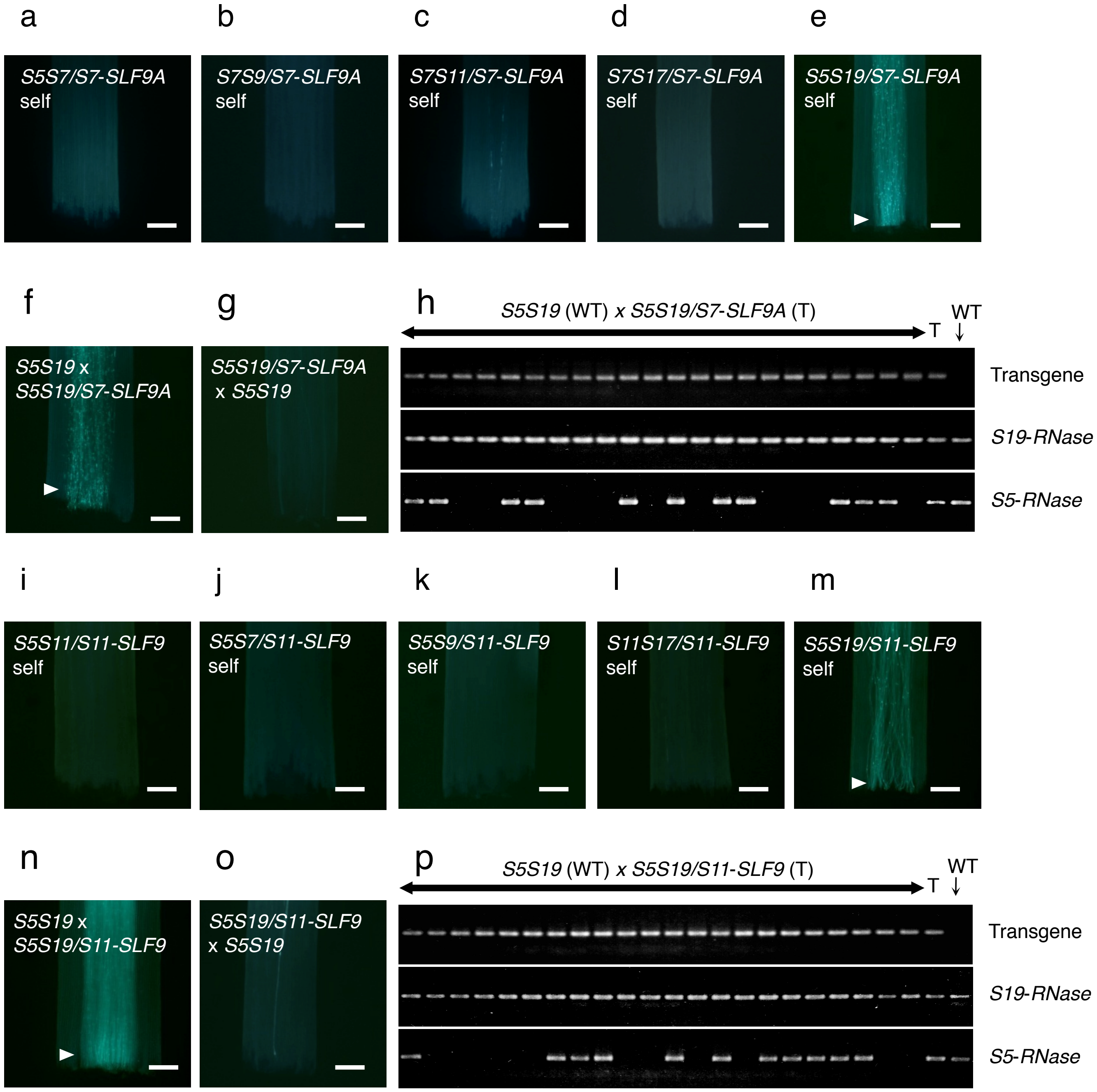


Supplementary Figure 4 Schematic representation of transgene constructs used for transformation experiments. The region between the right border (RB) and left border (LB) is integrated into transgenic plants. *Nos*, the gene encoding nopaline synthase; *pro*, promoter; *ter*, transcription terminator; *LAT52-pro*, pollen/pollen tube-specific *LAT52* promoter of tomato[57]; *35S-pro*, Cauliflower mosaic virus *35S* promoter; *S_5-SLF18-pro*, 2028 bp of the upstream region of the *S_5-SLF18* gene; *NPTII*, the gene encoding neomycin phosphotransferase II (conferring kanamycin resistance); *AtFT*, *Arabidopsis thaliana FLOWERING LOCUS T* gene (accelerating flowering and to shortening the experimental time period)[58]; *Venus*, the gene encoding enhanced yellow fluorescent protein[59]. Small arrows denote the locations of the forward and reverse primers used in PCR genotyping and RT-PCR analysis of each transgene (for primer sequences, see Supplementary Table 2).



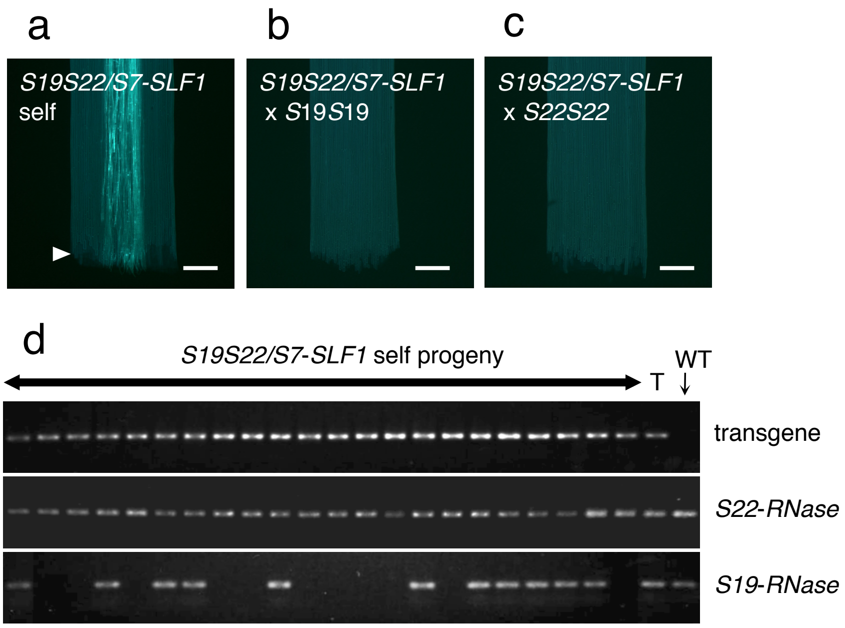
Supplementary Figure 5 Representative results of transgenic experiments to detect the *in vivo* interaction between type-3 SLFs and S_7-RNase. (**a–c**) Pollen tubes derived from S_5-*SLF3* transgenic plants were stained with aniline blue and monitored by fluorescence microscopy. The S_5S_{11}/S_5-*SLF3* (**a**), S_5S_{17}/S_5-*SLF3* (**b**) and S_5S_{19}/S_5-*SLF3* (**c**) transgenic plants retained SI, indicating that S_5-SLF3 did not recognize and detoxify S_5-, S_{11}-, S_{17}-, and S_{19}-RNases. (**d–h**) Pollen tubes derived from S_7-*SLF3*–transgenic plants were stained with aniline blue and monitored by fluorescence microscopy. All transgenic plants exhibited SI, indicating that S_7-SLF3 did not recognize and detoxify S_5-, S_7-, S_9-, S_{11}-, S_{17}-, and S_{19}-RNases. (**i–m**) Pollen tubes derived from S_{11}-*SLF3B*–transgenic plants were stained with aniline blue and monitored by fluorescence microscopy. All transgenic plants exhibited SI, indicating that S_{11}-SLF3B did not recognize and detoxify S_5-, S_7-, S_9-, S_{11}-, S_{17}-, and S_{19}-RNases. Bars = 200 μm.

sup. Fig. 5

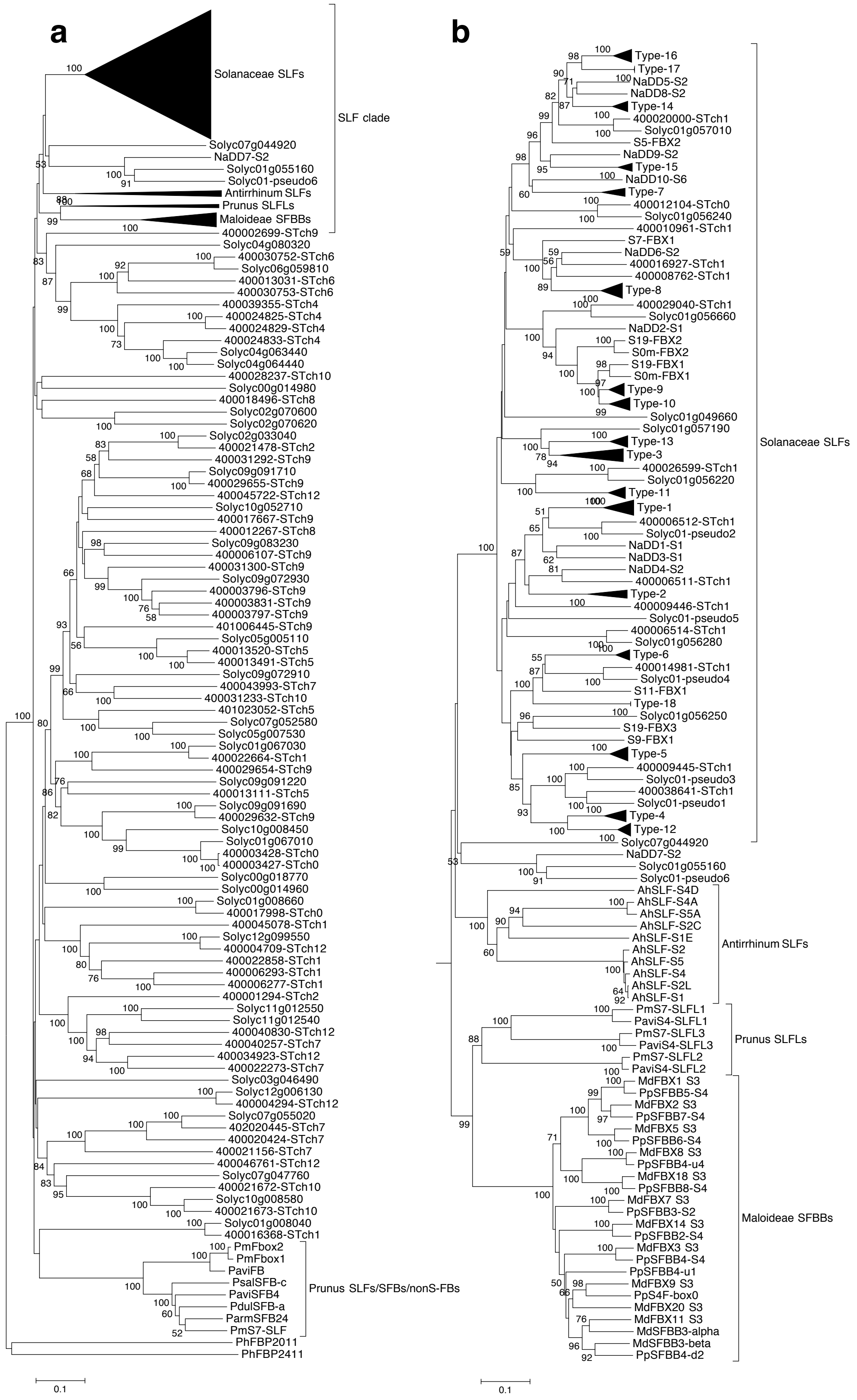

a
S5S7/S7-SLF9A self
b
S7S9/S7-SLF9A self
c
S7S11/S7-SLF9A self
d
S7S17/S7-SLF9A self
e
S5S19/S7-SLF9A self
f
S5S19 x S5S19/S7-SLF9A
g
S5S19/S7-SLF9A x S5S19
h
S5S19 (WT) x S5S19/S7-SLF9A (T)
T
WT
Transgene
S19-RNase
S5-RNase
i
S5S11/S11-SLF9 self
j
S5S7/S11-SLF9 self
k
S5S9/S11-SLF9 self
l
S11S17/S11-SLF9 self
m
S5S19/S11-SLF9 self
n
S5S19 x S5S19/S11-SLF9
o
S5S19/S11-SLF9 x S5S19
p
S5S19 (WT) x S5S19/S11-SLF9 (T)
T
WT
Transgene
S19-RNase
S5-RNase

sup. Fig. 6

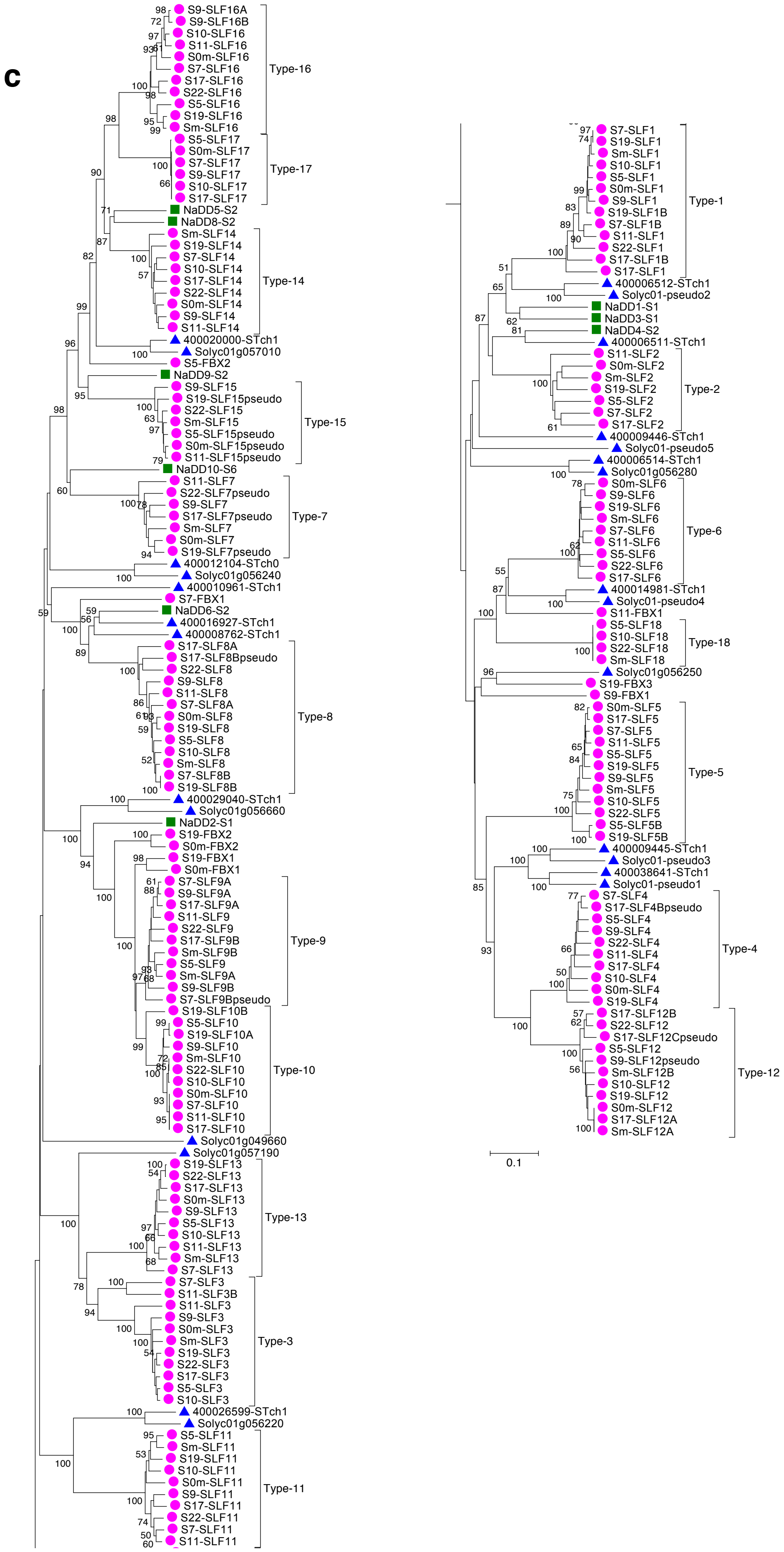
Supplementary Figure 6 Representative results of transgenic experiments to demonstrate *in vivo* interaction between type-9 SLFs (S_7-SLF9A, and S_{11}-SLF9) and S_{19}-RNase. (**a–g**) Pollen tube growth derived from S_7-*SLF9A*–transgenic plants. S_5S_7/S_7-*SLF9A* (**a**), S_7S_9/S_7-*SLF9A* (**b**), S_7S_{11}/S_7-*SLF9A* (**c**) and S_7S_{17}/S_7-*SLF9A* (**d**) retained SI, suggesting that S_7-SLF9A does not recognize S_5-, S_7-, S_9-, S_{11}- and S_{17}-RNases. S_5S_{19}/S_7-*SLF9A* (**e**) exhibited SC. The reciprocal cross (**f, g**) indicated the SI breakdown occurred in pollen. (**h**) PCR genotyping of 22 progeny plants obtained by crossing S_5S_{19} (WT) with pollen from S_5S_{19}/S_7-*SLF9A* (T). These results suggest that S_7-SLF9A recognizes S_{19}-RNase as a target. (**i-p**) Pollen tube growth derived from S_{11}-*SLF9*–transgenic plants. S_5S_{11}/S_{11}-*SLF9* (**i**), S_5S_7/S_{11}-*SLF9* (**j**), S_5S_9/S_{11}-*SLF9* (**k**) and $S_{11}S_{17}/S_{11}$-*SLF9* (**l**) retained SI, suggesting that S_{11}-SLF9 does not recognize S_5-, S_7-, S_9- S_{11}- and S_{17}-RNases. S_5S_{19}/S_{11}-*SLF9* (**m**) exhibited SC. The reciprocal cross (**n, o**) indicated the SI breakdown occurred in pollen. (**p**) PCR genotyping of 22 progeny plants obtained by crossing S_5S_{19} (WT) with pollen from S_5S_{19}/S_{11}-*SLF9* (T). These results suggest that S_{11}-SLF9 recognizes S_{19}-RNase as a target. Bars = 200 μm.



Supplementary Figure 7 Representative results of transgenic experiments to demonstrate the *in vivo* interaction between S_7-SLF1 and S_{22}-RNase. (**a**-**c**) Pollination phenotype of $S_{19}S_{22}/S_7$-*SLF1* transgenic plants. $S_{19}S_{22}/S_7$-*SLF1* exhibited breakdown of SI (a), whereas pistil of $S_{19}S_{22}/S_7$-*SLF1* retained incompatibility against pollen from S_{19}-homozygote (b) and S_{22}-homozygote (c). (**d**) PCR genotyping of 22 progeny plants obtained by selfing of $S_{19}S_{22}/S_7$-*SLF1* (T).

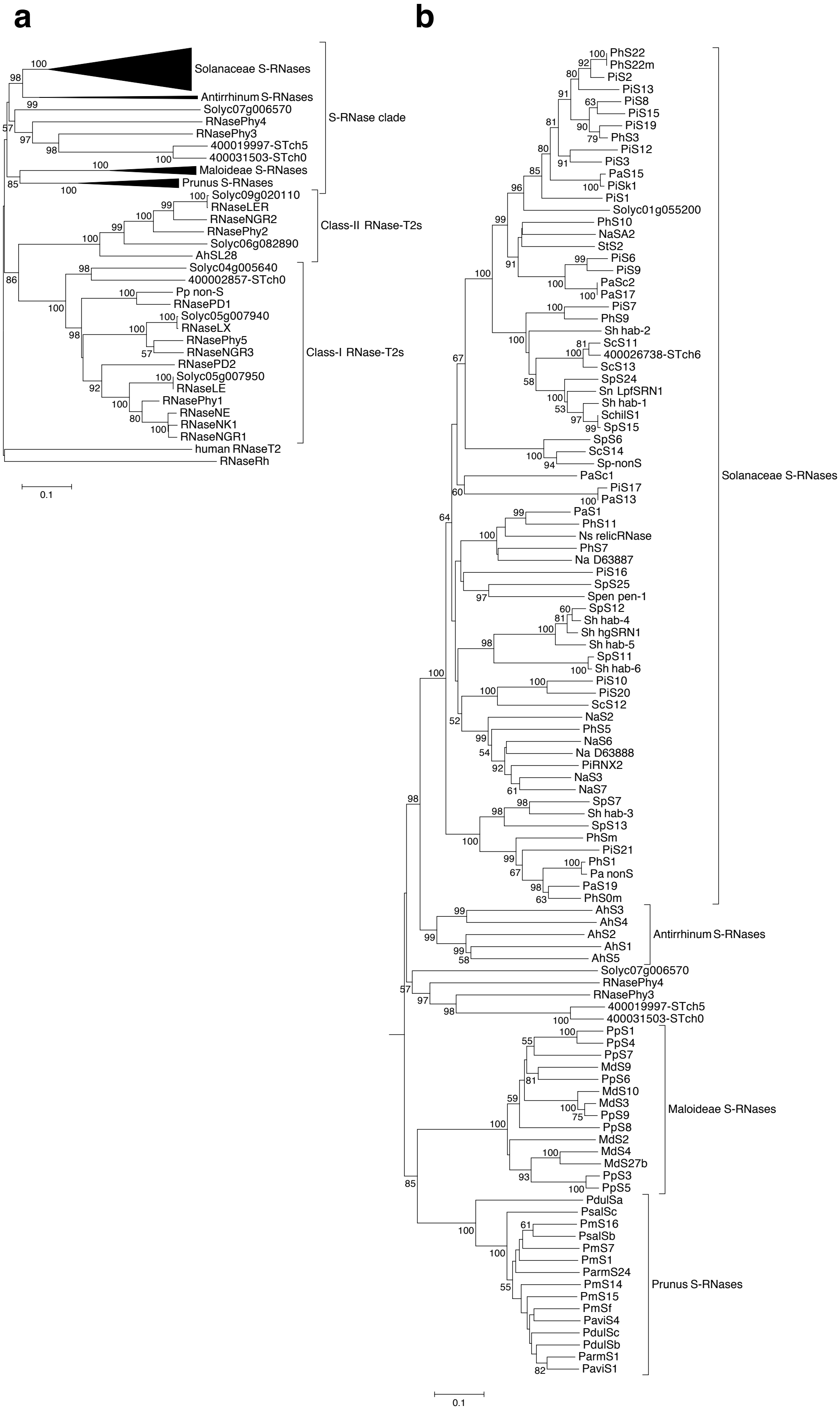

a
Solanaceae SLFs
SLF clade
Solyc07g044920
NaDD7-S2
Solyc01g055160
Solyc01-pseudo6
Antirrhinum SLFs
Prunus SLFLs
Maloideae SFBBs
400002699-STch9
Solyc04g080320
400030752-STch6
Solyc06g059810
400013031-STch6
400030753-STch6
400039355-STch4
400024825-STch4
400024829-STch4
400024833-STch4
Solyc04g063440
Solyc04g064440
400028237-STch10
Solyc00g014980
400018496-STch8
Solyc02g070600
Solyc02g070620
Solyc02g033040
400021478-STch2
400031292-STch9
Solyc09g091710
400029655-STch9
400045722-STch12
Solyc10g052710
400017667-STch9
400012267-STch8
Solyc09g083230
400006107-STch9
400031300-STch9
Solyc09g072930
400003796-STch9
400003831-STch9
400003797-STch9
401006445-STch9
Solyc05g005110
400013520-STch5
400013491-STch5
Solyc09g072910
400043993-STch7
400031233-STch10
401023052-STch5
Solyc07g052580
Solyc05g007530
Solyc01g067030
400022664-STch1
400029654-STch9
Solyc09g091220
400013111-STch5
Solyc09g091690
400029632-STch9
Solyc10g008450
Solyc01g067010
400003428-STch0
400003427-STch0
Solyc00g018770
Solyc00g014960
Solyc01g008660
400017998-STch0
400045078-STch1
Solyc12g099550
400004709-STch12
400022858-STch1
400006293-STch1
400006277-STch1
400001294-STch2
Solyc11g012550
Solyc11g012540
400040830-STch12
400040257-STch7
400034923-STch12
400022273-STch7
Solyc03g046490
Solyc12g006130
400004294-STch12
Solyc07g055020
402020445-STch7
400020424-STch7
400021156-STch7
400046761-STch12
Solyc07g047760
400021672-STch10
Solyc10g008580
400021673-STch10
Solyc01g008040
400016368-STch1
PmFbox2
PmFbox1
PaviFB
PsalSFB-c
PaviSFB4
PdulSFB-a
ParmSFB24
PmS7-SLF
Prunus SLFs/SFBs/nonS-FBs
PhFBP2011
PhFBP2411
0.1
b
Type-16
Type-17
NaDD5-S2
NaDD8-S2
Type-14
400020000-STch1
Solyc01g057010
S5-FBX2
NaDD9-S2
Type-15
NaDD10-S6
Type-7
400012104-STch0
Solyc01g056240
400010961-STch1
S7-FBX1
NaDD6-S2
400016927-STch1
400008762-STch1
Type-8
400029040-STch1
Solyc01g056660
NaDD2-S1
S19-FBX2
S0m-FBX2
S19-FBX1
S0m-FBX1
Type-9
Type-10
Solyc01g049660
Solyc01g057190
Type-13
Type-3
400026599-STch1
Solyc01g056220
Type-11
Type-1
400006512-STch1
Solyc01-pseudo2
NaDD1-S1
NaDD3-S1
NaDD4-S2
400006511-STch1
Type-2
400009446-STch1
Solyc01-pseudo5
400006514-STch1
Solyc01g056280
Type-6
400014981-STch1
Solyc01-pseudo4
S11-FBX1
Type-18
Solyc01g056250
S19-FBX3
S9-FBX1
Type-5
400009445-STch1
Solyc01-pseudo3
400038641-STch1
Solyc01-pseudo1
Type-4
Type-12
Solyc07g044920
Solanaceae SLFs
NaDD7-S2
Solyc01g055160
Solyc01-pseudo6
AhSLF-S4D
AhSLF-S4A
AhSLF-S5A
AhSLF-S2C
AhSLF-S1E
AhSLF-S2
AhSLF-S5
AhSLF-S4
AhSLF-S2L
AhSLF-S1
Antirrhinum SLFs
PmS7-SLFL1
PaviS4-SLFL1
PmS7-SLFL3
PaviS4-SLFL3
PmS7-SLFL2
PaviS4-SLFL2
Prunus SLFLs
MdFBX1 S3
PpSFBB5-S4
MdFBX2 S3
PpSFBB7-S4
MdFBX5 S3
PpSFBB6-S4
MdFBX8 S3
PpSFBB4-u4
MdFBX18 S3
PpSFBB8-S4
MdFBX7 S3
PpSFBB3-S2
MdFBX14 S3
PpSFBB2-S4
MdFBX3 S3
PpSFBB4-S4
PpSFBB4-u1
MdFBX9 S3
PpS4F-box0
MdFBX20 S3
MdFBX11 S3
MdSFBB3-alpha
MdSFBB3-beta
PpSFBB4-d2
Maloideae SFBBs
0.1

sup. Fig. 8


c
S9-SLF16A
S9-SLF16B
S10-SLF16
S11-SLF16
S0m-SLF16
S7-SLF16
S17-SLF16
S22-SLF16
S5-SLF16
S19-SLF16
Sm-SLF16
Type-16
S5-SLF17
S0m-SLF17
S7-SLF17
S9-SLF17
S10-SLF17
S17-SLF17
Type-17
NaDD5-S2
NaDD8-S2
Sm-SLF14
S19-SLF14
S7-SLF14
S10-SLF14
S17-SLF14
S22-SLF14
S0m-SLF14
S9-SLF14
S11-SLF14
Type-14
400020000-STch1
Solyc01g057010
S5-FBX2
NaDD9-S2
S9-SLF15
S19-SLF15pseudo
S22-SLF15
Sm-SLF15
S5-SLF15pseudo
S0m-SLF15pseudo
S11-SLF15pseudo
Type-15
NaDD10-S6
S11-SLF7
S22-SLF7pseudo
S9-SLF7
S17-SLF7pseudo
Sm-SLF7
S0m-SLF7
S19-SLF7pseudo
Type-7
400012104-STch0
Solyc01g056240
400010961-STch1
S7-FBX1
NaDD6-S2
400016927-STch1
400008762-STch1
S17-SLF8A
S17-SLF8Bpseudo
S22-SLF8
S9-SLF8
S11-SLF8
S7-SLF8A
S0m-SLF8
S19-SLF8
S5-SLF8
S10-SLF8
Sm-SLF8
S7-SLF8B
S19-SLF8B
Type-8
400029040-STch1
Solyc01g056660
NaDD2-S1
S19-FBX2
S0m-FBX2
S19-FBX1
S0m-FBX1
S7-SLF9A
S9-SLF9A
S17-SLF9A
S11-SLF9
S22-SLF9
S17-SLF9B
Sm-SLF9B
S5-SLF9
Sm-SLF9A
S9-SLF9B
S7-SLF9Bpseudo
Type-9
S19-SLF10B
S5-SLF10
S19-SLF10A
S9-SLF10
Sm-SLF10
S22-SLF10
S10-SLF10
S0m-SLF10
S7-SLF10
S11-SLF10
S17-SLF10
Type-10
Solyc01g049660
Solyc01g057190
S19-SLF13
S22-SLF13
S17-SLF13
S0m-SLF13
S9-SLF13
S5-SLF13
S10-SLF13
S11-SLF13
Sm-SLF13
S7-SLF13
Type-13
S7-SLF3
S11-SLF3B
S11-SLF3
S9-SLF3
S0m-SLF3
Sm-SLF3
S19-SLF3
S22-SLF3
S17-SLF3
S5-SLF3
S10-SLF3
Type-3
400026599-STch1
Solyc01g056220
S5-SLF11
Sm-SLF11
S19-SLF11
S10-SLF11
S0m-SLF11
S9-SLF11
S17-SLF11
S22-SLF11
S7-SLF11
S11-SLF11
Type-11
S7-SLF1
S19-SLF1
Sm-SLF1
S10-SLF1
S5-SLF1
S0m-SLF1
S9-SLF1
S19-SLF1B
S7-SLF1B
S11-SLF1
S22-SLF1
S17-SLF1B
S17-SLF1
Type-1
400006512-STch1
Solyc01-pseudo2
NaDD1-S1
NaDD3-S1
NaDD4-S2
400006511-STch1
S11-SLF2
S0m-SLF2
Sm-SLF2
S19-SLF2
S5-SLF2
S7-SLF2
S17-SLF2
Type-2
400009446-STch1
Solyc01-pseudo5
400006514-STch1
Solyc01g056280
S0m-SLF6
S9-SLF6
S19-SLF6
Sm-SLF6
S7-SLF6
S11-SLF6
S5-SLF6
S22-SLF6
S17-SLF6
Type-6
400014981-STch1
Solyc01-pseudo4
S11-FBX1
S5-SLF18
S10-SLF18
S22-SLF18
Sm-SLF18
Type-18
Solyc01g056250
S19-FBX3
S9-FBX1
S0m-SLF5
S17-SLF5
S7-SLF5
S11-SLF5
S5-SLF5
S19-SLF5
S9-SLF5
Sm-SLF5
S10-SLF5
S22-SLF5
S5-SLF5B
S19-SLF5B
Type-5
400009445-STch1
Solyc01-pseudo3
400038641-STch1
Solyc01-pseudo1
S7-SLF4
S17-SLF4Bpseudo
S5-SLF4
S9-SLF4
S22-SLF4
S11-SLF4
S17-SLF4
S10-SLF4
S0m-SLF4
S19-SLF4
Type-4
S17-SLF12B
S22-SLF12
S17-SLF12Cpseudo
S5-SLF12
S9-SLF12pseudo
Sm-SLF12B
S10-SLF12
S19-SLF12
S0m-SLF12
S17-SLF12A
Sm-SLF12A
Type-12
0.1

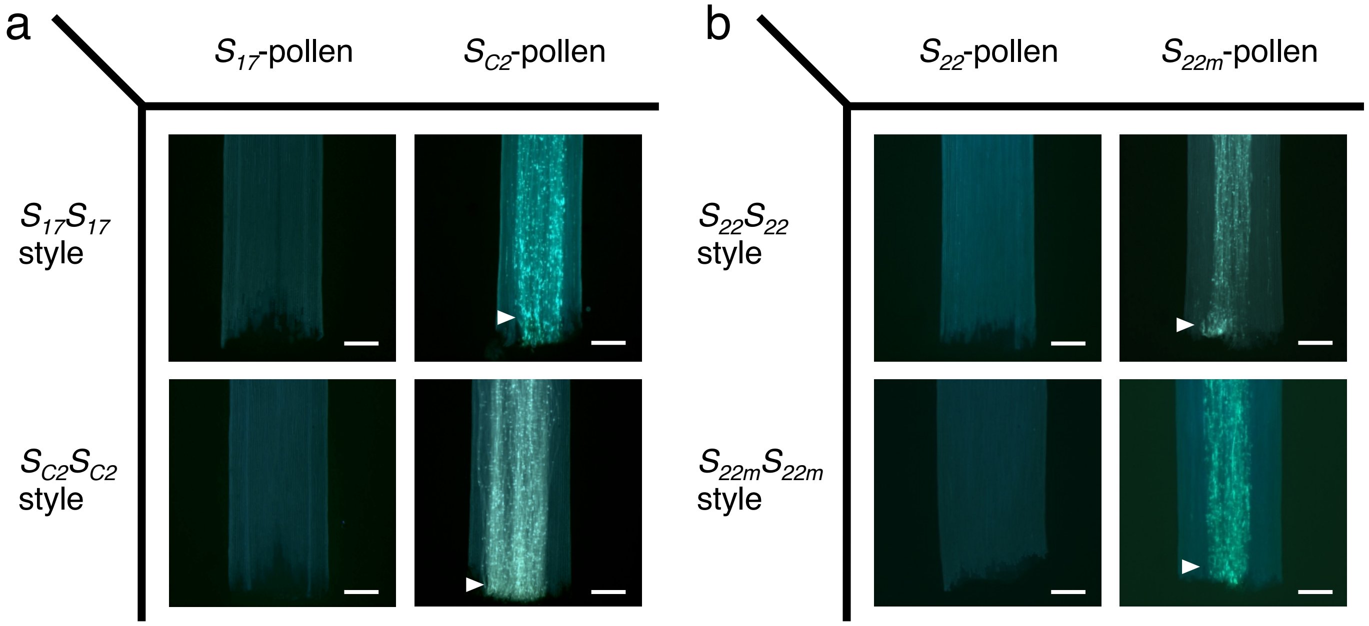
sup. Fig. 8

Supplementary Figure 8 Phylogenies of SLF-related F-boxes from species possessing S-RNase-based SI. (**a**) Whole tree constructed by using *Petunia* SLFs and all BLAST hits from the tomato and potato databases, as well as other SLF-related F-box proteins from Solanaceae, Plantaginaceae, and Rosaceae. PiFBP2011 and PiFBP2411 from *Petunia inflata* were used as the outgroup[60]. For other details, see Online Methods and the caption of Fig. 3. In this tree, Solanaceae SLF, Antirrhinum SLF, Prunus SLFL, and Maloideae SFBB clades are shown in compressed representation (black triangles). A subtree of Solanaceae SLFs is shown in Fig. 3a. (**b**) Subtree of SLF clade in (a) is shown. *Petunia* SLFs types are shown in compressed representation (black triangles). (**c**) Subtree of Solanaceae SLF clade (see Fig. 3a) is shown without compression. Round red markers indicate *SLF*s from genus *Petunia* (*P. hybrida*, *P. axillaris* and *P. inflata*); blue, genus *Solanum* (*Solanum lycopersicum*, *S. tuberosum* and their relatives); green, genus *Nicotiana*. 'PGSC0003DMG' is omitted from each potato gene ID to simplify, and '-STchx' is attached to indicate genes located on *S. tuberosum* chromosome x.


a
Solanaceae S-RNases
Antirrhinum S-RNases
Solyc07g006570
RNasePhy4
RNasePhy3
400019997-STch5
400031503-STch0
Maloideae S-RNases
Prunus S-RNases
S-RNase clade
Solyc09g020110
RNaseLER
RNaseNGR2
RNasePhy2
Solyc06g082890
AhSL28
Class-II RNase-T2s
Solyc04g005640
400002857-STch0
Pp non-S
RNasePD1
Solyc05g007940
RNaseLX
RNasePhy5
RNaseNGR3
RNasePD2
Solyc05g007950
RNaseLE
RNasePhy1
RNaseNE
RNaseNK1
RNaseNGR1
Class-I RNase-T2s
human RNaseT2
RNaseRh
0.1
b
PhS22
PhS22m
PiS2
PiS13
PiS8
PiS15
PiS19
PhS3
PiS12
PiS3
PaS15
PiSk1
PiS1
Solyc01g055200
PhS10
NaSA2
StS2
PiS6
PiS9
PaSc2
PaS17
PiS7
PhS9
Sh hab-2
ScS11
400026738-STch6
ScS13
SpS24
Sn LpfSRN1
Sh hab-1
SchilS1
SpS15
SpS6
ScS14
Sp-nonS
PaSc1
PiS17
PaS13
PaS1
PhS11
Ns relicRNase
PhS7
Na D63887
PiS16
SpS25
Spen pen-1
SpS12
Sh hab-4
Sh hgSRN1
Sh hab-5
SpS11
Sh hab-6
PiS10
PiS20
ScS12
NaS2
PhS5
NaS6
Na D63888
PiRNX2
NaS3
NaS7
SpS7
Sh hab-3
SpS13
PhSm
PiS21
PhS1
Pa nonS
PaS19
PhS0m
Solanaceae S-RNases
AhS3
AhS4
AhS2
AhS1
AhS5
Antirrhinum S-RNases
Solyc07g006570
RNasePhy4
RNasePhy3
400019997-STch5
400031503-STch0
PpS1
PpS4
PpS7
MdS9
PpS6
MdS10
MdS3
PpS9
PpS8
MdS2
MdS4
MdS27b
PpS3
PpS5
Maloideae S-RNases
PdulSa
PsalSc
PmS16
PsalSb
PmS7
PmS1
ParmS24
PmS14
PmS15
PmSf
PaviS4
PdulSc
PdulSb
ParmS1
PaviS1
Prunus S-RNases
0.1

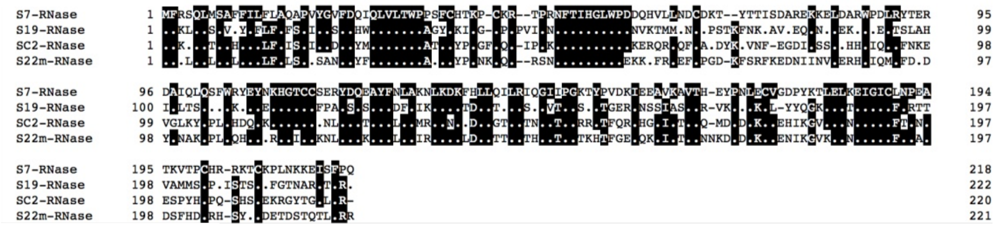
sup. Fig. 9

Supplementary Figure 9 Phylogenies of S-RNase-related RNase-T2s from species possessing S-RNase-based SI. (**a**) Whole tree constructed using *Petunia* S-RNases and all hits from BLAST searches of the tomato and potato databases, as well as other RNase-T2s from Solanaceae, Plantaginaceae and Rosaceae. Classification of RNase-T2 is made according to refs. 61 and 62. RNase-T2s from human and the filamentous fungus *Rhizopus niveus* were used as outgroup[63,64]. For other details, see METHODS and the caption of Fig. 3. In this tree, S-RNase clades from Solanaceae, Antirrhinum, Prunus, and Maloideae are shown in compressed representation (black triangles). A subtree of Solanaceae S-RNases clade is shown in Fig. 3b. (**b**) Subtree of S-RNase clade in (a) is shown without compression.

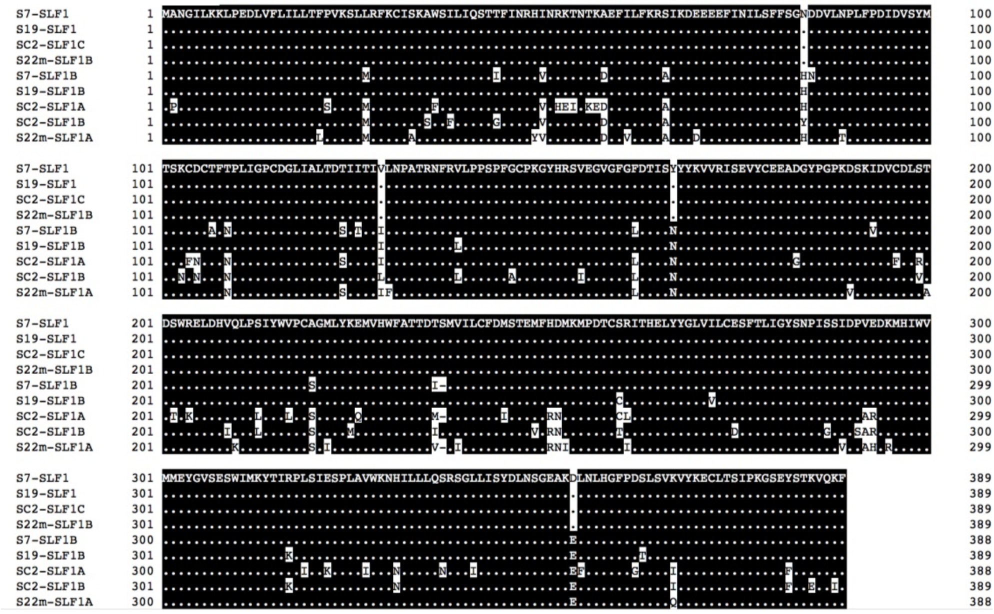


Supplementary Figure 10 S_{C2}- and S_{22m}-haplotypes are the pollen-side SC haplotypes. Reciprocal pollination tests between SC S_{C2}- and SI S_{17}-homozygous plants (**a**) and between SC S_{22m}- and SI S_{22}-homozygous plants (**b**). Pollen tubes were stained with aniline blue, and the compatibility was judged by the presence of a large number of pollen tubes at the basal end of the style (arrowhead). Bars = 200 µm.

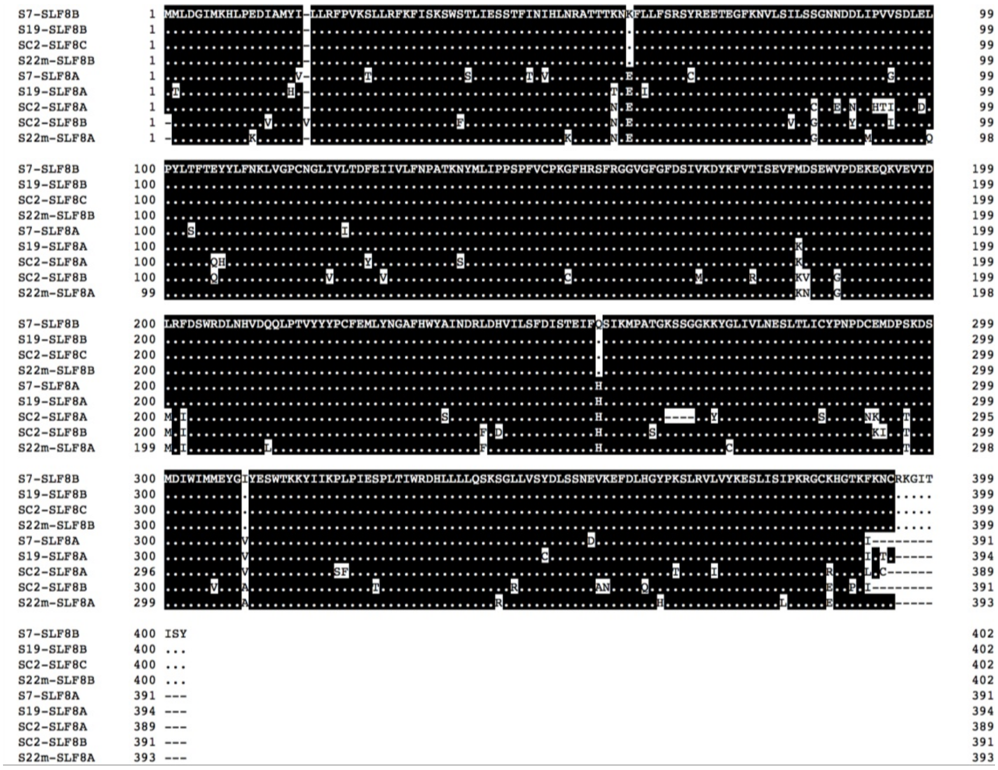
a. S-RNases



b. SLF1s

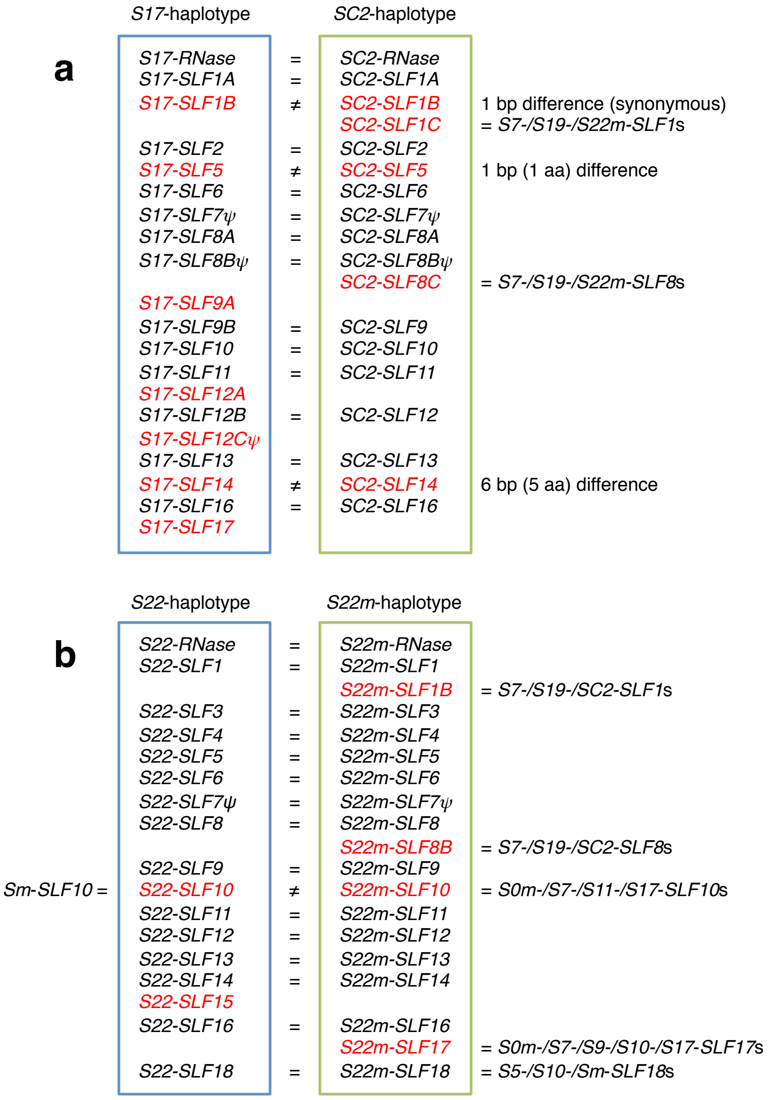


c. SLF8s



sup. Fig. 11

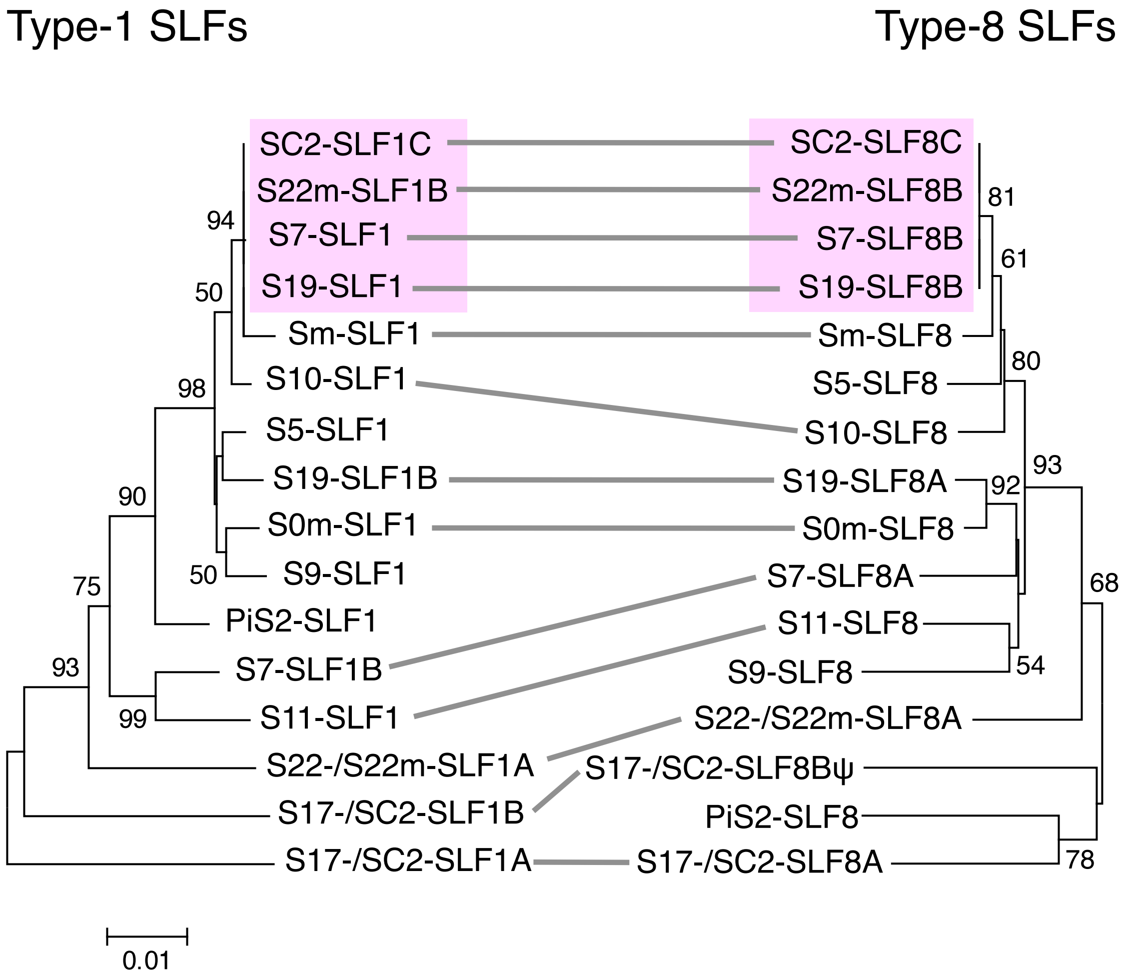
Supplementary Figure 11 S_7-, S_{19}-, S_{22m}-, S_{C2}-haplotypes share identical *SLF1* and *SLF8*. Alignment of deduced amino-acid sequences of S-RNases (**a**), SLF1s (**b**) and SLF8s (**c**) from S_7-, S_{19}-, S_{22m}-, and S_{C2}-haplotypes of *Petunia*. Deduced amino-acid sequences were aligned using MEGA5.2.2 and illustrated using the GENETYX-MAC (ver. 16.0.6). Amino-acid residues conserved in more than half of the aligned sequences are shown by darkened background. Amino-acid residues identical with the first line are indicated by dots. Gaps are indicated by hyphens.



S17-haplotype		*SC2*-haplotype	
S17-RNase	=	*SC2-RNase*	
S17-SLF1A	=	*SC2-SLF1A*	
S17-SLF1B	≠	*SC2-SLF1B*	1 bp difference (synonymous)
		SC2-SLF1C	= *S7-/S19-/S22m-SLF1*s
S17-SLF2	=	*SC2-SLF2*	
S17-SLF5	≠	*SC2-SLF5*	1 bp (1 aa) difference
S17-SLF6	=	*SC2-SLF6*	
S17-SLF7ψ	=	*SC2-SLF7ψ*	
S17-SLF8A	=	*SC2-SLF8A*	
S17-SLF8Bψ	=	*SC2-SLF8Bψ*	
		SC2-SLF8C	= *S7-/S19-/S22m-SLF8*s
S17-SLF9A			
S17-SLF9B	=	*SC2-SLF9*	
S17-SLF10	=	*SC2-SLF10*	
S17-SLF11	=	*SC2-SLF11*	
S17-SLF12A			
S17-SLF12B	=	*SC2-SLF12*	
S17-SLF12Cψ			
S17-SLF13	=	*SC2-SLF13*	
S17-SLF14	≠	*SC2-SLF14*	6 bp (5 aa) difference
S17-SLF16	=	*SC2-SLF16*	
S17-SLF17			

	S22-haplotype		*S22m*-haplotype	
	S22-RNase	=	*S22m-RNase*	
	S22-SLF1	=	*S22m-SLF1*	
			S22m-SLF1B	= *S7-/S19-/SC2-SLF1*s
	S22-SLF3	=	*S22m-SLF3*	
	S22-SLF4	=	*S22m-SLF4*	
	S22-SLF5	=	*S22m-SLF5*	
	S22-SLF6	=	*S22m-SLF6*	
	S22-SLF7ψ	=	*S22m-SLF7ψ*	
	S22-SLF8	=	*S22m-SLF8*	
			S22m-SLF8B	= *S7-/S19-/SC2-SLF8*s
	S22-SLF9	=	*S22m-SLF9*	
Sm-SLF10 =	*S22-SLF10*	≠	*S22m-SLF10*	= *S0m-/S7-/S11-/S17-SLF10*s
	S22-SLF11	=	*S22m-SLF11*	
	S22-SLF12	=	*S22m-SLF12*	
	S22-SLF13	=	*S22m-SLF13*	
	S22-SLF14	=	*S22m-SLF14*	
	S22-SLF15			
	S22-SLF16	=	*S22m-SLF16*	
			S22m-SLF17	= *S0m-/S7-/S9-/S10-/S17-SLF17*s
	S22-SLF18	=	*S22m-SLF18*	= *S5-/S10-/Sm-SLF18*s

Supplementary Figure 12 Self-compatible S_{C2}- and S_{22m}-haplotypes have different *SLF* repertoires from self-incompatible S_{17}- and S_{22}-haplotypes, respectively. Red characters indicate differential *SLF*s. ψ indicates pseudogene. (**a**) Comparisons of *SLF*-repertoires between S_{C2}- and S_{17}-haplotypes. No gene corresponding to S_{17}-*SLF9A*, S_{17}-*SLF12A* or S_{17}-*SLF17* was found from the S_{C2}-haplotype. 1–6-bp substitutions were detected in *SLF1*, *SLF5* and *SLF14*. (**b**) Comparisons of *SLF*-repertoires between S_{22}- and S_{22m}-haplotypes. Type-3, -4, -5, -6, -7, -8, -9, -11, -12, -13, -14 and -16 *SLF*s shared completely identical sequences, whereas the type-10 *SLF*s had four nucleotide differences affecting three amino acids. We hypothesized that this difference is the result of inter-haplotypic gene exchange, because S_{22}- and S_{22m}-*SLF10*s were identical with S_m-*SLF10* and S_{0m}-/S_7-/S_{11}-/S_{17}-*SLF10*, respectively. Type-15 *SLF* was not found from S_{22m}-haplotype, while type-17 *SLF* was not found from S_{22}-haplotype.



Supplementary Figure 13 Coevolutionary relationships between type-1 and type-8 SLFs. Neighbor-joining phylogenic trees of type-1 and -8 SLFs were created with MEGA 5.2.2. Both trees are shown in the same scale; the bar for each tree indicates the number of base substitutions per site. Numbers on the branches indicate bootstrap values >50% with 1,000 trials. Identical SLF1 and SLF8 shared among four different *S*-haplotypes are highlighted in pink. Horizontal gray lines indicated gene pairs on the same *S*-haplotypes holding similar branching patterns.

Supplementary Table 1 Repertoire of SLF genes identified in our research

***S5*-haplotype**

Gene	RPKM	Accession ID	References	Note
S5-SLF1	23.72	AB568390	ref. 9	interact with S9- and S17-RNases
S5-SLF2	2.28	AB568394	ref. 9	interact with S9- and S11-RNases
S5-SLF3	13.50	AB568399	ref. 9	interact with S7-RNases
S5-SLF4	3.06	AB568405	ref. 9	
S5-SLF5	2.37	AB568411	ref. 9	
S5-SLF5B	10.19	AB932964	this work	
S5-SLF6	34.20	AB568417	ref. 9	
S5-SLF8	5.74	AB932965	this work	
S5-SLF9	27.11	AB932966	this work	
S5-SLF10	18.07	AB932967	this work	
S5-SLF11	11.28	AB932968	this work	
S5-SLF12	8.66	AB932969	this work	
S5-SLF13	6.59	AB932970	this work	
S5-SLF15ψ	undetectable	AB932971	this work	1 bp insertion at position 107
S5-SLF16	22.18	AB932972	this work	
S5-SLF17	10.36	AB932973	this work	
S5-SLF18	123.97	AB568423	ref. 9	synonymous with S5-FBX, identical to S10-/S22-/S22m-SLF18s
S5-FBX2	14.80	AB932974	this work	
total tags number	590953			

***S7*-haplotype**

Gene	RPKM	Accession ID	References	Note
S7-SLF1	5.60	AB568391	ref. 9	interact with S9- and S17-RNases, identical to S19-/SC2-/S22m-SLF1s
S7-SLF1B	5.42	AB932975	this work	
S7-SLF2	3.30	AB568395	ref. 9	interact with S9-, S11-, and S19-RNases
S7-SLF3	2.20	AB932976	this work	
S7-SLF4	undetectable	AB568406	ref. 9	
S7-SLF5	4.29	AB568412	ref. 9	
S7-SLF6	4.52	AB568418	ref. 9	
S7-SLF8A	9.24	AB932977	this work	
S7-SLF8B	2.14	AB932978	this work	identical to S19-/SC2-/S22m-SLF8s
S7-SLF9A	25.75	AB932979	this work	interact with S19-RNase
S7-SLF9Bψ	10.89	AB932980	this work	deletion from position 646
S7-SLF10	36.14	AB932981	this work	
S7-SLF11	8.07	AB932982	this work	
S7-SLF13	27.53	AB568400	ref. 9	renamed from S7-SLF3
S7-SLF14	4.25	AB932983	this work	
S7-SLF16	25.96	AB932984	this work	
S7-SLF17	6.39	AB932985	this work	
S7-FBX1	1.26	AB932986	this work	
total tags number	634016			

Supplementary Table 1 (continued)

***S9*-haplotype**

Gene	RPKM	Accession ID	References	Note
S9-SLF1	undetectable	AB568392	ref. 9	interact with S17-RNase
S9-SLF3	28.33	AB568401	ref. 9	
S9-SLF4	9.17	AB568407	ref. 9	
S9-SLF5	1.10	AB568413	ref. 9	
S9-SLF6	3.38	AB568419	ref. 9	
S9-SLF7	30.54	AB932987	this work	
S9-SLF8	5.03	AB932988	this work	
S9-SLF9A	2.32	AB932989	this work	
S9-SLF9B	7.76	AB932990	this work	
S9-SLF10	40.51	AB932991	this work	
S9-SLF11	23.05	AB932992	this work	
S9-SLF12ψ	undetectable	AB932993	this work	1 bp deletion at position 193
S9-SLF13	2.85	AB932994	this work	
S9-SLF14	5.33	AB932995	this work	
S9-SLF15	undetectable	AB932996	this work	
S9-SLF16A	7.85	AB932997	this work	
S9-SLF16B	1.33	AB932998	this work	
S9-SLF17	8.27	AB932999	this work	
S9-FBX1	16.17	AB933000	this work	
total tags number	550736			

***S10*-haplotype**

Gene	RPKM	Accession ID	References	Note
S10-SLF1	—	AB933001	this work	
S10-SLF3	—	AB933002	this work	
S10-SLF4	—	AB933003	this work	
S10-SLF5	—	AB933004	this work	
S10-SLF8	—	AB933005	this work	
S10-SLF10	—	AB933006	this work	
S10-SLF11	—	AB933007	this work	
S10-SLF12	—	AB933008	this work	
S10-SLF13	—	AB933009	this work	
S10-SLF14	—	AB933010	this work	
S10-SLF16	—	AB933011	this work	
S10-SLF17	—	AB933012	this work	
S10-SLF18	—	AB933013	this work	identical to S5-/S22-/S22m-SLF18s
total tags number	no data			

Supplementary Table 1 (continued)

***S11*-haplotype**

Gene	RPKM	Accession ID	References	Note
S11-SLF1	16.41	AB568393	ref. 9	interact with S17-RNase
S11-SLF2	1.31	AB568396	ref. 9	interact with S9-RNase
S11-SLF3	21.95	AB568402	ref. 9	interact with S7-RNase
S11-SLF3B	2.34	AB933014	this work	
S11-SLF4	undetectable	AB568408	ref. 9	
S11-SLF5	2.55	AB568414	ref. 9	
S11-SLF6	1.15	AB568420	ref. 9	
S11-SLF7	undetectable	AB933015	this work	
S11-SLF8	undetectable	AB933016	this work	
S11-SLF9	1.36	AB933017	this work	interact with S19-RNase
S11-SLF10	29.63	AB933018	this work	
S11-SLF11	8.68	AB933019	this work	
S11-SLF13	4.39	AB933020	this work	
S11-SLF14	2.57	AB933021	this work	
S11-SLF15ψ	2.70	AB933022	this work	26 bp deletion at position 732
S11-SLF16	4.94	AB933023	this work	
S11-FBX1	2.61	AB933024	this work	
total tags number	545880			

***S17*-haplotype**

Gene	RPKM	Accession ID	References	Note
S17-SLF1	58.77	AY766153	ref. 21	synonymous with SLF-S17
S17-SLF1B	12.96	AY766155	ref. 21	synonymous with PaF1
S17-SLF2	9.23	AB568397	ref. 9	partial sequence
S17-SLF3	26.51	AB568403	ref. 9	
S17-SLF4A	4.57	AB568409	ref. 9	
S17-SLF4Bψ	1.42	AB933025	this work	2 bp insertion at position 802
S17-SLF5	2.55	AB568415	ref. 9	
S17-SLF6	14.98	AB568421	ref. 9	
S17-SLF7ψ	7.53	AB933026	this work	5 bp deletion at position 236
S17-SLF8A	4.27	AB933027	this work	
S17-SLF8Bψ	4.05	AB933028	this work	premature stop at position 535
S17-SLF9A	undetectable	AB933029	this work	
S17-SLF9B	30.29	AB933030	this work	
S17-SLF10	52.70	AB933031	this work	
S17-SLF11	28.40	AB933032	this work	
S17-SLF12A	undetectable	AB933033	this work	
S17-SLF12B	1.29	AB933034	this work	
S17-SLF12Cψ	2.42	AB933035	this work	943 bp insertion at position 523
S17-SLF13	5.07	AB933036	this work	
S17-SLF14	8.83	AB933037	this work	
S17-SLF16	23.63	AB933038	this work	
S17-SLF17	11.07	AB933039	this work	
total tags number	550612			

Supplementary Table 1 (continued)

***S19*-haplotype**

Gene	RPKM	Accession ID	References	Note
S19-SLF1	4.38	AY766154	ref. 21	synonymous with SLF-S19, identical to S7-/SC2-/S22m-SLF1s
S19-SLF1B	23.67	AB933040	this work	
S19-SLF2	32.32	AB568398	ref. 9	
S19-SLF3	50.63	AB568404	ref. 9	
S19-SLF4	5.66	AB568410	ref. 9	
S19-SLF5A	15.84	AB568416	ref. 9	
S19-SLF5B	19.31	AB933041	this work	
S19-SLF6	16.77	AB568422	ref. 9	
S19-SLF7ψ	20.25	AB933042	this work	29 bp insertion at position 821
S19-SLF8A	10.82	AB933043	this work	
S19-SLF8B	21.13	AB933044	this work	identical to S7-/SC2-/S22m-SLF8s
S19-SLF10A	26.60	AB933045	this work	
S19-SLF10B	20.90	AB933046	this work	
S19-SLF11	24.07	AB933047	this work	
S19-SLF12	8.70	AB933048	this work	
S19-SLF13	14.41	AB933049	this work	
S19-SLF14	21.03	AB933050	this work	
S19-SLF15ψ	10.23	AB933051	this work	1 bp insertion at position 905
S19-SLF16	19.34	AB933052	this work	
S19-FBX1	20.96	AB933053	this work	
S19-FBX2	31.13	AB933054	this work	
S19-FBX3	6.65	AB933055	this work	
total tags number	521109			

***S22*-haplotype**

Gene	RPKM	Accession ID	References	
S22-SLF1	—	AB933056	this work	
S22-SLF3	—	AB933057	this work	
S22-SLF4	—	AB933058	this work	
S22-SLF5	—	AB933059	this work	
S22-SLF6	—	AB933060	this work	
S22-SLF7ψ	—	AB933061	this work	31 bps deletions, frameshift
S22-SLF8	—	AB933062	this work	
S22-SLF9	—	AB933063	this work	
S22-SLF10	—	AB933064	this work	identical to Sm-SLF10
S22-SLF11	—	AB933065	this work	
S22-SLF12	—	AB933066	this work	
S22-SLF13	—	AB933067	this work	
S22-SLF14	—	AB933068	this work	
S22-SLF15	—	AB933069	this work	
S22-SLF16	—	AB933070	this work	
S22-SLF18	—	AB933071	this work	identical to S5-/S10-/S22m-/Sm-SLF18s
total tags number	no data			

Supplementary Table 1 (continued)

S_{0m}-haplotype

Gene	RPKM	Accession ID	References	Note
S0m-SLF1	15.14	AB933072	this work	
S0m-SLF2	8.15	AB933073	this work	partial sequence
S0m-SLF3	undetectable	AB933074	this work	
S0m-SLF4	7.05	AB933075	this work	
S0m-SLF5	undetectable	AB933076	this work	
S0m-SLF6	20.38	AB933077	this work	
S0m-SLF7	30.52	AB933078	this work	
S0m-SLF8	7.47	AB933079	this work	
S0m-SLF10	33.22	AB933080	this work	
S0m-SLF11	22.65	AB933081	this work	
S0m-SLF12	7.45	AB933082	this work	
S0m-SLF13	15.75	AB933083	this work	
S0m-SLF14	27.73	AB933084	this work	
S0m-SLF15ψ	7.26	AB933085	this work	1 bp insertion at position 78
S0m-SLF16	undetectable	AB933086	this work	
S0m-SLF17	undetectable	AB933087	this work	
S0m-FBX1	60.39	AB933088	this work	
S0m-FBX2	undetectable	AB933089	this work	
total tags number	101431			

S_m-haplotype

Gene	RPKM	Accession ID	References	Note
Sm-SLF1	—	AB933090	this work	
Sm-SLF2	—	AB933091	this work	
Sm-SLF3	—	AB933092	this work	
Sm-SLF5	—	AB933093	this work	
Sm-SLF6	—	AB933094	this work	
Sm-SLF7	—	AB933095	this work	
Sm-SLF8	—	AB933096	this work	
Sm-SLF9A	—	AB933097	this work	
Sm-SLF9B	—	AB933098	this work	
Sm-SLF10	—	AB933099	this work	
Sm-SLF11	—	AB933100	this work	
Sm-SLF12A	—	AB933101	this work	
Sm-SLF12B	—	AB933102	this work	
Sm-SLF13	—	AB933103	this work	
Sm-SLF14	—	AB933104	this work	
Sm-SLF15	—	AB933105	this work	
Sm-SLF16	—	AB933106	this work	
Sm-SLF18	—	AB933107	this work	identical to S5-/S10-/S22-/S22m-SLF18s
total tags number	no data			

Supplementary Table 1 (continued)

***SC2*-haplotype**

Gene	RPKM	Accession ID	References	Note
SC2-SLF1A	—	AY766153	ref. 21	identical to S17-SLF1
SC2-SLF1B	—	AY766155	ref. 21	identical to S17-SLF1B
SC2-SLF1C	—	AY766154	ref. 21	identical to S7-/S19-/S22m-SLF1s
SC2-SLF2	—	AB933108	this work	identical to S17-SLF2
SC2-SLF5	—	AB933109	this work	1 bp (1 aa) different from S17-SLF5
SC2-SLF6	—	AB933110	this work	identical to S17-SLF6
SC2-SLF7ψ	—	AB933111	this work	identical to S17-SLF7ψ
SC2-SLF8A	—	AB933112	this work	identical to S17-SLF8A
SC2-SLF8Bψ	—	AB933113	this work	identical to S17-SLF8Bψ
SC2-SLF8C		AB933114	this work	identical to S7-/S19-/S22m-SLF8s
SC2-SLF9	—	AB933115	this work	identical to S17-SLF9B
SC2-SLF10	—	AB933116	this work	identical to S17-SLF10
SC2-SLF11	—	AB933117	this work	identical to S17-SLF11
SC2-SLF12	—	AB933118	this work	identical to S17-SLF12B
SC2-SLF13	—	AB933119	this work	identical to S17-SLF13
SC2-SLF14	—	AB933120	this work	6 bps (5 aas) different from S17-SLF14
SC2-SLF16	—	AB933121	this work	identical to S17-SLF16
total tags number	no data			

S_{22m}-haplotype

Gene	RPKM	Accession ID	References	Note
S22m-SLF1A	—	AB933122	this work	identical to S22-SLF1
S22m-SLF1B	—	AB933123	this work	identical to S7-/S19-/SC2-SLF1s
S22m-SLF3	—	AB933124	this work	identical to S22-SLF3
S22m-SLF4	—	AB933125	this work	identical to S22-SLF4
S22m-SLF5	—	AB933126	this work	identical to S22-SLF5
S22m-SLF6	—	AB933127	this work	identical to S22-SLF6
S22m-SLF7ψ	—	AB933128	this work	identical to S22-SLF7ψ
S22m-SLF8A	—	AB933129	this work	identical to S22-SLF8
S22m-SLF8B	—	AB933130	this work	identical to S7-/S19-/SC2-SLF8s
S22m-SLF9	—	AB933131	this work	identical to S22-SLF9
S22m-SLF10	—	AB933132	this work	identical to S0m-/S7-/S11-/S17-SLF10s
S22m-SLF11	—	AB933133	this work	identical to S22-SLF11
S22m-SLF12	—	AB933134	this work	identical to S22-SLF12
S22m-SLF13	—	AB933135	this work	identical to S22-SLF13
S22m-SLF14	—	AB933136	this work	identical to S22-SLF14
S22m-SLF16	—	AB933137	this work	identical to S22-SLF16
S22m-SLF17	—	AB933138	this work	identical to S0m-/S7-/S9-/S10-/S17-SLF17s
S22m-SLF18	—	AB933139	this work	identical to S5-/S10-/S22-/Sm-SLF18s
total tags number	no data			

ψ following a gene name indicates pseudogene. For *SLF*s of the S_5-, S_7-, S_9-, S_{11}-, S_{17}-, S_{19}- and S_{0m}-haplotypes, relative expression levels are shown in RPKM (Reads Per Kilobase of exon model per Million mapped reads), and total numbers of ESTs are shown at the bottom of each table. GenBank accession IDs and references are also shown.

Supplementary Table 2 List of primer sequences

	Name	Primer		Target / Purpose
Type-7 specific amplification	SLF7-F1	CAA AGT ATA TTT TAC ATT GCA TTG CAG A	F	Type-7 *SLF*s / genomic PCR
	SLF7-F2	GGG TTT TAG AAG ACT ATG GCG ATC	F	Type-7 *SLF*s / 3' RACE, genomic PCR
	SLF7-F3	GTT GAG AAA GTG GAA GAT CGA TGT	F	Type-7 *SLF*s / 3' RACE, genomic PCR
	SLF7-F4	ATG ACT CTC TAA CAC TGA TCT GTT ACC G	F	Type-7 *SLF*s / 3' RACE, expression analysis
	SLF7-R1	GAG AAG GGT AAG CTC TAT TTA AAT TGG	R	Type-7 *SLF*s / genomic PCR
	SLF7-R2	GTA CTC CTT CAT TGT CCA AAT TTC CA	R	Type-7 *SLF*s / 5' RACE, genomic PCR
	SLF7-R3	TTC CGT TCT TCC AAA CCA ATG AG	R	Type-7 *SLF*s / 5' RACE, genomic PCR
	SLF7-R4	TGA GCT CTC TAA AAA TTT TGA ACT TGA GTA CTA	R	Type-7 *SLF*s / genomic PCR, expression analysis
Type-8 specific amplification	SLF8-F1	TCA AAG GAT CGG AGG TAT TAC AGA GA	F	Type-8 *SLF*s / genomic PCR
	SLF8-F2	GAA ACA TTT TTT ATT GCA TTG AAG AGA AC	F	Type-8 *SLF*s / genomic PCR
	SLF8-F3	GGT TTT GAC TCG ATT GTG AAG GAC T	F	Type-8 *SLF*s / 3' RACE
	SLF8-F4	AAG CAA AAG TGG ACT TCT TGT TTC CTA C	F	Type-8 *SLF*s / 3' RACE, expression analysis
	SLF8-R1	ATT TAG GCT GAA AAC TAC TTT CCA ATC A	R	Type-8 *SLF*s / genomic PCR, expression analysis
	SLF8-R2	CCT TTT TTG GAA TTG AAA TCA AGC	R	Type-8 *SLF*s / 5' RACE
	SLF8-R3	CTC CAA GAA TCA AAA CGC AAA TCA	R	Type-8 *SLF*s / 5' RACE
Type-9 specific amplification	SLF9-F1	ATC CAA CTG AAA TGA GGT CTT AAA GCA	F	Type-9 *SLF*s, *S19-FBX1, 2* and *S0m-FBX1* / genomic PCR
	SLF9-F2	GCC GTG GTA CCA AAA AGG CAA	F	Type-9 *SLF*s, *S0m-*/*S19-FBX1* and *2* / genomic PCR
	SLF9-F3	GAA GTT AAG GAA TTA GAT TTG CAT GGT CT	F	Type-9 *SLF*s / 3' RACE, expression analysis
	SLF9/10-F1	AAT GAA GGA ATA CGG TGA AAA GGA G	F	Type-9 and -10 *SLF*s, *S0m-*/*S19-FBX1* and *2* / 3' RACE
	SLF9/10-F2	GAA TCC CCA TTA GCA GTT TGG AAG	F	Type-9 and -10 *SLF*s, *S0m-*/*S19-FBX1* and *2* / 3' RACE
	SLF9-R1	CCA TTG ATC TGT AAG TTG TTG CTG C	R	Type-9 *SLF*s / genomic PCR
	SLF9-R2	GAA GTT CTA TGC AAT CCT TAT TTC TTG G	R	Type-9 *SLF*s and *S0m-*/*S19-FBX1* / 5' RACE
	SLF9-R3	CGA ATT AAG ATC ATA GGC AAT CAA ATG T	R	Type-9 *SLF*s and *S0m-*/*S19-FBX1* / 5' RACE
	SLF9-R4	AAT ATG GCT TCC ATT GAT CTG TAA GTT G	R	Type-9 *SLF*s / genomic PCR, expression analysis
Type-10 specific amplification	SLF10-F1	CCG AAG TAA GAT CCA ACT AAA ATG ATG T	F	Type-10 *SLF*s / genomic PCR
	SLF10-F2	GAA GTC CAG GAA TTA GAT TTA CAT GGT TA	F	Type-10 *SLF*s / 5' RACE, expression analysis
	SLF9/10-F1	AAT GAA GGA ATA CGG TGA AAA GGA G	F	Type-9 and -10 *SLF*s, *S0m-*/*S19-FBX1* and *2* / 3' RACE
	SLF9/10-F2	GAA TCC CCA TTA GCA GTT TGG AAG	F	Type-9 and -10 *SLF*s, *S0m-*/*S19-FBX1* and *2* / 3' RACE
	SLF10-R1	TAG TAT TCA GAT GTG TTA GGT TGT TGC C	R	Type-10 *SLF*s / genomic PCR, expression analysis
	SLF10-R2	ATT AAA TAC GAT AGT GGT AAG GGA ATC TGT	R	Type-10 *SLF*s / 5' RACE
	SLF10-R3	CAG CAG TGG TGG TCA AAT GTG G	R	Type-10 *SLF*s / 5' RACE
Type-11 specific amplification	SLF11-F1	ATG TTT GAC GGG TCG CTC CTT	F	Type-11 *SLF*s / genomic PCR
	SLF11-F2	ATT ACT ACA CAA TCA TTC CCA TAT AGC ACA	F	Type-11 *SLF*s / 3' RACE, genomic PCR
	SLF11-F3	TTG TTG GAG AGA CCT GGA TCT TAC G	F	Type-11 *SLF*s / 3' RACE, expression analysis
	SLF11-R1	AAT TAA AAG TGT GGA AAT CTT CAC AAA GAA	R	Type-11 *SLF*s / 5' RACE, genomic PCR
	SLF11-R2	GAG GCC ATA ACC TTT ATT GTC CCA	R	Type-11 *SLF*s / 5' RACE, genomic PCR, expression analysis
Type-12 specific amplification	SLF12-F1	AAG GGA GTA AAG CTG CTA TTT TGA	F	Type-12 *SLF*s / genomic PCR
	SLF12-F2	CTT CCA GTA AAG TTT CTC TTG CGA TTC	F	Type-12 *SLF*s / 3' RACE, expression analysis
	SLF12-F3	TCA CGC TCT CAC AAA ATC TTC CAC T	F	Type-12 *SLF*s / 3' RACE
	SLF12-R1	AGT ATT AAA ATC CCA CGA TGA AAA AG	R	Type-12 *SLF*s / genomic PCR, expression analysis
	SLF12-R2	TAA TTG TGT ATT TCT TTG TCC AAG ACT CAT	R	Type-12 and -4 *SLF*s / 5' RACE
	SLF12-R3	GGA ACT TAC ATT CAT CAC AGC AAC CAG	R	Type-12 *SLF*s / 5' RACE
Type-13 specific amplification	SLF13-F1	AAA TGT TAT TAC ACA CAC AAT CCT TGA A	F	Type-13 *SLF*s / 3' RACE, genomic PCR
	SLF13-F2	TGG TTT GAT TCT TTT GAC AGA CTC GTT	F	Type-13 *SLF*s / 3' RACE, expression analysis
	S7-SLF13-R	CTT AAG TTG GGG TGT TTT ACC TTC TC	R	Type-13 *SLF*s / genomic PCR
	SLF13-R1	AAG ATC TCC ATA CAC ACG TGA AAC TCT AAT	R	Type-13 *SLF*s / 5' RACE
	SLF13-R3	AAA ACA GAG AAG TAA ACG CAT TTG TCC	R	Type-13 *SLF*s / 5' RACE, genomic PCR, expression analysis
Type-14 specific amplification	SLF14-F1	AGC TGA TAC TAC TCA AAG AAA CCT AAC TC	F	Type-14 *SLF*s / genomic PCR
	SLF14-F2	ATT CTC TTC AAG CGC TCG TTC AA	F	Type-14 *SLF*s / 3' RACE
	SLF14-F3	ATC TCA TTG GTT CGG AAA CAC AAA TAC	F	Type-14 *SLF*s / 3' RACE, expression analysis
	SLF14/16-F1	TGT CTC TCC AGA TTT AGA AGT GCC ATA	F	Type-14 and -16 *SLF*s / 3' RACE
	SLF14/16-F2	GGA GAG AGG TAG AAA ATG TGG ATC AAC	F	Type-14 and -16 *SLF*s / 3' RACE
	SLF14-R1	TTA TTA TTG ATA GGC TTT TAC ACA ATT TAA	R	Type-14 *SLF*s / genomic PCR
	SLF14-R2	AAG CAT TTC TAA TAA CTG AAC TAA CTT AGG GA	R	Type-14 *SLF*s / 5' RACE, genomic PCR, expression analysis
	SLF14-R3	GAA CGA TGG AAA CCT AGT GGA CTG	R	Type-14 *SLF*s / 5' RACE
	SLF14-R4	GTT GCT GGA TTA GAT AAT ACT GTA GTT ACT TT	R	Type-14 *SLF*s / 5' RACE

	SLF14/16-R1	ACT ACG AGG CCA TAA CAC TTC CTG T	R	Type-14 and -16 *SLF*s / 5' RACE
	SLF14/16-R2	CTG GAG AAA CAT GGT GAA GGT CAT AA	R	Type-14 and -16 *SLF*s / 5' RACE
Type-15 specific amplification	SLF15-F1	TTA GAG CTA TTA CAC TGC AAA GGA ACC A	F	Type-15 *SLF*s / genomic PCR
	SLF15-F2	CTG AAG TAC AAT GTG CAT TGC TTT GA	F	Type-15 *SLF*s / 3' RACE
	SLF15-F3	GTG AAA TTA TGG AAA GAT TGC CTA AAG A	F	Type-15 *SLF*s / 3' RACE
	SLF15-F4	GGA TAA TGA TGG AAT ACG GTG TGG A	F	Type-15 *SLF*s / 3' RACE, expression analysis
	SLF15-R1	GGA ATG CAT AAC CTG AAA CGA CAA	R	Type-15 *SLF*s / 5' RACE, genomic PCR
	SLF15-R2	TTT TGG GCA TTT GGT ACT ATG CTC T	R	Type-15 *SLF*s / 5' RACE
	SLF15-R3	CCC AGT TAA AAA GTT ATC GAG AAG TAG GT	R	Type-15 *SLF*s / 5' RACE, genomic PCR, expression analysis
Type-16 specific amplification	SLF16-F1	ATG TCC CTA AAA TTC TAC AGT GAA CAT TGA	F	Type-16 *SLF*s / genomic PCR
	SLF16-F2	GTG CAT TGG TAT CCG TGT GGC	F	Type-16 *SLF*s / 3' RACE, expression analysis
	SLF14/16-F1	TGT CTC TCC AGA TTT AGA AGT GCC ATA	F	Type-16 and -14 *SLF*s / 3' RACE
	SLF14/16-F2	GGA GAG AGG TAG AAA ATG TGG ATC AAC	F	Type-16 and -14 *SLF*s / 3' RACE
	SLF16-R1	TAG CTA AAG AAT ATG AAT GAA AAG AAA GAT CC	R	Type-16 *SLF*s / genomic PCR
	SLF16-R2	CCG AAG AGA GAG TTA TAG AAA TGC TGG T	R	Type-16 *SLF*s / genomic PCR
	SLF16-R3	ATG CTG GTT TTA TAT TTT GAA GTT AGA GAG	R	Type-16 *SLF*s / 5' RACE, genomic PCR, expression analysis
	SLF14/16-R1	ACT ACG AGG CCA TAA CAC TTC CTG T	R	Type-16 and -14 *SLF*s / 5' RACE
	SLF14/16-R2	CTG GAG AAA CAT GGT GAA GGT CAT AA	R	Type-16 and -14 *SLF*s / 5' RACE
Type-17 specific amplification	SLF17-F1	GCG CAC ACA TAA AAA ACA TTT CCT AA	F	Type-17 *SLF*s / genomic PCR
	SLF17-F2	TAT GTG CAT TGG TAT CCC AGT GCT	F	Type-17 *SLF*s / 3' RACE, expression analysis
	SLF17-R1	TAA GTC AAG TCT CTA CCA GTT GGA CTC G	R	Type-17 *SLF*s / genomic PCR, expression analysis
	SLF17-R2	TAT GCT CGC GGT CTT TTG GAA	R	Type-17 and -16 *SLF*s / 5' RACE
	SLF17-R3	AAC CAA TGA GAG GCC CCT TTG TA	R	Type-17 *SLF*s / 5' RACE
Type-18 specific amplification	S5-FBX-F1	CCT CAT GCA ATG AAT TGC TCA AGC AGT	F	Type-18 *SLF*s / genomic PCR
	S5-FBX-F2	GAT CAA TCG ACT GCT CAA GGA AAA	F	Type-18 *SLF*s / 3' RACE
	S5-FBX-SF	TCG TCG GTT GTT TGG ATA ATG AAA G	F	Type-18 *SLF*s / 3' RACE, expression analysis
	S5-FBX-R1	TTG ATT GGA CTC TAT TGG AAT TAG GTG	R	Type-18 *SLF*s / genomic PCR
	S5-FBX-R2	TCA AAA ACC AAC AAA TAA CCC TTC CAA	R	Type-18 *SLF*s / 5' RACE
	S5-FBX-R3	CAA TCC AAT GGC AAG CTC CCT TGT	R	Type-18 *SLF*s / 5' RACE
	S5-FBX-SR	TAC ATG AGA GTT ACA AAT CAA CCC AAA G	R	Type-18 *SLF*s / genomic PCR, expression analysis
Allele-specific amplificarion for SLF	S5-SLF9-F	ACA ATA TAG GAA TGC CAG ATG CT	F	*S5-SLF9* / genotyping
	S5-SLF9-R	CTC TTC ACG ACA GAA AGT TTT TCA	R	*S5-SLF9* / genotyping
	S5-SLF12-F	CCG ATT ATG AAA TTG CAT GAA GAT ATT G	F	*S5-SLF12* / genotyping
	S5-SLF12-R	CCG TAC AGT TAA GAT CAT CAC CAT TAC C	R	*S5-SLF12* / genotyping
	S5-SLF16-F	AAG GAG TAT GGT ATA AAC GAG TCT TGG TG	F	*S5-SLF16* / genotyping
	S5-SLF16-R	AAG GAG TAT GGT ATA AAC GAG TCT TGG TG	R	*S5-SLF16* / genotyping
	S5-FBX-SF	CAC CTA ATT CCA ATA GAG TCC AAT CAA TA	F	*S5-, S10-, S22-, Sm-SLF18* / genotyping, expression analysis
	S5-FBX-SR	TAC ATG AGA GTT ACA AAT CAA CCC AAA G	R	*S5-, S10-, S22-, Sm-SLF18* / genotyping, expression analysis
	S5-FBX2-F1	AAA CCG AAA CAA TAT TCC CCA AAG TAG	F	*S5-FBX2* / genomic cloning
	S5-FBX2-R1	AAA AGG TTG CAG AAA TCC TGG TGA TA	R	*S5-FBX2* / genomic cloning
	S5-FBX2-F2	ACG GCC TGG TAA TCC TGA ATG AG	F	*S5-FBX2* / genotyping, expression analysis
	S5-FBX2-R2	GAT AAT CCT CTC CAA AGT TGT TGA ACG	R	*S5-FBX2* / genotyping, expression analysis
	S7-SLF11-F	GAT GAA CTC AAG GGA TTC AAT TTC CA	F	*S7-SLF11* / genotyping
	S7/S11-SLF11-R	TTC TCA AAG AAA TTG TAA CAG ATT AGT GCC	R	*S7-SLF11* / genotyping
	S7-SLF13-F	CCA AGG AGG GAG AGT AGT CCA ATG	F	*S7-SLF13* / genotyping
	S7-SLF13-R	CTT AAG TTG GGG TGT TTT ACC TTC TC	R	*S7-SLF13* / genotyping
	S7-SLF14-F	TTT GCT ATT GAA TCA CCA TTG GCT ATC	F	*S7-SLF14* / genotyping
	S7-SLF14-R	TGC GCG AGT ATT ATT GAG CTT GTG	R	*S7-SLF14* / genotyping
	S7-SLF16-F	GTT AGT CAA CAT TGC ATC ACA AGA AAG A	F	*S7-SLF16* / genotyping
	S7-SLF16-R	TTC CTT CGC AAT CTG TTA AAA CCA A	R	*S7-SLF16* / genotyping
	S7-FBX1-F1	GGT TTG ATT GCT TTG ACA GAT TTT GAA	F	*S7-FBX1* / 3' RACE, genotyping, expression analysis
	S7-FBX1-R1	AAG AAT TAC CAT TGT GTC TGT GTC TGT ATC	R	*S7-FBX1* / 5' RACE, genotyping, expression analysis
	S7-FBX1-F2	ATG GAT TCA GAT TGG ATT CCC GT	F	*S7-FBX1* / 3' RACE, genomic PCR
	S7-FBX1-R2	TCC CAT GTG AAA GAT CTC GAA ATG T	R	*S7-FBX1* / 5' RACE, genomic PCR
	S9-SLF7-F	AAT CGA TCC TAC AAA AGA CTT CAT GGA G	F	*S9-SLF7* / genotyping
	S9-SLF7-R	ACA AAA AGA TGT TCA AAA GCA GGT GTT	R	*S9-SLF7* / genotyping
	S9-SLF10-F	AAA TGG GCA ATG CAC AAT ACA AGT T	F	*S9-SLF10* / genotyping
	S9-SLF10-R	CCA GGC CAT AAG ACT TTC CAT CC	R	*S9-SLF10* / genotyping

	S9-SLF11-F	CTA AAA CAT GGT ACG CGC TCG TC	F	*S9-SLF11* / genotyping
	S9-SLF11-R	AAC TAA CTT GTA ATA ATT TTC AGC CAG GG	R	*S9-SLF11* / genotyping
	S9-SLF13-F	TTT ACG GTG TTG GAT TTG GCG	F	*S9-SLF13* / genotyping
	S9-SLF13-R	ATA TTG CCA AAG GGG ATT CGA C	R	*S9-SLF13* / genotyping
	S9-SLF15-F	GTG GTC TTG GTG ATG ATG ATC TTT G	F	*S9-SLF15* / genotyping
	S9-SLF15-R	AAA AAA AAG AAT TAC CAT TGT ATT TGC AC	R	*S9-SLF15* / genotyping
	S9-FBX1-F1	AGA GTG CAA CAT CGT ATA ACA GAG CC	F	*S9-FBX1* / 3' RACE, genomic PCR
	S9-FBX1-F2	CAA TGG ACC TAG TTA TGG CCT CCT	F	*S9-FBX1* / 3' RACE, genotyping, expression analysis
	S9-FBX1-R1	AGA TTT GGT GGG TAT TCG GTG CTA	R	*S9-FBX1* / genomic PCR, genotyping, expression analysis
	S11-SLF8-F	CAG CGA CGA TCT TAT CCC CAT TA	F	*S11-SLF8* / genotyping
	S11-SLF8-R	CAT CAT TAT CCA AAT GTC CAT TAA ATC A	R	*S11-SLF8* / genotyping
	S11-SLF11-F	CTG ATG AAC TCA AGG AAT TCA ATT TCA G	F	*S11-SLF11* / genotyping
	S7/S11-SLF11-R	TTC TCA AAG AAA TTG TAA CAG ATT AGT GCC	R	*S11-SLF11* / genotyping
	S11-FBX1-F1	TTA CCC CTA CCC AGA GCC TGT G	F	*S11-FBX1* / 3' RACE, genomic PCR
	S11-FBX1-F2	GGA TTA AAA AGT ACA CAA TTA CAG GCC	F	*S11-FBX1* / 3' RACE, genotyping, expression analysis
	S11-FBX1-R1	CGT TAT CTT ACA AGC CAA ACA AGC	R	*S11-FBX1* / 5' RACE, genotyping, expression analysis
	S11-FBX1-R2	GGA TAC CCG TCG TTA ACA ATG	R	*S11-FBX1* / 5' RACE, genomic PCR
	SLF8-F2	GAA ACA TTT TTT ATT GCA TTG AAG AGA AC	F	*S17-SLF8A* / genotyping
	S17-SLF8A-F	GAA TCT TTT GTT GGA TCC ATC TTG TTA	R	*S17-SLF8A* / genotyping
	S17-SLF12B-F	AAG ATG CTG GAC GGA ATT ATT ATG AAG	F	*S17-SLF12B/Cψ* / genotyping
	S17-SLF12B-R	CTC TCT CCC TAT TCA GGA TAC CCG A	R	*S17-SLF12B/Cψ* / genotyping
	S19-SLF10B-F	CAA GTA GTC CAA CAG AAA AAT TCA CG	F	*S19-SLF10B* / genotyping
	S19-SLF10B-R	TTT CAT AAT GGA GGC AAA AGA AGC	R	*S19-SLF10B* / genotyping
	S19-FBX1-F	CCT GGT GAT TTT GTG TAA GTC GCT	F	*S19-FBX1, S0m-FBX1* / 3' RACE, genotyping
	S19-FBX1-R	GTT AGG TTG TTG CCG AAA TCA AAG	R	*S19-FBX1* / genomic PCR, genotyping
	S19-FBX2-F	CTT CTT CCT ATT GAA TCC CCG TTG	F	*S19-FBX2, S0m-FBX2* / 3' RACE, genomic PCR, genotyping
	S19-FBX2-R	GTG AGT ATC TAA AAT GGT TGA ACT TCA GC	R	*S19-FBX2* /genomic PCR, genotypig
	S19-FBX3-F1	AAA TAC ACA CTA GAA TGT TAA GAG TCA	F	*S19-FBX3* / 3 'RACE, genomic PCR
	S19-FBX3-F2	AGA AGT TTA CTG GAT AGA TCA TGG	F	*S19-FBX3* / 3' RACE, genomic PCR, genotyping
	S19-FBX3-R1	GCT AAT GGA GAT ACA ATA CGA AGA	R	*S19-FBX3* / genomic PCR, genotyping
	SLF9-F2	GCC GTG GTA CCA AAA AGG CAA	F	*S0m-FBX2, Type-9 SLFs, S19-FBX1 and 2* / genomic PCR
	S0m-FBX2-R	TGG AAG GAA ATG GAG ATA ATG TTG AAA	R	*S0m-FBX2* / genomic PCR
*S-RNase*s amplification	SRNC1-U	HWK GCA ACT MGT ITT AAC ATG GCC	F	*S-RNase* conserved region 1
	SRNC5-L	WSG VKY RAA RCA TAT ICC TAT CTC	R	*S-RNase* conserved region 5
Allele-specific amplification for S-RNase	S0m-RN-F	ACT TCA GAA TGT TTC AGT TTC AG	F	*S0m-RNase* / genotyping
	S0m-RN-R	AAC AGG TTT ACT TTT GCT AAT TAT	R	*S0m-RNase* / genotyping
	S22-RN-F	TTT TCG TCT AGA GTT CTG TCC TGG C	F	*S22-RNase* / genotyping
	S22-RN-R	CGC ATT TGA GGT CAG GAT CTT TG	R	*S22-RNase* / genotyping
	S10-RN-F	GGC CAG ATA ATG AGC AAA GAC GT	F	*S10-RNase* / genotyping
	S10-RN-R	CAA AAA AGA AAG AAA TGG AAA GTC AAA C	R	*S10-RNase* / genotyping
	Sm-RN-F	AGA ATT GCC CGA TAA AAC CG	F	*Sm-RNase* / genotyping
	Sm-RN-R	TTC TGA TTG ACT GTA GAC ATC TG	R	*Sm-RNase* / genotyping
Vector construction	S5-T3-BamHI-F	AAG GAT CCA TGA CGG CCA TGA AGA AAT TGC	F	Cloning of *S5-SLF3* ORF
	S11-T3-SacI-R	AAT GAG CTC TAA AAA TTC TGA ACT TGT GTA CTA C	R	Cloning of *S5-SLF3* ORF
	T9-BamHI-F	TGG ATC CAT GAA GGA ATT GCC CCA AG	F	Cloning of *S7-* and *S11-SLF9*s ORF
	T9-SacI-R	AGA GCT CTC CCC ACT TCT AAA ATT GTT CAA	R	Cloning of *S7-* and *S11-SLF9*s ORF
Transgene detection	SLF3-F1	CAT TCA ATT GTC CTA GTG TGA TGG AGT	F	*S5-SLF3*-transgene / genotyping, expression analysis
	SLF9/10-F1	AAT GAA GGA ATA CGG TGA AAA GGA G	F	*S7-* and *S11-SLF9*-transgene / genotyping, expression analysis
	NosR	ACC GGC AAC AGG ATT CAA TC	R	*Nos* terminator / genotyping, expression analysis
RT-PCR control	UB-F	CCT AAC CGG CAA AAC CAT CAC CT	F	*Petunia ubiquitin / expression analysis*
	UB-R	GCA CTT ATC AAC AAC AGG ACG ACA ACA	R	*Petunia ubiquitin / expression analysis*

Supplementary Table 3 Summary of pairwise peptide-sequence identities among S-genes

(**a**) Type-1 SLFs Max. = 100.0 % Min. = 86.1 % Ave. = 92.0 %

	S9-SLF1	Sm-SLF1	S22-SLF1	PiS11-SLF1	S11-SLF1	S7-SLF1	S19-SLF1	S10-SLF1	S5-SLF1	S0m-SLF1	S19-SLF1B	PiS2-SLF1	S7-SLF1B	PiS13-SLF1	PiS7-SLF1	PiS1-SLF1	S17-SLF1B	S17-SLF1	PiS3-SLF1
PiS5-SLF1	97.2 %	96.1 %	90.2 %	92.8 %	92.5 %	97.2 %	97.2 %	98.2 %	97.7 %	97.7 %	97.9 %	94.9 %	94.3 %	90.0 %	90.0 %	89.5 %	89.7 %	86.6 %	86.4 %
S9-SLF1	-	96.4 %	90.2 %	92.5 %	92.5 %	97.4 %	97.4 %	97.9 %	97.4 %	97.9 %	97.7 %	94.6 %	92.8 %	90.2 %	89.7 %	89.7 %	89.2 %	86.3 %	86.4 %
Sm-SLF1		-	90.5 %	92.0 %	91.8 %	99.0 %	99.0 %	97.9 %	96.9 %	96.9 %	96.7 %	94.6 %	94.1 %	90.2 %	89.5 %	89.2 %	88.9 %	86.6 %	86.1 %
S22-SLF1			-	91.2 %	91.0 %	91.0 %	91.0 %	90.5 %	91.0 %	91.3 %	90.7 %	92.8 %	93.0 %	91.0 %	88.9 %	88.2 %	88.4 %	87.6 %	86.6 %
PiS11-SLF1				-	97.4 %	93.1 %	93.1 %	92.8 %	93.3 %	93.1 %	93.1 %	93.3 %	96.1 %	91.0 %	89.9 %	88.9 %	89.5 %	87.6 %	87.4 %
S11-SLF1					-	92.8 %	92.8 %	92.8 %	93.1 %	92.8 %	93.1 %	93.3 %	95.6 %	91.8 %	90.7 %	89.2 %	89.2 %	87.3 %	87.1 %
S7-SLF1						-	100.0 %	99.0 %	97.9 %	97.9 %	97.7 %	95.6 %	93.1 %	91.3 %	90.5 %	90.2 %	90.0 %	87.4 %	87.1 %
S19-SLF1							-	99.0 %	97.9 %	97.9 %	97.7 %	95.6 %	93.1 %	91.3 %	90.5 %	90.2 %	90.0 %	87.4 %	87.1 %
S10-SLF1								-	98.5 %	97.9 %	98.7 %	95.1 %	93.1 %	90.7 %	90.5 %	90.2 %	90.0 %	86.9 %	86.6 %
S5-SLF1									-	97.9 %	98.2 %	95.6 %	93.3 %	91.3 %	90.2 %	90.2 %	89.7 %	87.4 %	87.4 %
S0m-SLF1										-	97.7 %	95.6 %	95.1 %	90.7 %	90.5 %	89.7 %	90.2 %	87.4 %	87.7 %
S19-SLF1B											-	94.9 %	93.3 %	91.5 %	90.7 %	90.7 %	90.5 %	87.6 %	87.4 %
PiS2-SLF1												-	95.4 %	92.3 %	90.2 %	89.7 %	90.5 %	88.7 %	88.4 %
S7-SLF1B													-	92.8 %	91.5 %	90.5 %	90.2 %	87.9 %	88.7 %
PiS13-SLF1														-	92.0 %	91.0 %	90.5 %	88.7 %	89.5 %
PiS7-SLF1															-	91.5 %	91.0 %	87.1 %	88.7 %
PiS1-SLF1																-	89.5 %	87.4 %	88.4 %
S17-SLF1B																	-	88.1 %	87.4 %
S17-SLF1																		-	86.4 %

(**b**) Type-2 SLFs Max. = 88.3 % Min. = 72.8 % Ave. = 82.4 %

	S17-SLF2	S11-SLF2	S5-SLF2	S19-SLF2	Sm-SLF2	S0m-SLF2	PiS1-SLF2
S7-SLF2	87.1 %	84.7 %	85.2 %	83.9 %	83.5 %	85.9 %	72.8 %
S17-SLF2	-	84.4 %	85.3 %	85.3 %	83.8 %	86.2 %	74.5 %
S11-SLF2		-	83.3 %	82.6 %	82.8 %	86.2 %	73.5 %
S5-SLF2			-	85.1 %	84.6 %	83.7 %	74.7 %
S19-SLF2				-	86.2 %	87.7 %	75.0 %
Sm-SLF2					-	88.3 %	75.2 %
S0m-SLF2						-	76.0 %

(**c**) Type-3 SLFs Max. = 99.0 % Min. = 72.0 % Ave. = 88.9 %

	S17-SLF3	S10-SLF3	S22-SLF3	S19-SLF3	PiS2-SLF3	S0m-SLF3	Sm-SLF3	S9-SLF3	S11-SLF3	S11-SLF3B	S7-SLF3
S5-SLF3	99.0 %	99.0 %	98.7 %	98.2 %	97.9 %	97.1 %	97.1 %	97.4 %	89.0 %	76.2 %	73.4 %
S17-SLF3	-	97.9 %	97.7 %	97.1 %	96.9 %	96.1 %	96.1 %	96.4 %	88.7 %	76.5 %	73.6 %
S10-SLF3		-	98.2 %	97.7 %	97.9 %	97.1 %	96.6 %	97.4 %	89.5 %	76.5 %	73.6 %
S22-SLF3			-	98.4 %	97.9 %	96.9 %	95.8 %	96.1 %	89.0 %	76.0 %	73.6 %
S19-SLF3				-	97.1 %	96.4 %	95.6 %	95.6 %	88.2 %	76.0 %	73.6 %
PiS2-SLF3					-	97.7 %	96.6 %	95.8 %	89.5 %	76.2 %	73.4 %
S0m-SLF3						-	95.8 %	95.6 %	88.2 %	76.5 %	73.6 %
Sm-SLF3							-	95.1 %	87.4 %	74.7 %	72.0 %
S9-SLF3								-	89.3 %	75.7 %	72.6 %
S11-SLF3									-	74.4 %	72.3 %
S11-SLF3B										-	85.1 %

(**d**) Type-4 SLFs Max. = 97.3 % Min. = 89.4 % Ave. = 93.4 %

	S11-SLF4	S0m-SLF4	S5-SLF4	PiS2-SLF4	S7-SLF4	S17-SLF4Bψ	S9-SLF4	S17-SLF4	S10-SLF4	S19-SLF4
S22-SLF4	93.7 %	91.9 %	94.9 %	93.7 %	95.2 %	93.9 %	94.2 %	92.9 %	92.1 %	89.4 %
S11-SLF4	-	91.8 %	94.8 %	94.0 %	95.8 %	94.5 %	94.0 %	93.3 %	92.8 %	89.6 %
S0m-SLF4		-	93.3 %	92.6 %	93.5 %	92.6 %	93.3 %	92.1 %	92.1 %	89.9 %
S5-SLF4			-	96.3 %	96.5 %	95.3 %	95.5 %	94.5 %	94.0 %	90.9 %
PiS2-SLF4				-	95.8 %	94.5 %	94.8 %	93.8 %	93.1 %	90.6 %
S7-SLF4					-	97.3 %	95.8 %	95.3 %	94.8 %	91.6 %
S17-SLF4Bψ						-	94.8 %	94.0 %	93.5 %	90.4 %
S9-SLF4							-	93.8 %	93.5 %	90.9 %
S17-SLF4								-	92.3 %	91.1 %
S10-SLF4									-	91.6 %

100%
more than 90 %, less than 100 %
more than 80 %, less than 90 %
more than 70 %, less than 80 %
less than 70 %

Supplementary Table 3 (Continued)

(**e**) Type-5 SLFs Max. = 99.2 % Min. = 91.2 % Ave. = 95.5 %

	PiS3-SLF5	S11-SLF5	S0m-SLF5	S17-SLF5	PiS2-SLF5	S5-SLF5	S19-SLF5	S9-SLF5	Sm-SLF5	S10-SLF5	S22-SLF5	S5-SLF5B	S19-SLF5B
S7-SLF5	99.2 %	98.2 %	98.5 %	98.2 %	98.2 %	98.2 %	97.9 %	97.2 %	96.4 %	95.1 %	94.3 %	92.5 %	93.0 %
PiS3-SLF5	-	97.9 %	98.2 %	97.9 %	97.9 %	97.9 %	97.7 %	96.9 %	96.1 %	94.8 %	94.3 %	92.3 %	92.7 %
S11-SLF5		-	98.2 %	97.9 %	97.9 %	97.9 %	97.7 %	96.9 %	96.1 %	94.8 %	94.3 %	92.5 %	93.0 %
S0m-SLF5			-	99.2 %	98.2 %	98.2 %	97.9 %	97.2 %	96.6 %	95.4 %	94.6 %	92.8 %	93.3 %
S17-SLF5				-	97.9 %	97.9 %	97.7 %	96.9 %	96.1 %	95.1 %	94.1 %	92.3 %	92.7 %
PiS2-SLF5					-	98.2 %	97.9 %	96.9 %	96.6 %	94.8 %	94.6 %	92.3 %	92.7 %
S5-SLF5						-	97.7 %	96.9 %	96.1 %	94.8 %	94.1 %	92.5 %	93.0 %
S19-SLF5							-	96.6 %	95.9 %	94.6 %	93.8 %	92.0 %	92.5 %
S9-SLF5								-	95.6 %	94.3 %	93.0 %	91.8 %	92.2 %
Sm-SLF5									-	95.4 %	95.4 %	92.8 %	93.3 %
S10-SLF5										-	93.6 %	92.8 %	93.3 %
S22-SLF5											-	91.2 %	91.7 %
S5-SLF5B												-	99.0 %

100%
more than 90 %, less than 100 %
more than 80 %, less than 90 %
more than 70 %, less than 80 %
less than 70 %

(**f**) Type-6 SLFs Max. = 99.0 % Min. = 93.1 % Ave. = 94.9 %

	S0m-SLF6	Sm-SLF6	S7-SLF6	S11-SLF6	S19-SLF6	S17-SLF6	PiS2-SLF6	PiS3-SLF6	S5-SLF6	S22-SLF6
S9-SLF6	96.4 %	95.4 %	94.9 %	95.2 %	95.9 %	94.7 %	95.4 %	95.4 %	94.9 %	94.9 %
S0m-SLF6	-	94.1 %	93.6 %	93.9 %	94.4 %	93.1 %	93.9 %	93.9 %	93.1 %	93.6 %
Sm-SLF6		-	93.9 %	94.9 %	95.4 %	93.9 %	94.7 %	94.7 %	94.4 %	93.9 %
S7-SLF6			-	95.9 %	94.4 %	93.4 %	94.1 %	94.6 %	93.9 %	93.6 %
S11-SLF6				-	95.9 %	94.9 %	95.7 %	96.2 %	94.7 %	94.9 %
S19-SLF6					-	95.4 %	96.2 %	96.4 %	95.2 %	94.9 %
S17-SLF6						-	97.7 %	97.7 %	93.9 %	93.6 %
PiS2-SLF6							-	99.0 %	95.2 %	94.4 %
PiS3-SLF6								-	95.2 %	94.4 %
S5-SLF6									-	94.4 %

(**g**) Type-7 SLFs Max. = 99.2 % Min. = 87.3 % Ave. = 91.9 %

	PiS2-SLF7	S17-SLF7ψ	S22-SLF7ψ	Sm-SLF7	S19-SLF7ψ	S0m-SLF7	S11-SLF7	PiS1-SLF7
S9-SLF7	99.2 %	93.1 %	92.1 %	91.8 %	92.6 %	93.1 %	89.0 %	88.8 %
PiS2-SLF7	-	93.0 %	92.0 %	91.7 %	92.5 %	93.0 %	88.9 %	88.6 %
S17-SLF7ψ		-	91.8 %	91.3 %	92.1 %	92.3 %	88.5 %	88.1 %
S22-SLF7ψ			-	91.6 %	91.6 %	91.6 %	87.8 %	87.3 %
Sm-SLF7				-	93.6 %	92.9 %	90.8 %	90.1 %
S19-SLF7ψ					-	96.4 %	93.4 %	93.0 %
S0m-SLF7						-	92.6 %	92.2 %
S11-SLF7							-	98.4 %

(**h**) Type-8 SLFs Max. = 100.0 % Min. = 88.2 % Ave. = 93.8 %

	S7-SLF8B	S19-SLF8B	S10-SLF8	S5-SLF8	Sm-SLF8	S9-SLF8	S0m-SLF8	S19-SLF8A	S11-SLF8	S22-SLF8	S17-SLF8A	PiS2-SLF8	S17-SLF8Bψ	Ungrouped S7-FBX1
S7-SLF8A	96.4 %	96.4 %	95.1 %	95.1 %	95.7 %	95.8 %	95.9 %	95.9 %	95.1 %	92.1 %	89.8 %	89.5 %	89.3 %	67.5 %
S7-SLF8B	-	100.0 %	97.7 %	97.7 %	98.2 %	97.7 %	97.5 %	97.2 %	96.4 %	94.4 %	91.3 %	90.9 %	90.5 %	68.6 %
S19-SLF8B		-	97.7 %	97.7 %	98.2 %	97.7 %	97.5 %	97.2 %	96.4 %	94.4 %	91.3 %	90.9 %	90.5 %	68.6 %
S10-SLF8			-	96.7 %	97.5 %	96.6 %	96.4 %	96.4 %	95.7 %	93.1 %	90.6 %	89.6 %	90.0 %	68.1 %
S5-SLF8				-	96.9 %	96.9 %	96.4 %	96.4 %	95.1 %	93.1 %	90.0 %	90.0 %	89.5 %	68.1 %
Sm-SLF8					-	97.1 %	96.4 %	96.4 %	95.7 %	93.6 %	91.1 %	90.4 %	89.8 %	68.8 %
S9-SLF8						-	96.9 %	96.9 %	96.4 %	93.5 %	91.1 %	90.6 %	90.4 %	68.3 %
S0m-SLF8							-	98.5 %	95.7 %	93.6 %	91.3 %	90.4 %	90.5 %	68.9 %
S19-SLF8A								-	95.7 %	93.9 %	91.3 %	90.6 %	90.8 %	68.4 %
S11-SLF8									-	92.1 %	90.6 %	90.1 %	89.3 %	67.8 %
S22-SLF8										-	90.0 %	90.6 %	91.3 %	67.3 %
S17-SLF8A											-	90.3 %	88.2 %	66.0 %
PiS2-SLF8												-	88.7 %	66.0 %
S17-SLF8Bψ													-	67.1 %

Supplementary Table 3 (Continued)

(**i**) Type-9 SLFs Max. = 100.0 % Min. = 92.7 % Ave. = 95.1 %

															Ungrouped	
		S17-SLF9A	S7-SLF9A	S9-SLF9A	S11-SLF9	S5-SLF9	Sm-SLF9A	Sm-SLF9B	S22-SLF9	PiS1-SLF9	PiS2-SLF9	S9-SLF9B	S17-SLF9B	S7-SLF9Bψ	S0m-FBX1	S19-FBX1
	PiS3-SLF9	97.1 %	97.1 %	97.6 %	95.5 %	94.7 %	95.2 %	94.1 %	94.7 %	94.9 %	94.9 %	94.1 %	95.2 %	95.3 %	87.0 %	87.0 %
	S17-SLF9A	-	97.9 %	98.4 %	96.3 %	94.2 %	95.2 %	94.5 %	95.0 %	95.2 %	95.2 %	94.0 %	95.5 %	96.7 %	87.7 %	86.9 %
	S7-SLF9A		-	99.0 %	96.9 %	94.8 %	95.5 %	95.0 %	95.5 %	95.5 %	95.5 %	94.8 %	96.1 %	97.2 %	87.7 %	87.4 %
	S9-SLF9A			-	97.4 %	95.3 %	96.0 %	95.5 %	96.1 %	96.0 %	96.0 %	95.0 %	96.6 %	97.7 %	88.2 %	88.0 %
	S11-SLF9				-	93.7 %	94.4 %	94.5 %	95.0 %	94.4 %	94.4 %	93.7 %	94.8 %	95.8 %	86.6 %	86.6 %
	S5-SLF9					-	97.3 %	96.1 %	94.0 %	94.1 %	94.1 %	92.7 %	94.0 %	94.9 %	86.6 %	86.1 %
	Sm-SLF9A						-	96.5 %	94.7 %	94.9 %	94.9 %	93.4 %	94.7 %	93.5 %	87.0 %	86.7 %
	Sm-SLF9B							-	94.0 %	93.6 %	93.6 %	93.4 %	94.0 %	94.0 %	86.6 %	86.1 %
	S22-SLF9								-	94.4 %	94.4 %	93.2 %	94.8 %	93.0 %	86.6 %	86.1 %
	PiS1-SLF9									-	100.0 %	93.4 %	94.7 %	94.0 %	86.5 %	85.9 %
	PiS2-SLF9										-	93.4 %	94.7 %	94.0 %	86.5 %	85.9 %
	S9-SLF9B											-	94.5 %	94.0 %	85.6 %	85.6 %
	S17-SLF9B												-	95.8 %	86.9 %	86.9 %
	S7-SLF9Bψ													-	91.2 %	90.2 %
Ungrouped	S0m-FBX1														-	91.9 %

(**j**) Type-10 SLFs Max. = 100.0 % Min. = 92.0 % Ave. = 97.1 %

															Ungrouped	
		PiS3-SLF10	S5-SLF10	S19-SLF10A	S9-SLF10	PiS2-SLF10	S7-SLF10	S11-SLF10	S17-SLF10	S0m-SLF10	S10-SLF10	Sm-SLF10	S22-SLF10	S19-SLF10B	S0m-FBX1	S19-FBX1
	PiS1-SLF10	98.1 %	98.9 %	98.7 %	98.7 %	97.9 %	97.3 %	97.3 %	97.3 %	97.3 %	97.6 %	97.9 %	97.9 %	93.6 %	85.9 %	88.8 %
	PiS3-SLF10	-	97.6 %	97.3 %	97.3 %	96.6 %	96.0 %	96.0 %	96.0 %	96.0 %	96.3 %	96.6 %	96.6 %	92.6 %	84.6 %	87.8 %
	S5-SLF10		-	99.7 %	98.2 %	97.1 %	97.3 %	97.3 %	97.3 %	97.3 %	97.4 %	97.6 %	97.6 %	92.7 %	85.1 %	88.0 %
	S19-SLF10A			-	97.9 %	96.8 %	97.1 %	97.1 %	97.1 %	97.1 %	97.1 %	97.4 %	97.4 %	92.4 %	84.8 %	87.7 %
	S9-SLF10				-	98.2 %	97.3 %	97.3 %	97.3 %	97.3 %	97.6 %	97.9 %	97.9 %	92.9 %	85.8 %	88.5 %
	PiS2-SLF10					-	96.8 %	96.8 %	96.8 %	96.8 %	97.1 %	97.4 %	97.4 %	92.6 %	85.7 %	88.3 %
	S7-SLF10						-	100.0 %	100.0 %	100.0 %	98.9 %	99.2 %	99.2 %	92.0 %	84.9 %	87.5 %
	S11-SLF10							-	100.0 %	100.0 %	98.9 %	99.2 %	99.2 %	92.0 %	84.9 %	87.5 %
	S17-SLF10								-	100.0 %	98.9 %	99.2 %	99.2 %	92.0 %	84.9 %	87.5 %
	S0m-SLF10									-	98.9 %	99.2 %	99.2 %	92.0 %	84.9 %	87.5 %
	S10-SLF10										-	99.7 %	99.7 %	92.0 %	85.2 %	87.5 %
	Sm-SLF10											-	100.0 %	92.3 %	85.4 %	87.8 %
	S22-SLF10												-	92.3 %	85.4 %	87.8 %
	S19-SLF10B													-	86.9 %	88.7 %
Ungrouped	S0m-FBX1														-	91.9 %

(**k**) Type-11 SLFs Max. = 97.2 % Min. = 91.2 % Ave. = 93.7 %

	Sm-SLF11	S19-SLF11	S10-SLF11	S7-SLF11	S11-SLF11	S22-SLF11	S9-SLF11	S17-SLF11	S0m-SLF11
S5-SLF11	97.2 %	95.1 %	95.6 %	94.9 %	95.1 %	93.8 %	92.2 %	93.1 %	92.6 %
Sm-SLF11	-	94.6 %	94.4 %	94.1 %	94.4 %	93.3 %	91.4 %	92.3 %	91.8 %
S19-SLF11		-	94.4 %	93.6 %	94.4 %	93.3 %	91.9 %	92.6 %	92.8 %
S10-SLF11			-	93.6 %	94.4 %	93.1 %	91.9 %	92.3 %	93.3 %
S7-SLF11				-	97.2 %	95.6 %	93.5 %	94.6 %	92.1 %
S11-SLF11					-	96.7 %	94.5 %	96.2 %	93.1 %
S22-SLF11						-	93.5 %	94.9 %	91.5 %
S9-SLF11							-	95.1 %	91.2 %
S17-SLF11								-	91.3 %

100%
more than 90 %, less than 100 %
more than 80 %, less than 90 %
more than 70 %, less than 80 %
less than 70 %

Supplementary Table 3 (Continued)

(**l**) Type-12 SLFs Max. = 100.0 % Min. = 91.9 % Ave. = 95.9 %

	S0m-SLF12	Sm-SLF12A	S19-SLF12	S10-SLF12	Sm-SLF12B	S9-SLF12ψ	S5-SLF12	S22-SLF12	S17-SLF12B	S17-SLF12Cψ
S17-SLF12A	100.0 %	100.0 %	97.7 %	96.9 %	96.2 %	95.9 %	97.5 %	94.9 %	96.2 %	92.9 %
S0m-SLF12	-	100.0 %	97.7 %	96.9 %	96.2 %	95.9 %	97.5 %	94.9 %	96.2 %	92.9 %
Sm-SLF12A		-	97.7 %	96.9 %	96.2 %	95.9 %	97.5 %	94.9 %	96.2 %	92.9 %
S19-SLF12			-	97.2 %	96.4 %	96.2 %	96.9 %	95.2 %	96.2 %	93.4 %
S10-SLF12				-	96.7 %	96.9 %	96.2 %	94.9 %	95.9 %	92.9 %
Sm-SLF12B					-	96.7 %	95.4 %	94.7 %	95.4 %	92.4 %
S9-SLF12ψ						-	95.4 %	93.9 %	94.9 %	91.9 %
S5-SLF12							-	95.2 %	96.7 %	93.4 %
S22-SLF12								-	97.2 %	95.7 %
S17-SLF12B									-	94.7 %

(**m**) Type-13 SLFs Max. = 99.7 % Min. = 91.2 % Ave. = 95.3 %

	Sm-SLF13	S5-SLF13	S10-SLF13	S17-SLF13	S22-SLF13	S19-SLF13	S0m-SLF13	S9-SLF13	S7-SLF13
S11-SLF13	96.9 %	94.8 %	95.3 %	95.1 %	95.9 %	95.6 %	96.1 %	94.6 %	92.5 %
Sm-SLF13	-	95.9 %	94.8 %	94.6 %	96.9 %	96.6 %	95.6 %	94.1 %	91.2 %
S5-SLF13		-	97.2 %	94.6 %	96.4 %	96.1 %	95.4 %	95.6 %	92.3 %
S10-SLF13			-	95.4 %	95.6 %	95.4 %	96.6 %	95.4 %	94.1 %
S17-SLF13				-	97.7 %	97.4 %	96.6 %	95.1 %	92.5 %
S22-SLF13					-	99.7 %	97.4 %	95.9 %	92.8 %
S19-SLF13						-	97.2 %	95.6 %	92.5 %
S0m-SLF13							-	95.9 %	93.6 %
S9-SLF13								-	92.5 %

(**p**) Type-16 SLFs Max. = 99.0 % Min. = 90.9 % Ave. = 94.2 %

	S9-SLF16B	S11-SLF16	S0m-SLF16	S7-SLF16	S22-SLF16	S17-SLF16	S5-SLF16	S10-SLF16	Sm-SLF16	S19-SLF16
S9-SLF16A	99.0 %	97.4 %	95.9 %	93.9 %	92.3 %	92.3 %	92.4 %	97.4 %	98.4 %	92.7 %
S9-SLF16B	-	96.9 %	95.7 %	93.4 %	91.8 %	91.8 %	91.9 %	96.9 %	94.0 %	92.2 %
S11-SLF16		-	96.4 %	94.4 %	92.8 %	92.8 %	93.0 %	98.0 %	93.2 %	93.0 %
S0m-SLF16			-	94.1 %	92.8 %	92.8 %	93.0 %	96.9 %	95.6 %	93.5 %
S7-SLF16				-	92.6 %	91.8 %	90.9 %	95.1 %	94.8 %	91.5 %
S22-SLF16					-	96.4 %	93.2 %	93.9 %	95.0 %	94.5 %
S17-SLF16						-	92.4 %	94.4 %	94.5 %	94.3 %
S5-SLF16							-	94.0 %	95.3 %	94.8 %
S10-SLF16								-	91.5 %	94.0 %
Sm-SLF16									-	98.4 %

(**n**) Type-14 SLFs Max. = 97.4 % Min. = 93.6 % Ave. = 95.2 %

	S7-SLF14	S19-SLF14	S0m-SLF14	S9-SLF14	S22-SLF14	S11-SLF14	S17-SLF14	Sm-SLF14
S10-SLF14	97.4 %	95.7 %	93.8 %	94.1 %	93.8 %	95.4 %	94.6 %	93.6 %
S7-SLF14	-	96.3 %	94.8 %	95.6 %	94.8 %	95.4 %	95.1 %	94.6 %
S19-SLF14		-	95.6 %	95.6 %	95.3 %	95.6 %	94.8 %	95.0 %
S0m-SLF14			-	96.9 %	95.6 %	96.7 %	95.1 %	94.6 %
S9-SLF14				-	95.6 %	97.2 %	95.4 %	94.3 %
S22-SLF14					-	95.9 %	94.1 %	94.1 %
S11-SLF14						-	96.9 %	94.1 %
S17-SLF14							-	94.1 %

(**o**) Type-15 SLFs Max. = 99.0 % Min. = 93.4 % Ave. = 96.3 %

	S5-SLF15ψ	S11-SLF15ψ	S0m-SLF15ψ	S22-SLF15	S19-SLF15ψ	S9-SLF15
Sm-SLF15	98.5 %	98.2 %	98.2 %	98.0 %	95.2 %	93.6 %
S5-SLF15ψ	-	98.2 %	98.2 %	98.0 %	95.2 %	93.4 %
S11-SLF15ψ		-	99.0 %	97.7 %	95.5 %	93.9 %
S0m-SLF15ψ			-	98.2 %	95.5 %	93.6 %
S22-SLF15				-	95.7 %	93.9 %
S19-SLF15ψ					-	95.2 %

(**q**) Type-17 SLFs Max. = 100.0 % Min. = 99.7 % Ave. = 99.9 %

	S9-SLF17	S10-SLF17	S17-SLF17	S0m-SLF17	S5-SLF17
S7-SLF17	100.0 %	100.0 %	100.0 %	100.0 %	99.7 %
S9-SLF17	–	100.0 %	100.0 %	100.0 %	99.7 %
S10-SLF17		–	100.0 %	100.0 %	99.7 %
S17-SLF17			–	100.0 %	99.7 %
S0m-SLF17				–	99.7 %

(**r**) Type-18 SLFs

	S10−SLF18	S22−SLF18	Sm−SLF18
S5−SLF18	100.0 %	100.0 %	100.0 %
S10−SLF18	–	100.0 %	100.0 %
S22−SLF18		–	100.0 %

100%
more than 90 %, less than 100 %
more than 80 %, less than 90 %
more than 70 %, less than 80 %
less than 70 %

Supplementary Table 3 (Continued)

(**s**) SLFs of S5-haplotype Max. = 92.5 % Min. = 44.2 % Ave. = 52.0 %

	S5-SLF2	S5-SLF3	S5-SLF4	S5-SLF5	S5-SLF5B	S5-SLF6	S5-SLF8	S5-SLF9	S5-SLF10	S5-SLF11	S5-SLF12	S5-SLF13	S5-SLF15ψ	S5-SLF16	S5-SLF17	S5-SLF18	S5-FBX2
S5-SLF1	58.4 %	51.0 %	47.2 %	53.4 %	52.9 %	48.5 %	55.0 %	52.1 %	49.5 %	54.1 %	48.5 %	49.5 %	52.2 %	52.0 %	52.6 %	47.6 %	50.8 %
S5-SLF2	-	52.1 %	51.8 %	53.6 %	52.3 %	49.5 %	54.3 %	53.3 %	51.3 %	53.0 %	51.3 %	50.4 %	50.0 %	51.3 %	50.9 %	46.8 %	54.6 %
S5-SLF3		-	51.7 %	50.9 %	49.3 %	47.3 %	52.2 %	51.9 %	51.2 %	54.9 %	50.3 %	70.3 %	55.6 %	54.1 %	54.5 %	47.8 %	56.0 %
S5-SLF4			-	56.8 %	55.1 %	53.4 %	48.7 %	48.3 %	46.4 %	45.7 %	75.6 %	47.0 %	48.9 %	48.6 %	50.0 %	50.0 %	51.3 %
S5-SLF5				-	92.5 %	53.0 %	50.3 %	50.6 %	48.6 %	48.5 %	56.7 %	48.0 %	51.7 %	50.1 %	50.3 %	52.9 %	51.5 %
S5-SLF5B					-	51.8 %	48.3 %	51.2 %	48.8 %	47.8 %	56.5 %	46.4 %	50.4 %	49.9 %	51.3 %	50.9 %	50.1 %
S5-SLF6						-	47.3 %	47.5 %	47.4 %	47.6 %	52.7 %	44.4 %	49.2 %	47.7 %	47.8 %	59.0 %	47.8 %
S5-SLF8							-	51.0 %	48.0 %	53.6 %	49.2 %	51.4 %	53.6 %	55.7 %	53.9 %	47.4 %	53.4 %
S5-SLF9								-	89.0 %	49.6 %	45.5 %	49.5 %	53.8 %	51.3 %	50.9 %	44.8 %	54.3 %
S5-SLF10									-	48.1 %	44.2 %	48.2 %	54.6 %	50.3 %	49.9 %	44.2 %	53.8 %
S5-SLF11										-	49.4 %	53.4 %	51.7 %	50.0 %	49.6 %	45.3 %	54.1 %
S5-SLF12											-	46.4 %	48.6 %	47.8 %	48.2 %	48.5 %	49.2 %
S5-SLF13												-	51.5 %	52.2 %	52.9 %	45.9 %	52.2 %
S5-SLF15ψ													-	63.9 %	62.4 %	46.7 %	63.1 %
S5-SLF16														-	79.2 %	45.5 %	70.7 %
S5-SLF17															-	44.5 %	67.9 %
S5-SLF18																-	47.1 %

(**t**) SLFs of S7-haplotype Max. = 97.2 % Min. = 45.4 % Ave. = 53.4 %

	S7-SLF1B	S7-SLF2	S7-SLF3	S7-SLF4	S7-SLF5	S7-SLF6	S7-SLF8A	S7-SLF8B	S7-SLF9A	S7-SLF9Bψ	S7-SLF10	S7-SLF11	S7-SLF13	S7-SLF14	S7-SLF16	S7-SLF17	S7-FBX1
S7-SLF1	95.1 %	58.4 %	49.9 %	47.7 %	53.2 %	49.5 %	54.1 %	54.6 %	51.9 %	51.2 %	49.2 %	53.6 %	49.2 %	53.1 %	52.1 %	51.6 %	53.8 %
S7-SLF1B	-	59.6 %	51.0 %	48.5 %	54.6 %	50.3 %	53.6 %	54.1 %	52.1 %	50.7 %	49.1 %	53.2 %	49.9 %	52.9 %	51.8 %	51.0 %	53.3 %
S7-SLF2		-	50.9 %	51.5 %	51.4 %	48.4 %	52.4 %	53.2 %	52.9 %	51.4 %	50.5 %	51.8 %	50.3 %	53.3 %	53.5 %	52.0 %	52.3 %
S7-SLF3			-	51.8 %	53.7 %	49.0 %	53.5 %	53.8 %	51.8 %	50.9 %	50.4 %	53.9 %	66.0 %	52.5 %	49.9 %	52.0 %	52.5 %
S7-SLF4				-	58.7 %	53.7 %	49.1 %	50.1 %	49.2 %	48.8 %	48.2 %	47.0 %	48.6 %	50.0 %	51.2 %	50.8 %	50.4 %
S7-SLF5					-	52.3 %	49.6 %	50.0 %	50.6 %	52.5 %	48.1 %	47.7 %	49.1 %	50.5 %	50.3 %	50.0 %	53.9 %
S7-SLF6						-	46.2 %	47.8 %	48.2 %	48.2 %	47.2 %	47.3 %	45.4 %	47.6 %	46.7 %	46.2 %	47.8 %
S7-SLF8A							-	96.4 %	50.3 %	47.3 %	47.2 %	52.4 %	52.5 %	53.0 %	54.6 %	53.1 %	67.5 %
S7-SLF8B								-	51.3 %	48.6 %	47.7 %	53.6 %	52.9 %	54.0 %	56.1 %	54.7 %	68.6 %
S7-SLF9A									-	97.2 %	88.3 %	50.9 %	51.8 %	54.7 %	51.6 %	51.2 %	52.2 %
S7-SLF9Bψ										-	88.4 %	49.3 %	47.7 %	53.4 %	48.4 %	47.8 %	49.8 %
S7-SLF10											-	48.1 %	48.8 %	52.9 %	49.7 %	49.5 %	49.7 %
S7-SLF11												-	53.4 %	51.5 %	48.5 %	48.3 %	54.6 %
S7-SLF13													-	53.5 %	52.3 %	53.7 %	54.3 %
S7-SLF14														-	75.8 %	72.8 %	53.9 %
S7-SLF16															-	78.5 %	55.6 %
S7-SLF17																-	54.7 %

100%
more than 90 %, less than 100 %
more than 80 %, less than 90 %
more than 70 %, less than 80 %
less than 70 %

Supplementary Table 3 (Continued)

(**u**) SLFs of S9-haplotype Max. = 99.0 % Min. = 43.9 % Ave. = 53.2 %

	S9-SLF3	S9-SLF4	S9-SLF5	S9-SLF6	S9-SLF7	S9-SLF8	S9-SLF9A	S9-SLF9B	S9-SLF10	S9-SLF11	S9-SLF12ψ	S9-SLF13	S9-SLF14	S9-SLF15	S9-SLF16A	S9-SLF16B	S9-SLF17	S9-FBX1
S9-SLF1	50.3 %	46.0 %	52.9 %	49.7 %	55.2 %	55.1 %	51.7 %	50.6 %	49.4 %	51.7 %	46.6 %	47.2 %	53.1 %	54.6 %	51.0 %	50.5 %	51.0 %	52.6 %
S9-SLF3	-	50.6 %	50.0 %	46.5 %	53.7 %	52.6 %	53.9 %	53.2 %	51.7 %	53.8 %	49.2 %	69.0 %	55.7 %	55.0 %	54.0 %	52.9 %	53.5 %	51.2 %
S9-SLF4		-	57.1 %	53.7 %	49.6 %	49.6 %	48.4 %	48.1 %	46.5 %	45.5 %	78.2 %	47.8 %	48.4 %	49.1 %	49.2 %	48.7 %	50.0 %	50.9 %
S9-SLF5			-	52.8 %	51.7 %	50.1 %	50.9 %	49.7 %	48.2 %	48.8 %	56.7 %	47.7 %	50.8 %	51.3 %	49.7 %	49.2 %	50.7 %	52.7 %
S9-SLF6				-	49.4 %	47.2 %	47.7 %	46.6 %	47.4 %	46.6 %	51.4 %	43.9 %	48.2 %	50.1 %	46.5 %	46.3 %	47.5 %	53.4 %
S9-SLF7					-	50.6 %	50.8 %	50.9 %	50.9 %	50.9 %	49.9 %	49.5 %	63.6 %	60.2 %	60.5 %	60.0 %	58.9 %	52.3 %
S9-SLF8						-	51.6 %	50.8 %	49.5 %	52.4 %	50.4 %	51.0 %	54.1 %	54.2 %	56.4 %	56.1 %	54.2 %	51.4 %
S9-SLF9A							-	95.0 %	90.0 %	50.8 %	45.7 %	51.8 %	54.4 %	55.1 %	51.4 %	50.9 %	51.7 %	49.6 %
S9-SLF9B								-	87.1 %	49.2 %	45.2 %	51.0 %	53.9 %	53.5 %	50.4 %	49.9 %	50.6 %	49.6 %
S9-SLF10									-	49.2 %	44.2 %	49.1 %	52.6 %	54.3 %	49.6 %	49.3 %	50.1 %	49.2 %
S9-SLF11										-	45.6 %	51.7 %	52.6 %	51.4 %	50.0 %	49.2 %	49.5 %	51.9 %
S9-SLF12ψ											-	48.2 %	47.7 %	48.2 %	47.7 %	47.2 %	48.8 %	50.8 %
S9-SLF13												-	51.7 %	51.4 %	51.5 %	50.5 %	52.6 %	48.8 %
S9-SLF14													-	65.1 %	75.5 %	75.0 %	73.3 %	51.5 %
S9-SLF15														-	65.0 %	64.5 %	63.1 %	53.3 %
S9-SLF16A															-	99.0 %	78.9 %	49.9 %
S9-SLF16B																-	78.4 %	49.4 %
S9-SLF17																	-	50.0 %

(**v**) SLFs of S11-haplotype Max. = 87.2 % Min. = 44.4 % Ave. = 52.3 %

	S11-SLF2	S11-SLF3	S11-SLF3B	S11-SLF4	S11-SLF5	S11-SLF6	S11-SLF7	S11-SLF8	S11-SLF9	S11-SLF10	S11-SLF11	S11-SLF13	S11-SLF14	S11-SLF15ψ	S11-SLF16	S11-FBX1
S11-SLF1	56.8 %	49.6 %	50.9 %	47.0 %	52.8 %	50.5 %	54.5 %	53.6 %	50.8 %	47.8 %	52.7 %	49.9 %	51.9 %	51.5 %	49.5 %	50.1 %
S11-SLF2	-	52.8 %	51.8 %	48.5 %	51.4 %	47.8 %	54.4 %	52.7 %	52.6 %	49.0 %	54.4 %	50.1 %	53.9 %	49.1 %	53.7 %	47.5 %
S11-SLF3		-	74.4 %	50.1 %	49.9 %	47.0 %	53.5 %	53.2 %	52.6 %	50.8 %	53.8 %	69.5 %	57.6 %	54.3 %	54.5 %	47.7 %
S11-SLF3B			-	50.5 %	50.0 %	48.6 %	54.9 %	55.2 %	53.0 %	51.7 %	54.7 %	67.4 %	53.2 %	53.9 %	50.1 %	48.3 %
S11-SLF4				-	56.6 %	53.2 %	50.0 %	50.0 %	47.8 %	46.3 %	46.7 %	47.3 %	48.2 %	48.9 %	49.0 %	54.3 %
S11-SLF5					-	52.8 %	50.4 %	51.0 %	50.9 %	48.3 %	48.0 %	48.8 %	50.6 %	51.4 %	49.5 %	54.0 %
S11-SLF6						-	48.6 %	48.5 %	48.4 %	47.2 %	48.9 %	44.4 %	49.7 %	50.0 %	46.0 %	64.3 %
S11-SLF7							-	50.4 %	52.3 %	51.3 %	51.3 %	50.9 %	63.5 %	58.7 %	58.5 %	48.8 %
S11-SLF8								-	52.1 %	49.3 %	54.1 %	53.4 %	54.9 %	53.1 %	55.9 %	49.6 %
S11-SLF9									-	87.2 %	49.9 %	50.9 %	56.3 %	54.7 %	51.7 %	47.8 %
S11-SLF10										-	48.7 %	48.8 %	54.1 %	54.8 %	49.7 %	46.0 %
S11-SLF11											-	53.6 %	53.1 %	51.4 %	49.6 %	47.4 %
S11-SLF13												-	52.9 %	50.9 %	51.0 %	47.4 %
S11-SLF14													-	65.7 %	76.0 %	47.5 %
S11-SLF15ψ														-	64.4 %	51.7 %
S11-SLF16															-	45.9 %

100%
more than 90 %, less than 100 %
more than 80 %, less than 90 %
more than 70 %, less than 80 %
less than 70 %

Supplementary Table 3 (Continued)

(**w**) SLFs of S17-haplotype Max. = 96.2 % Min. = 43.2 % Ave. = 52.9 %

	S17-SLF1B	S17-SLF2	S17-SLF3	S17-SLF4	S17-SLF4Bψ	S17-SLF5	S17-SLF6	S17-SLF7ψ	S17-SLF8A	S17-SLF8Bψ	S17-SLF9A	S17-SLF9B	S17-SLF10	S17-SLF11	S17-SLF12A	S17-SLF12B	S17-SLF12Cψ	S17-SLF13	S17-SLF14	S17-SLF16	S17-SLF17
S17-SLF1	87.9 %	58.6 %	50.1 %	48.1 %	47.0 %	53.3 %	49.7 %	53.9 %	51.9 %	50.4 %	48.7 %	50.0 %	46.8 %	50.4 %	46.6 %	47.1 %	45.3 %	49.1 %	51.4 %	51.0 %	49.5 %
S17-SLF1B	-	56.6 %	51.5 %	49.0 %	47.7 %	53.7 %	52.0 %	56.6 %	54.0 %	52.3 %	49.9 %	51.2 %	47.9 %	50.8 %	47.6 %	48.4 %	46.3 %	49.6 %	52.1 %	52.0 %	50.8 %
S17-SLF2		-	49.9 %	49.0 %	48.6 %	52.0 %	48.6 %	54.4 %	51.7 %	50.6 %	53.2 %	53.7 %	51.7 %	51.0 %	49.6 %	49.3 %	48.2 %	50.1 %	53.0 %	51.6 %	51.2 %
S17-SLF3			-	50.7 %	50.9 %	51.2 %	48.2 %	53.5 %	52.5 %	51.9 %	52.5 %	53.5 %	51.6 %	53.4 %	50.3 %	50.8 %	50.0 %	70.6 %	56.0 %	54.0 %	54.5 %
S17-SLF4				-	94.0 %	56.6 %	53.4 %	48.2 %	49.1 %	48.6 %	47.6 %	47.6 %	46.7 %	45.4 %	74.8 %	75.1 %	73.0 %	46.9 %	47.7 %	49.0 %	49.2 %
S17-SLF4Bψ					-	57.4 %	52.9 %	49.9 %	48.9 %	48.3 %	48.2 %	48.5 %	47.3 %	45.5 %	75.6 %	75.6 %	73.6 %	48.2 %	47.7 %	50.0 %	50.0 %
S17-SLF5						-	53.0 %	50.4 %	50.5 %	49.9 %	51.4 %	51.3 %	49.6 %	48.0 %	57.0 %	57.2 %	54.2 %	49.3 %	50.1 %	51.0 %	50.4 %
S17-SLF6							-	49.0 %	47.6 %	48.1 %	47.7 %	48.5 %	47.8 %	46.3 %	50.6 %	51.1 %	49.9 %	44.1 %	49.0 %	48.3 %	47.0 %
S17-SLF7ψ								-	51.0 %	50.5 %	51.8 %	52.0 %	50.4 %	50.6 %	49.0 %	49.2 %	49.2 %	51.0 %	63.3 %	61.8 %	58.9 %
S17-SLF8A									-	88.2 %	51.0 %	50.5 %	47.8 %	51.0 %	49.3 %	50.1 %	47.5 %	51.7 %	52.1 %	54.8 %	53.9 %
S17-SLF8Bψ										-	51.3 %	50.1 %	48.7 %	52.0 %	48.0 %	49.0 %	47.2 %	50.5 %	52.3 %	55.2 %	53.8 %
S17-SLF9A											-	95.5 %	88.0 %	49.4 %	44.7 %	45.2 %	44.7 %	50.0 %	53.9 %	51.9 %	50.9 %
S17-SLF9B												-	87.3 %	49.6 %	45.2 %	45.7 %	44.7 %	51.5 %	54.2 %	52.7 %	50.6 %
S17-SLF10													-	47.4 %	43.5 %	43.5 %	43.2 %	48.6 %	52.8 %	51.6 %	49.5 %
S17-SLF11														-	46.1 %	45.8 %	45.6 %	51.3 %	51.2 %	48.8 %	49.1 %
S17-SLF12A															-	96.2 %	92.9 %	47.8 %	48.1 %	48.0 %	48.0 %
S17-SLF12B																-	94.7 %	47.5 %	48.7 %	48.7 %	48.5 %
S17-SLF12Cψ																	-	47.8 %	47.7 %	47.4 %	48.6 %
S17-SLF13																		-	51.1 %	50.8 %	52.6 %
S17-SLF14																			-	76.8 %	73.0 %
S17-SLF16																				-	78.6 %

(**x**) SLFs of S19-haplotyped Max. = 100.0 % Min. = 43.5 % Ave. = 53.7 %

	S19-SLF1B	S19-SLF2	S19-SLF3	S19-SLF4	S19-SLF5	S19-SLF5B	S19-SLF6	S19-SLF7ψ	S19-SLF8A	S19-SLF8B	S19-SLF10A	S19-SLF10B	S19-SLF11	S19-SLF12	S19-SLF13	S19-SLF14	S19-SLF15ψ	S19-SLF16	S19-FBX1	S19-FBX2	S19-FBX3
S19-SLF1	97.7 %	60.4 %	50.3 %	48.2 %	53.7 %	53.2 %	50.3 %	55.4 %	55.2 %	54.6 %	49.5 %	51.6 %	53.3 %	48.1 %	49.5 %	54.2 %	54.5 %	52.2 %	51.7 %	51.4 %	51.4 %
S19-SLF1B	-	60.9 %	51.5 %	48.7 %	53.9 %	53.4 %	50.3 %	56.2 %	55.8 %	55.1 %	49.2 %	51.6 %	54.1 %	48.1 %	50.0 %	55.2 %	54.7 %	53.3 %	51.7 %	51.7 %	51.7 %
S19-SLF2		-	52.7 %	50.9 %	51.7 %	50.9 %	48.8 %	54.9 %	53.8 %	53.9 %	51.4 %	53.0 %	53.4 %	50.9 %	51.7 %	54.6 %	51.8 %	54.1 %	52.9 %	53.4 %	52.4 %
S19-SLF3			-	51.4 %	50.1 %	49.6 %	48.1 %	54.0 %	53.4 %	51.9 %	50.6 %	52.5 %	55.7 %	50.3 %	69.0 %	56.4 %	54.7 %	54.4 %	50.9 %	51.2 %	52.6 %
S19-SLF4				-	56.8 %	55.4 %	54.2 %	49.9 %	49.1 %	49.2 %	45.4 %	46.8 %	46.0 %	74.0 %	46.3 %	47.7 %	48.2 %	50.1 %	47.4 %	48.0 %	58.2 %
S19-SLF5					-	92.5 %	54.1 %	50.1 %	50.5 %	49.7 %	48.1 %	48.1 %	48.0 %	56.7 %	48.8 %	51.4 %	52.4 %	50.7 %	49.2 %	51.7 %	57.7 %
S19-SLF5B						-	52.8 %	50.4 %	49.1 %	48.3 %	48.8 %	49.6 %	48.6 %	57.0 %	47.0 %	52.0 %	51.4 %	51.4 %	49.5 %	52.4 %	57.7 %
S19-SLF6							-	49.1 %	48.3 %	47.1 %	47.4 %	47.9 %	48.1 %	50.9 %	44.6 %	48.8 %	50.6 %	47.8 %	48.7 %	50.3 %	53.7 %
S19-SLF7ψ								-	51.3 %	51.1 %	51.5 %	52.7 %	53.3 %	49.6 %	51.4 %	63.9 %	59.4 %	61.7 %	52.7 %	54.2 %	54.5 %
S19-SLF8A									-	97.2 %	49.4 %	49.6 %	53.2 %	49.4 %	52.6 %	55.4 %	53.8 %	56.5 %	49.6 %	51.4 %	52.5 %
S19-SLF8B										-	48.3 %	49.6 %	52.9 %	49.9 %	52.2 %	54.9 %	53.8 %	57.0 %	49.2 %	51.8 %	52.5 %
S19-SLF10A											-	92.1 %	48.8 %	43.5 %	48.7 %	53.5 %	54.7 %	50.8 %	87.7 %	76.6 %	50.3 %
S19-SLF10B												-	51.7 %	45.9 %	50.5 %	54.5 %	56.1 %	53.4 %	88.7 %	77.1 %	51.3 %
S19-SLF11													-	48.9 %	53.8 %	53.5 %	50.8 %	51.4 %	49.4 %	51.9 %	50.3 %
S19-SLF12														-	47.5 %	49.4 %	47.2 %	49.1 %	43.8 %	46.0 %	57.0 %
S19-SLF13															-	52.5 %	50.9 %	52.5 %	48.7 %	49.7 %	49.0 %
S19-SLF14																-	66.1 %	76.9 %	54.5 %	53.8 %	54.2 %
S19-SLF15ψ																	-	65.9 %	54.4 %	55.6 %	52.8 %
S19-SLF16																		-	52.1 %	52.1 %	52.5 %
S19-FBX1																			-	80.2 %	52.2 %
S19-FBX2																				-	52.8 %

100%
more than 90 %, less than 100 %
more than 80 %, less than 90 %
more than 70 %, less than 80 %
less than 70 %

Supplementary Table 3 (Continued)

(**y**) S-RNases Max. = 94.1 % Min. = 35.2 % Ave. = 52.9 %

	PiS2-RNase	PiS13-RNase	PiS3-RNase	PiS12-RNase	PiS1-RNase	S10-RNase	S17-RNase	S9-RNase	PiS7-RNase	S7-RNase	S11-RNase	S5-RNase	Sm-RNase	S19-RNase	S0m-RNase
S22-RNase	94.1 %	85.3 %	81.7 %	76.8 %	71.1 %	60.6 %	61.0 %	53.2 %	54.7 %	43.4 %	42.9 %	43.6 %	39.9 %	43.4 %	42.6 %
PiS2-RNase	-	86.5 %	80.2 %	77.4 %	71.2 %	63.1 %	60.4 %	53.6 %	54.7 %	45.2 %	42.0 %	45.5 %	40.9 %	43.3 %	41.1 %
PiS13-RNase		-	81.6 %	76.7 %	70.6 %	60.1 %	54.9 %	50.6 %	54.7 %	36.4 %	35.2 %	42.4 %	39.1 %	40.5 %	39.7 %
PiS3-RNase			-	84.0 %	72.6 %	63.2 %	62.5 %	55.4 %	54.7 %	45.7 %	43.0 %	45.1 %	40.9 %	44.4 %	42.7 %
PiS12-RNase				-	75.0 %	65.0 %	58.5 %	52.8 %	57.5 %	39.6 %	35.8 %	41.3 %	38.8 %	40.0 %	39.5 %
PiS1-RNase					-	65.0 %	58.3 %	55.6 %	56.3 %	44.8 %	41.2 %	44.7 %	39.9 %	44.0 %	41.5 %
S10-RNase						-	68.0 %	60.2 %	59.0 %	45.4 %	43.1 %	49.8 %	41.2 %	43.6 %	43.1 %
S17-RNase							-	57.3 %	54.0 %	47.0 %	45.7 %	47.1 %	42.7 %	45.9 %	47.5 %
S9-RNase								-	84.9 %	47.2 %	45.5 %	47.2 %	43.8 %	45.0 %	44.5 %
PiS7-RNase									-	43.3 %	39.1 %	41.3 %	40.5 %	41.5 %	39.6 %
S7-RNase										-	68.7 %	51.6 %	46.9 %	47.5 %	47.5 %
S11-RNase											-	50.2 %	44.5 %	48.9 %	48.9 %
S5-RNase												-	47.1 %	46.2 %	47.1 %
Sm-RNase													-	72.8 %	73.8 %
S19-RNase														-	86.5 %

100%
more than 90 %, less than 100 %
more than 80 %, less than 90 %
more than 70 %, less than 80 %
less than 70 %

Pairwise comparisons among allelic *SLF*s of the same type (**a–r**), among *SLF*s of each *S*-haplotype (**s–x**), or among allelic *S-RNase*s (**y**). Shading shows the level of identity. Each value was computed by using the GENETYX-MAC (ver. 16.0.6).

Supplementary Table 4 Summary of transformation experiments

				Transgene	self pollination	
Plant ID		*S*-genotype[a]		expression[b]	seed set[c]	Phenotype
S7-SLF1	#41	*S5S22*	*S11S22* x #14 (*S5S17/S7-SLF1*)[d]	+++	+++	SC
S7-SLF1	#42	*S11S19*	*S7S11* x #37 (*S5S19/S7-SLF1*)[d]	+++	-	SI
S7-SLF1	#43	*S11S19*	*S7S11* x #40 (*S17S19/S7-SLF1*)[d]	+++	-	SI
S7-SLF1	#44	*S11S22*	#42 x *S11S22*	+++	+++	SC
S7-SLF1	#45	*S19S22*	#42 x *S11S22*	+++	+++	SC
S7-SLF1	#46	*S19S22*	#43 x *S11S22*	+++	+++	SC
S5-SLF3	#1	*S5S11*	T0	+++	-	SI
S5-SLF3	#2	*S5S17*	T0	+++	-	SI
S5-SLF3	#3	*S11S7*	*S7S7* x #1	++	+++	SC
S5-SLF3	#4	*S11S7*	*S7S7* x #1	++	+++	SC
S5-SLF3	#5	*S9S11*	*S9S9* x #1	+	-	SI
S5-SLF3	#6	*S5S17*	*S17S17* x #1	+++	-	SI
S5-SLF3	#7	*S5S17*	*S17S17* x #1	+++	-	SI
S5-SLF3	#8	*S5S19*	*S19S19* x #1	+	-	SI
S5-SLF3	#9	*S5S9*	*S9S11* x #2	+++	-	SI
S5-SLF3	#10	*S5S11*	*S9S11* x #2	+++	-	SI
S5-SLF3	#11	*S5S11*	*S9S11* x #2	+++	-	SI
S5-SLF3	#12	*S9S17*	*S9S11* x #2	+++	-	SI
S5-SLF3	#13	*S5S7*	*S7S7* x #2	+++	+++	SC
S5-SLF3	#14	*S5S7*	*S7S7* x #2	+++	+++	SC
S5-SLF3	#15	*S5S19*	*S19S19* x #2	+++	-	SI
S5-SLF3	#16	*S5S19*	*S19S19* x #2	+++	-	SI
S7-SLF3	#1	*S5S7*	T0	+++	-	SI
S7-SLF3	#2	*S5S7*	T0	+++	-	SI
S7-SLF3	#3	*S5S7*	T0	+++	-	SI
S7-SLF3	#4	*S5S7*	T0	+++	-	SI
S7-SLF3	#5	*S5S7*	T0	+++	-	SI
S7-SLF3	#6	*S5S17*	T0	+++	-	SI
S7-SLF3	#7	*S5S17*	T0	+++	-	SI
S7-SLF3	#8	*S5S17*	T0	+++	-	SI
S7-SLF3	#9	*S7S9*	T0	+++	-	SI
S7-SLF3	#10	*S7S9*	T0	++	-	SI
S7-SLF3	#11	*S7S9*	T0	++	-	SI
S7-SLF3	#12	*S7S9*	T0	+++	-	SI
S7-SLF3	#13	*S7S11*	#1 x *S11S11*	+++	-	SI
S7-SLF3	#14	*S7S11*	#2 x *S11S11*	+++	-	SI
S7-SLF3	#15	*S7S11*	#3 x *S11S11*	+++	-	SI
S7-SLF3	#16	*S7S19*	#1 x *S5S19*	+++	-	SI
S7-SLF3	#17	*S7S19*	#3 x *S5S19*	+++	-	SI
S7-SLF3	#18	*S5S19*	#6 x *S5S19*	+++	-	SI
S11-SLF3B	#1	*S5S17*	T0	+++	-	SI
S11-SLF3B	#2	*S5S17*	T0	+++	-	SI
S11-SLF3B	#3	*S5S17*	T0	+++	-	SI
S11-SLF3B	#4	*S5S11*	T0	++	-	SI
S11-SLF3B	#5	*S5S11*	T0	+++	-	SI

S11-SLF3B	#6	*S5S9*	*S9S11* x #1	+++	-	SI
S11-SLF3B	#7	*S5S9*	*S9S11* x #1	+++	-	SI
S11-SLF3B	#8	*S5S11*	*S9S11* x #1	+++	-	SI
S11-SLF3B	#9	*S5S11*	*S9S11* x #1	+++	-	SI
S11-SLF3B	#10	*S11S17*	*S11S11* x #1	+++	-	SI
S11-SLF3B	#11	*S11S17*	*S11S11* x #1	+++	-	SI
S11-SLF3B	#12	*S5S7*	*S7S19* x #1	+++	-	SI
S11-SLF3B	#13	*S5S19*	*S7S19* x #1	+++	-	SI
S11-SLF3B	#14	*S5S19*	*S7S19* x #1	+++	-	SI
S11-SLF3B	#15	*S5S7*	*S7S19* x #1	++	-	SI
S11-SLF3B	#16	*S5S19*	*S7S19* x #1	+++	-	SI
S11-SLF3B	#17	*S7S17*	*S7S19* x #1	+++	-	SI
S11-SLF3B	#18	*S5S9*	*S9S11* x #3	++	-	SI
S11-SLF3B	#19	*S9S17*	*S9S11* x #3	++	-	SI
S11-SLF3B	#20	*S9S17*	*S9S11* x #3	++	-	SI
S11-SLF3B	#21	*S11S17*	*S9S11* x #3	+++	-	SI
S11-SLF3B	#22	*S5S7*	*S7S19* x #3	+++	-	SI
S11-SLF3B	#23	*S7S17*	*S7S19* x #3	+++	-	SI
S11-SLF3B	#24	*S17S19*	*S7S19* x #3	++	-	SI

S7-SLF9	#1	*S5S17*	T0	+++	-	SI
S7-SLF9	#2	*S5S17*	T0	+++	-	SI
S7-SLF9	#3	*S5S17*	T0	+++	-	SI
S7-SLF9	#4	*S5S9*	*S9S11* x #1	+++	-	SI
S7-SLF9	#5	*S5S11*	*S9S11* x #1	+++	-	SI
S7-SLF9	#6	*S5S11*	*S9S11* x #1	++	-	SI
S7-SLF9	#7	*S5S7*	*S7S19* x #1	+++	-	SI
S7-SLF9	#8	*S5S7*	*S7S19* x #1	+++	-	SI
S7-SLF9	#9	*S7S17*	*S7S19* x #1	++	-	SI
S7-SLF9	#10	*S5S19*	*S7S19* x #1	+++	+++	SC
S7-SLF9	#11	*S17S19*	*S7S19* x #1	+++	+++	SC
S7-SLF9	#12	*S5S9*	*S9S11* x #2	+++	-	SI
S7-SLF9	#13	*S5S11*	*S9S11* x #2	+++	-	SI
S7-SLF9	#14	*S11S17*	*S9S11* x #2	+++	-	SI
S7-SLF9	#15	*S5S7*	*S7S19* x #2	+++	-	SI
S7-SLF9	#16	*S5S7*	*S7S19* x #2	+++	-	SI
S7-SLF9	#17	*S5S19*	*S7S19* x #2	+++	+++	SC
S7-SLF9	#18	*S17S19*	*S7S19* x #2	+++	+++	SC
S7-SLF9	#19	*S5S9*	*S9S11* x #3	+++	-	SI
S7-SLF9	#20	*S5S9*	*S9S11* x #3	+++	-	SI
S7-SLF9	#21	*S11S17*	*S9S11* x #3	+++	-	SI
S7-SLF9	#22	*S5S7*	*S7S19* x #3	+++	-	SI
S7-SLF9	#23	*S5S7*	*S7S19* x #3	+++	-	SI
S7-SLF9	#24	*S5S19*	*S7S19* x #3	+++	+++	SC
S7-SLF9	#25	*S5S19*	*S7S19* x #3	+++	+++	SC
S7-SLF9	#26	*S7S9*	*S7S7* x #4	++	-	SI
S7-SLF9	#27	*S7S11*	*S7S7* x #5	++	-	SI
S7-SLF9	#28	*S7S17*	*S7S7* x #11	+++	-	SI
S7-SLF9	#29	*S7S19*	*S7S7* x #11	++	+++	SC
S7-SLF9	#30	*S7S9*	*S7S7* x #12	+++	-	SI
S7-SLF9	#31	*S7S11*	*S7S7* x #13	++	-	SI
S7-SLF9	#32	*S7S17*	*S7S7* x #18	+++	-	SI

S7-SLF9	#33	*S7S19*	*S7S7* x #18	+++	+++	SC
S7-SLF9	#34	*S7S9*	*S7S7* x #19	+++	-	SI
S7-SLF9	#35	*S7S11*	*S7S7* x #21	++	-	SI
S7-SLF9	#36	*S7S17*	*S7S7* x #21	+++	-	SI
S11-SLF9	#1	*S5S17*	T0	+++	-	SI
S11-SLF9	#2	*S5S17*	T0	+++	-	SI
S11-SLF9	#3	*S5S11*	T0	+++	-	SI
S11-SLF9	#4	*S5S9*	*S9S11* x #1	+++	-	SI
S11-SLF9	#5	*S5S11*	*S9S11* x #1	+++	-	SI
S11-SLF9	#6	*S9S17*	*S9S11* x #1	+++	-	SI
S11-SLF9	#7	*S11S17*	*S9S11* x #1	++	-	SI
S11-SLF9	#8	*S5S7*	*S7S19* x #1	+++	-	SI
S11-SLF9	#9	*S5S19*	*S7S19* x #1	+++	+++	SC
S11-SLF9	#10	*S17S19*	*S7S19* x #1	+++	+++	SC
S11-SLF9	#11	*S5S11*	*S9S11* x #2	+++	-	SI
S11-SLF9	#12	*S11S17*	*S9S11* x #2	+++	-	SI
S11-SLF9	#13	*S5S7*	*S7S19* x #2	+++	-	SI
S11-SLF9	#14	*S5S19*	*S7S19* x #2	+	+++	SC
S11-SLF9	#15	*S5S19*	*S7S19* x #2	+++	+++	SC
S11-SLF9	#16	*S9S11*	*S5S9* x #3	+++	-	SI
S11-SLF9	#17	*S11S17*	*S5S17* x #3	+++	-	SI
S11-SLF9	#18	*S5S19*	*S7S19* x #3	+++	+++	SC
S11-SLF9	#19	*S5S19*	*S7S19* x #3	+++	+++	SC

---

[a] The *S*-haplotype of each transgenic plant that is homoallelic with respect to the transgene is indicated in blue. For each self-compatible (SC) transgenic plant, the *S*-haplotype of pollen that exhibited competitive interaction with the transgene is indicated in red (see also Supplementary Table 6).

[b] "+++" indicates the transcript of a transgene yielding a strong band after 26 cycles of amplification; "++" indicates the transcript of a transgene yielding a strong band after 28 cycles of amplification; "+" indicates the transcript of a transgene yielding a weak or moderate-intensity band after 28 cycles of amplification.

[c] SC and SI phenotypes were judged by the number of the obtained seeds per pod after self-pollination. "+++" indicates more than 100 seeds set per pod; "++" indicates 51–100 seeds set per pod; "+" indicates 10–50 seeds set per pod; and "-" indicates fewer than 10 seeds set per pod. In this work, all self-pollination tests resulted in complete SC phenotype of "+++" or complete SI phenotype of "-". All results were consistently reproduced from at least three independent self-pollinations.

[d] These plants are derived from our previous work[9].

Supplementary Table 5 Analyses of progenies of the transformants that exhibited breakdown of SI

Population		*S*-haplotype segregation				
Genetic cross	No. of progeny plants analyzed	Possible genotypes of progeny plants	Observed ratio[a]	Expected ratio[b]	Chi square	P-value
S5S22 x *S5S22/S7-SLF1*	44	*S5S5/TG* : *S5S22/TG* : *S22S22/TG*	0: 21: 23	0: 1: 1	0.09	0.76
				1: 2: 1	24.14	5.74E-06
S11S22 x *S11S22/S7-SLF1*	30	*S11S11/TG* : *S11S22/TG* : *S22S22/TG*	0: 16: 14	0: 1: 1	0.13	0.72
				1: 2: 1	13.20	1.36E-03
S19S22 x *S19S22/S7-SLF1*	36	*S19S19/TG* : *S19S22/TG* : *S22S22/TG*	0: 17: 19	0: 1: 1	0.11	0.74
				1: 2: 1	20.17	4.18E-05
S5S7 x *S5S7/S5-SLF3*	52	*S5S5/TG* : *S5S7/TG* : *S7S7/TG*	0: 28: 24	0: 1: 1	0.31	0.58
				1: 2: 1	22.46	1.33E-05
S5S19 x *S5S19/S7-SLF9*	64	*S5S5/TG* : *S5S19/TG* : *S19S19/TG*	0: 35: 29	0: 1: 1	0.56	0.45
				1: 2: 1	26.84	1.48E-06
S7S19 x *S7S19/S7-SLF9*	47	*S7S7/TG* : *S7S19/TG* : *S19S19/TG*	0: 20: 27	0: 1: 1	1.04	0.31
				1: 2: 1	32.06	1.09E-07
S5S19 x *S5S19/S11-SLF9*	67	*S5S5/TG* : *S5S19/TG* : *S19S19/TG*	0: 32: 35	0: 1: 1	0.13	0.71
				1: 2: 1	36.70	1.07E-08
S17S19/S11-SLF9 self	36	*S17S17/TG* : *S17S19/TG* : *S19S19/TG*	0: 14: 22	0: 1: 1	1.78	0.18
				1: 2: 1	28.67	5.96E-07

[a] All progeny plants inherited the transgene (*TG*).

[b] Upper ratios are values predicted by competitive interaction; lower ratios are values predicted by simple mendelian inheritance.

Supplementary Table 6 Sequence information of genes extracted from whole genome database

(**a**) *SLF*-related F-box genes from tomato

Gene_ID	Location	Motif	Query	E value
Solyc00g014960	SL2.50ch00:11,078,697..11,082,983	F-box	S7-SLF5	3.00E-25
Solyc00g014980	SL2.50ch00:11,087,048..11,093,479	F-box	S7-SLF13	9.00E-25
Solyc00g018770	SL2.50ch00:11,667,234..11,668,418	F-box + FBA1	S7-SLF5	2.00E-25
Solyc01g008040	SL2.50ch01:2,196,519..2,197,816	F-box + FBA3	S7-SLF5	1.00E-23
Solyc01g008660	SL2.50ch01:2,721,644..2,722,893	F-box	S7-SLF4	2.00E-32
Solyc01g049660	SL2.50ch01:45,830,690..45,831,775	FBA3 (ψ)	S7-SLF14	1.00E-101
Solyc01g055160	SL2.50ch01:50,895,887..50,897,056	F-box + FBA1	S7-SLF6	1.00E-43
Solyc01g056220	SL2.50ch01:52,558,634..52,559,465	F-box (ψ)	S7-SLF11	3.00E-80
Solyc01g056240	SL2.50ch01:52,616,290..52,616,775	F-box + FBA3 (ψ)	S7-SLF14	1.00E-44
Solyc01g056250	SL2.50ch01:52,683,255..52,683,869	F-box (ψ)	S7-SLF5	4.00E-56
Solyc01g056280	SL2.50ch01:52,762,364..52,763,564	F-box + FBA1	S7-FBX	1.00E-116
Solyc01_pseudo1	SL2.50ch01:52,780,047..52,781,174	F-box + FBA3 (ψ)	S7-SLF4	1.00E-158
Solyc01_pseudo2	SL2.50ch01:53,340,413..53,341,578	F-box + FBA3 (ψ)	S7-SLF1A	1.00E-136
Solyc01_pseudo3	SL2.50ch01:53,365,318..53,366,359	F-box + FBA3 (ψ)	S7-SLF4	1.00E-103
Solyc01g056660	SL2.50ch01:55,528,778..55,529,745	F-box + FBA1	S7-SLF9A	1.00E-125
Solyc01_pseudo6	SL2.50ch01:55,974,384..55,975,615	F-box + FBA1 (ψ)	S7-SLF8A	2.00E-34
Solyc01g057010	SL2.50ch01:57,933,154..57,934,326	F-box + FBA1	S7-SLF8A	1.00E-132
Solyc01g057190	SL2.50ch01:59,694,709..59,695,872	F-box + FBA1	S7-SLF13	1.00E-176
Solyc01_pseudo4	SL2.50ch01:60,535,674..60,536,864	F-box + FBA3	S7-SLF6	1.00E-153
Solyc01_pseudo5	SL2.50ch01:63,731,624..63,732,791	FBA3 (ψ)	S7-SLF5	2.00E-50
Solyc01g067010	SL2.50ch01:75,348,972..75,350,445	F-box + FBA3	S7-SLF3	1.00E-24
Solyc01g067030	SL2.50ch01:75,366,631..75,368,093	F-box	S7-SLF8A	1.00E-23
Solyc02g033040	SL2.50ch02:29,703,075..29,704,514	F-box + FBA1	S7-SLF13	1.00E-24
Solyc02g070600	SL2.50ch02:40,317,008..40,319,433	F-box + FBA3	S7-SLF4	6.00E-21
Solyc02g070620	SL2.50ch02:40,323,600..40,325,396	F-box + FBA3	S7-SLF8A	1.00E-21
Solyc03g046490	SL2.50ch03:12,935,141..12,936,370	F-box + FBA3	S7-SLF2	3.00E-21
Solyc04g063440	SL2.50ch04:55,565,206..55,566,423	F-box + FBA3	S7-SLF2	1.00E-31
Solyc04g064440	SL2.50ch04:55,581,853..55,583,076	F-box + FBA1	S7-SLF1A	2.00E-36
Solyc04g080320	SL2.50ch04:64,549,641..64,550,714	F-box + FBA1	S7-SLF8A	7.00E-23
Solyc05g005110	SL2.50ch05:115,571..116,788	F-box + FBA1	S7-SLF13	2.00E-28
Solyc05g007530	SL2.50ch05:2,085,583..2,086,701	F-box + FBA1	S7-SLF2	8.00E-23
Solyc06g059810	SL2.50ch06:37,714,157..37,717,327	F-box + FBA1	S7-SLF2	1.00E-21
Solyc07g044920	SL2.50ch07:57,969,707..57,970,804	F-box + FBA3	S7-SLF8A	2.00E-45
Solyc07g047760	SL2.50ch07:58,956,909..58,958,366	F-box + FBA3	S7-SLF14	9.00E-29
Solyc07g052580	SL2.50ch07:61,061,992..61,063,899	F-box + FBA1	S7-SLF8A	6.00E-20
Solyc07g055020	SL2.50ch07:63,166,956..63,175,330	F-box + FBA1	S7-SLF3	2.00E-24
Solyc09g072910	SL2.50ch09:65,599,205..65,600,644	F-box + FBA1	S7-SLF3	1.00E-21
Solyc09g072930	SL2.50ch09:65,606,864..65,608,024	F-box + FBA1	S7-SLF2	3.00E-27
Solyc09g083230	SL2.50ch09:68,890,249..68,891,394	F-box	S7-SLF13	6.00E-28
Solyc09g091220	SL2.50ch09:70,525,090..70,526,286	F-box	S7-SLF5	2.00E-23
Solyc09g091690	SL2.50ch09:70,938,293..70,939,459	F-box	S7-SLF8A	2.00E-31
Solyc09g091710	SL2.50ch09:70,946,048..70,947,256	F-box	S7-SLF6	3.00E-28
Solyc10g008450	SL2.50ch10:2,574,498..2,575,547	F-box + FBA1	S7-SLF8A	2.00E-20
Solyc10g008580	SL2.50ch10:2,686,335..2,687,492	F-box + FBA3	S7-SLF4	2.00E-34
Solyc10g052710	SL2.50ch10:53,260,744..53,261,892	F-box + FBA1	S7-SLF3	2.00E-21
Solyc11g012540	SL2.50ch11:5,353,456..5,355,147	F-box	S7-SLF8A	2.00E-21
Solyc11g012550	SL2.50ch11:5,357,146..5,365,080	F-box	S7-SLF8A	2.00E-23
Solyc12g006130	SL2.50ch12:690,070..691,290	F-box + FBA1	S7-SLF13	3.00E-25
Solyc12g099550	SL2.50ch12:66,661,677..66,663,236	F-box + FBA1	S7-SLF17	7.00E-27

(**b**) *S-RNase*-related ribonuclease genes from tomato

Gene_ID	Location	Motif	Query	E value
Solyc01g055200	SL2.50ch01:51,700,660..51,701,422	signal + RNase T2	S7-RNase	2.00E-59
Solyc04g005640	SL2.50ch04:417,342..420,221	signal + RNase T2	S7-RNase	1.00E-19
Solyc05g007940	SL2.50ch05:2,366,284..2,369,405	signal + RNase T2	S7-RNase	2.00E-21
Solyc05g007950	SL2.50ch05:2,373,133..2,374,737	signal + RNase T2	S7-RNase	4.00E-20
Solyc06g082890	SL2.50ch06:48,522,779..48,529,899	signal + RNase T2	S7-RNase	3.00E-14
Solyc07g006570	SL2.50ch07:1,383,208..1,384,976	signal + RNase T2	S7-RNase	3.00E-13
Solyc09g020110	SL2.50ch09:18,416,997..18,428,931	signal + RNase T2	S7-RNase	9.00E-14

Supplementary Table 6 (Continued)

(**c**) *SLF*-related F-box genes from potato

Gene_ID	Peptide_ID	Location	Motif	Query	E value
PGSC0003DMG400017998	PGSC0003DMP400031381	ST4.03ch00:25,449,469..25,453,906	F-box	S7-SLF5	1.00E-26
PGSC0003DMG400003427	PGSC0003DMP400006117	ST4.03ch00:29,442,018..29,443,907	F-box	S7-SLF3	5.00E-23
PGSC0003DMG400003428	PGSC0003DMP400006118	ST4.03ch00:29,447,942..29,449,474	F-box	S7-SLF3	9.00E-23
PGSC0003DMG400012104	PGSC0003DMP400021387	ST4.03ch00:38,789,791..38,791,074	F-box + FBA1	S7-SLF16	1.00E-106
PGSC0003DMG400016368	PGSC0003DMP400028605	ST4.03ch01:3,708,814..3,710,345	F-box	S7-SLF5	1.00E-22
PGSC0003DMG400008762	PGSC0003DMP400015399	ST4.03ch01:26,225,626..26,226,959	F-box + FBA1	S7-SLF8A	1.00E-132
PGSC0003DMG400009445	PGSC0003DMP400016698	ST4.03ch01:26,409,150..26,410,277	F-box + FBA1	S7-SLF4	1.00E-121
PGSC0003DMG400009446	PGSC0003DMP400016699	ST4.03ch01:26,846,171..26,847,775	F-box + FBA1	S7-SLF2	1.00E-111
PGSC0003DMG400026599	PGSC0003DMP400046220	ST4.03ch01:28,485,606..28,486,790	F-box	S7-SLF11	1.00E-125
PGSC0003DMG400006514	PGSC0003DMP400011540	ST4.03ch01:28,825,314..28,825,912	F-box + FBA1	S7-SLF14	1.00E-46
PGSC0003DMG400006512	PGSC0003DMP400011538	ST4.03ch01:28,898,538..28,899,707	F-box + FBA3	S7-SLF1A	1.00E-158
PGSC0003DMG400006511	PGSC0003DMP400011537	ST4.03ch01:28,953,578..28,954,744	F-box + FBA1	S7-SLF2	1.00E-124
PGSC0003DMG400010961	PGSC0003DMP400019375	ST4.03ch01:29,555,279..29,556,511	F-box + FBA1	S7-SLF8A	3.00E-95
PGSC0003DMG400029040	PGSC0003DMP400050586	ST4.03ch01:30,452,407..30,453,378	F-box + FBA1	S7-SLF9	1.00E-122
PGSC0003DMG400020000	PGSC0003DMP400034705	ST4.03ch01:32,070,813..32,071,627	F-box + FBA1 (ψ)	S7-SLF14	1.00E-100
PGSC0003DMG400045078	PGSC0003DMP400067182	ST4.03ch01:32,798,728..32,799,843	F-box + FBA1	S7-SLF4	7.00E-21
PGSC0003DMG400038641	PGSC0003DMP400060745	ST4.03ch01:32,916,913..32,918,037	F-box + FBA3	S7-SLF4	1.00E-125
PGSC0003DMG400014981	PGSC0003DMP400026348	ST4.03ch01:33,421,528..33,422,865	F-box + FBA3	S7-SLF6	1.00E-136
PGSC0003DMG400016927	PGSC0003DMP400029579	ST4.03ch01:40,763,687..40,764,427	F-box + FBA1	S7-SLF8A	2.00E-88
PGSC0003DMG400022664	PGSC0003DMP400039281	ST4.03ch01:58,222,546..58,224,447	F-box + FBA1	S7-SLF5	1.00E-23
PGSC0003DMG400022858	PGSC0003DMP400039629	ST4.03ch01:60,036,805..60,038,756	F-box + FBA3	S7-SLF9	4.00E-27
PGSC0003DMG400006277	PGSC0003DMP400011123	ST4.03ch01:60,245,380..60,247,024	F-box + FBA3	S7-SLF2	1.00E-22
PGSC0003DMG400006293	PGSC0003DMP400011158	ST4.03ch01:60,422,085..60,423,307	F-box + FBA1	S7-SLF3	3.00E-21
PGSC0003DMG400021478	PGSC0003DMP400037241	ST4.03ch02:17,440,094..17,444,430	F-box + FBA1	S7-SLF5	1.00E-22
PGSC0003DMG400001294	PGSC0003DMP400002321	ST4.03ch02:46,711,089..46,712,488	F-box	S7-SLF13	7.00E-25
PGSC0003DMG400039355	PGSC0003DMP400061459	ST4.03ch04:57,788,313..57,789,497	F-box	S7-SLF2	5.00E-29
PGSC0003DMG400024833	PGSC0003DMP400043043	ST4.03ch04:57,810,515..57,811,675	F-box + FBA3	S7-SLF2	3.00E-29
PGSC0003DMG400024829	PGSC0003DMP400043032	ST4.03ch04:57,860,547..57,862,051	F-box	S7-SLF2	1.00E-23
PGSC0003DMG400024825	PGSC0003DMP400043028	ST4.03ch04:57,890,755..57,892,929	F-box	S7-SLF2	1.00E-25
PGSC0003DMG401023052	PGSC0003DMP400039944	ST4.03ch05:5,462,979..5,464,210	F-box	S7-SLF13	8.00E-23
PGSC0003DMG400013491	PGSC0003DMP400023858	ST4.03ch05:9,172,804..9,178,547	F-box + FBA1	S7-SLF13	8.00E-28
PGSC0003DMG400013520	PGSC0003DMP400023917	ST4.03ch05:9,273,070..9,278,152	F-box + FBA1	S7-SLF9	4.00E-29
PGSC0003DMG400013111	PGSC0003DMP400023213	ST4.03ch05:49,049,885..49,051,148	F-box	S7-SLF9	3.00E-25
PGSC0003DMG400030753	PGSC0003DMP400053555	ST4.03ch06:41,330,354..41,331,682	F-box + FBA3	S7-SLF13	5.00E-22
PGSC0003DMG400030752	PGSC0003DMP400053554	ST4.03ch06:41,337,764..41,338,969	F-box	S7-SLF2	2.00E-21
PGSC0003DMG400013031	PGSC0003DMP400023092	ST4.03ch06:41,352,637..41,353,830	F-box + FBA1	S7-SLF2	7.00E-21
PGSC0003DMG400040257	PGSC0003DMP400062361	ST4.03ch07:3,828,392..3,829,411	F-box	S7-SLF5	1.00E-20
PGSC0003DMG400021156	PGSC0003DMP400036681	ST4.03ch07:42,476,500..42,485,182	F-box + FBA1	S7-SLF2	9.00E-33
PGSC0003DMG400020424	PGSC0003DMP400035471	ST4.03ch07:50,094,896..50,104,856	F-box	S7-SLF2	2.00E-28
PGSC0003DMG402020445	PGSC0003DMP400035515	ST4.03ch07:50,126,875..50,132,629	F-box + FBA1	S7-SLF5	8.00E-24
PGSC0003DMG400043993	PGSC0003DMP400066097	ST4.03ch07:54,136,309..54,137,370	F-box + FBA3	S7-SLF3	5.00E-23
PGSC0003DMG400022273	PGSC0003DMP400038588	ST4.03ch07:55,683,647..55,690,807	F-box	S7-SLF1A	2.00E-24
PGSC0003DMG400018496	PGSC0003DMP400032228	ST4.03ch08:3,886,902..3,888,342	F-box + FBA1	S7-SLF16	5.00E-28
PGSC0003DMG400012267	PGSC0003DMP400021719	ST4.03ch08:56,165,635..56,166,828	F-box	S7-SLF5	3.00E-25
PGSC0003DMG400002699	PGSC0003DMP400004838	ST4.03ch09:3,209,305..3,210,537	F-box	S7-SLF2	4.00E-23
PGSC0003DMG400017667	PGSC0003DMP400030874	ST4.03ch09:43,584,212..43,586,601	F-box	S7-SLF6	2.00E-22
PGSC0003DMG400003796	PGSC0003DMP400006766	ST4.03ch09:50,930,115..50,932,391	F-box + FBA1	S7-SLF2	7.00E-23
PGSC0003DMG400003797	PGSC0003DMP400006767	ST4.03ch09:50,943,971..50,946,723	F-box	S7-SLF2	5.00E-26
PGSC0003DMG400003831	PGSC0003DMP400006820	ST4.03ch09:50,974,797..50,975,936	F-box + FBA1	S7-SLF2	8.00E-26
PGSC0003DMG401006445	PGSC0003DMP400011435	ST4.03ch09:54,462,904..54,469,210	F-box	S7-SLF3	5.00E-23
PGSC0003DMG400006107	PGSC0003DMP400010841	ST4.03ch09:55,170,298..55,171,874	F-box	S7-SLF9	2.00E-23
PGSC0003DMG400029654	PGSC0003DMP400051661	ST4.03ch09:58,511,594..58,513,725	F-box + FBA1	S7-SLF5	1.00E-20
PGSC0003DMG400029632	PGSC0003DMP400051618	ST4.03ch09:58,571,145..58,573,019	F-box	S7-SLF2	1.00E-26
PGSC0003DMG400029655	PGSC0003DMP400051662	ST4.03ch09:58,581,556..58,582,764	F-box	S7-SLF5	9.00E-26
PGSC0003DMG400031300	PGSC0003DMP400054533	ST4.03ch09:58,849,836..58,850,966	F-box	S7-SLF2	4.00E-27
PGSC0003DMG400031292	PGSC0003DMP400054521	ST4.03ch09:58,851,437..58,854,176	F-box	S7-SLF5	7.00E-23
PGSC0003DMG400021673	PGSC0003DMP400037580	ST4.03ch10:4,120,452..4,121,979	F-box + FBA1	S7-SLF5	1.00E-30
PGSC0003DMG400021672	PGSC0003DMP400037579	ST4.03ch10:4,123,154..4,124,335	F-box	S7-SLF5	7.00E-28
PGSC0003DMG400031233	PGSC0003DMP400054430	ST4.03ch10:48,844,750..48,845,709	F-box + FBA3	S7-SLF13	7.00E-24
PGSC0003DMG400028237	PGSC0003DMP400049085	ST4.03ch10:56,055,611..56,057,397	F-box + FBA1	S7-SLF9	7.00E-23
PGSC0003DMG400046761	PGSC0003DMP400068865	ST4.03ch12:995,124..996,059	F-box + FBA1	S7-SLF2	1.00E-23
PGSC0003DMG400004294	PGSC0003DMP400007644	ST4.03ch12:6,242,643..6,244,440	F-box + FBA1	S7-SLF3	2.00E-21
PGSC0003DMG400045722	PGSC0003DMP400067826	ST4.03ch12:20,809,067..20,810,263	F-box	S7-SLF3	5.00E-22
PGSC0003DMG400040830	PGSC0003DMP400062934	ST4.03ch12:27,411,668..27,412,774	F-box	S7-SLF5	3.00E-21
PGSC0003DMG400034923	PGSC0003DMP400057027	ST4.03ch12:53,231,209..53,232,237	F-box	S7-SLF13	6.00E-22
PGSC0003DMG400004709	PGSC0003DMP400008352	ST4.03ch12:60,211,092..60,212,744	F-box + FBA1	S7-SLF5	6.00E-27

(**d**) *S-RNase*-related ribonuclease genes from potato

Gene_ID	Peptide_ID	Location	Motif	Query	E value
PGSC0003DMG400026738	PGSC0003DMP400046458	ST4.03ch00:3,948,530..3,949,620	signal + RNase T2	S7-RNase	1.00E-46
PGSC0003DMG400031503	PGSC0003DMP400054831	ST4.03ch00:35,480,463..35,481,718	RNase T2	S7-RNase	8.00E-11
PGSC0003DMG400002857	PGSC0003DMP400005163	ST4.03ch04:262,942..265,137	RNase T2	S7-RNase	1.00E-17
PGSC0003DMG400019997	PGSC0003DMP400034699	ST4.03ch05:2,484,873..2,485,866	signal + RNase T2	S7-RNase	8.00E-12

Gray shading highlights *S*-genes that belong to Solanaceae *SLF*s or *S-RNase*s clades (see Fig. 3).

Supplementary table 7 Sequence information of *SLF*-related F-box genes, extracted from published data

Gene	Accession ID	Source	References	Note
Solanaceae SLFs				
PiS1-SLF1	AY500390	*Petunia inflata*	ref. 22	synonymous with PiSLF1
PiS1-SLF2	EF614191	*Petunia inflata*	ref. 56	synonymous with PiSLFLc-S1
PiS1-SLF7	EF614190	*Petunia inflata*	ref. 56	synonymous with PiSLFLa-S1
PiS1-SLF9	AY363970	*Petunia inflata*	ref. 37	synonymous with S1-A113
PiS1-SLF10	AY363973	*Petunia inflata*	ref. 37	synonymous with S1-A134
PiS2-SLF1	AY500391	*Petunia inflata*	ref. 22	synonymous with PiSLF2
PiS2-SLF3	EF614187	*Petunia inflata*	ref. 56	synonymous with PiSLFLd-S2
PiS2-SLF4	KF524351	*Petunia inflata*	ref. 23	
PiS2-SLF5	KF524352	*Petunia inflata*	ref. 23	
PiS2-SLF6	KF524353	*Petunia inflata*	ref. 23	
PiS2-SLF7	EF614189	*Petunia inflata*	ref. 56	synonymous with PiSLFLa-S2
PiS2-SLF8	EF614188	*Petunia inflata*	ref. 56	synonymous with PiSLFLb-S2
PiS2-SLF9	AY363971	*Petunia inflata*	ref. 37	synonymous with S2-A113
PiS2-SLF10	AY363974	*Petunia inflata*	ref. 37	synonymous with S2-A134
PiS3-SLF1	AY500392	*Petunia inflata*	ref. 22	synonymous with PiSLF3
PiS3-SLF5	KF524354	*Petunia inflata*	ref. 23	
PiS3-SLF6	KF524355	*Petunia inflata*	ref. 23	
PiS3-SLF9	AY363972	*Petunia inflata*	ref. 37	synonymous with S3-A113
PiS3-SLF10	AY363975	*Petunia inflata*	ref. 37	synonymous with S3-A134
PiS5-SLF1	KC590092	*Petunia inflata*	ref. 65	
PiS7-SLF1	KC590093	*Petunia inflata*	ref. 65	
PiS11-SLF1	KC590094	*Petunia inflata*	ref. 65	
PiS13-SLF1	KC590095	*Petunia inflata*	ref. 65	
NaDD1-S1	EF420251	*Nicotiana alata*	ref. 66	
NaDD2-S1	EF420252	*Nicotiana alata*	ref. 66	
NaDD3-S1	EF420253	*Nicotiana alata*	ref. 66	
NaDD4-S2	EF420254	*Nicotiana alata*	ref. 66	
NaDD5-S2	EF420255	*Nicotiana alata*	ref. 66	
NaDD6-S2	EF420256	*Nicotiana alata*	ref. 66	
NaDD7-S2	EF420257	*Nicotiana alata*	ref. 66	
NaDD8-S2	EF420258	*Nicotiana alata*	ref. 66	
NaDD9-S2	EF420259	*Nicotiana alata*	ref. 66	
NaDD10-S6	EF420260	*Nicotiana alata*	ref. 66	
Antirrhinum SLFs				
AhSLF-S2	AJ297974	*Antirrhinum hispanicum*	ref. 67	
AhSLF-S2L	AJ297975	*Antirrhinum hispanicum*	ref. 67	
AhSLF-S1	AJ515535	*Antirrhinum hispanicum*	ref. 68	
AhSLF-S4	AJ515534	*Antirrhinum hispanicum*	ref. 68	
AhSLF-S5	AJ515536	*Antirrhinum hispanicum*	ref. 68	
AhSLF-S1E	AJ515535	*Antirrhinum hispanicum*	ref. 68	
AhSLF-S2C	DQ462204	*Antirrhinum hispanicum*	ref. 68	
AhSLF-S4A	AJ515534	*Antirrhinum hispanicum*	ref. 68	
AhSLF-S4D	AJ515534	*Antirrhinum hispanicum*	ref. 68	
AhSLF-S5A	AJ515536	*Antirrhinum hispanicum*	ref. 68	
Maloideae SLFs/SFBBs				
MdFBX1-S3	AB539844	*Malus x domestica*	ref. 69	
MdFBX2-S3	AB539845	*Malus x domestica*	ref. 69	
MdFBX3-S3	AB539846	*Malus x domestica*	ref. 69	
MdFBX5-S3	AB539848	*Malus x domestica*	ref. 69	
MdFBX7-S3	AB539850	*Malus x domestica*	ref. 69	
MdFBX8-S3	AB539851	*Malus x domestica*	ref. 69	
MdFBX9-S3	AB539852	*Malus x domestica*	ref. 69	
MdFBX11-S3	AB539854	*Malus x domestica*	ref. 69	

MdFBX14-S3	AB539857	*Malus x domestica*	ref. 69	
MdFBX18-S3	AB539861	*Malus x domestica*	ref. 69	
MdFBX20-S3	AB539863	*Malus x domestica*	ref. 69	
MdSFBB3-alpha	AB270795	*Malus x domestica*	ref. 70	
MdSFBB3-beta	AB270796	*Malus x domestica*	ref. 70	
PpS4FBX0	AB308360	*Pyrus pyrifolia*	ref. 71	synonymous with PpSFBB1-S4 and PpSFBB4-d1
PpSFBB2-S4	AB270798	*Pyrus pyrifolia*	ref. 70	synonymous with PpSFBB4-β
PpSFBB3-S2	AB545982	*Pyrus pyrifolia*	ref. 72	synonymous with PpSFBB2-u5
PpSFBB4-S4	AB621610	*Pyrus pyrifolia*	ref. 73	
PpSFBB5-S4	AB545981	*Pyrus pyrifolia*	ref. 72	synonymous with PpSFBB4-u2
PpSFBB6-S4	AB270797	*Pyrus pyrifolia*	ref. 70	synonymous with PpSFBB4-α
PpSFBB7-S4	AB545981	*Pyrus pyrifolia*	ref. 72	synonymous with PpSFBB4-u3
PpSFBB8-S4	AB270799	*Pyrus pyrifolia*	ref. 70	synonymous with PpSFBB4-γ
PpSFBB4-u1	AB545981	*Pyrus pyrifolia*	ref. 72	
PpSFBB4-u4	AB545981	*Pyrus pyrifolia*	ref. 72	
PpSFBB4-d2	AB545981	*Pyrus pyrifolia*	ref. 72	
Prunus SLFLs				
PmS7-SLFL1	AB092624	*Prunus mume*	ref. 74	
PmS7-SLFL2	AB092626	*Prunus mume*	ref. 74	
PmS7-SLFL3	AB092627	*Prunus mume*	ref. 74	
PaviSLFL1-S4	AB280953	*Prunus avium*	ref. 75	
PaviSLFL2-S4	AB280954	*Prunus avium*	ref. 75	
PaviSLFL3-S4	AB280955	*Prunus avium*	ref. 75	
Prunus SLF/SFB/nonS-FBs				
ParmSFB24	HQ615603	*Prunus armeniaca*	ref. 76	
PaviSFB4	AB111521	*Prunus avium*	ref. 77	
PdulSFB-a	FJ362524	*Prunus dulcis*	Guo, C., Li, J., Luo, S. & He, T. Direct Submission	
PmS7-SLF	AB092622	*Prunus mume*	ref. 74	
PsalSFB-c	DQ849084	*Prunus salicina*	ref. 78	
PaviFB	JQ322648	*Prunus avium*	ref. 79	
PmFbox1	JX141276	*Prunus mume*	ref. 80	
PmFbox2	JX141277	*Prunus mume*	ref. 80	
(Outgroop)				
PiFBP2011	DQ250019	*Petunia hybrida*	ref. 60	
PiFBP2411	DQ250020	*Petunia hybrida*	ref. 60	

Supplementary table 8 Sequence information of *S-RNase*-related RNase-T2 genes used in phylogenetic analysis

Gene	Accession ID	Source	References	Note
Class-III: Solanaceae S-RNases				
PaS1-RNase	AF239908	*Petunia axillaris*	ref. 81	
PaS13-RNase	AF239909	*Petunia axillaris*	ref. 81	
PaS15-RNase	AF239910	*Petunia axillaris*	ref. 81	
PaS17-RNase	AY180050	*Petunia axillaris*	ref. 52	
PaS19-RNase	AY766156	*Petunia axillaris*	ref. 52	
PaSc1-RNase	AY180048	*Petunia axillaris*	ref. 52	self-compatible allele
PaSc2-RNase	AY180049	*Petunia axillaris*	ref. 52	self-compatible allele
Pa-nonS-RNase	AF239907	*Petunia axillaris*	ref. 81	non-S RNase
PhS1-RNase	U07362	*Petunia hybrida*	ref. 82	
PhS3-RNase	U07363	*Petunia hybrida*	ref. 82	
PhS5-RNase	AB016522	*Petunia hybrida*	ref. 51	synonymous with SB1, identical with Sv
PhS7-RNase	AB568388	*Petunia hybrida*	ref. 9	
PhS9-RNase	AB016523	*Petunia hybrida*	ref. 51	synonymous with SB2, identical with S3L
PhS10-RNase	AB933140	*Petunia hybrida*	This work	identical with Sx
PhS11-RNase	AB568389	*Petunia hybrida*	ref. 9	identical with PiS11
PhS22-RNase	AB933141	*Petunia hybrida*	This work	
PhS22m-RNase	AB933142	*Petunia hybrida*	This work	self-compatible allele
PhSm-RNase	AB933143	*Petunia hybrida*	This work	self-compatible allele
PhS0m-RNase	AB933144	*Petunia hybrida*	This work	identical with PhS0, self-compatible allele
PiS1-RNase	M67990	*Petunia inflata*	ref. 83	
PiS2-RNase	AF301533	*Petunia inflata*	ref. 84	
PiS3-RNase	M67991	*Petunia inflata*	ref. 83	
PiS6-RNase	AF301167	*Petunia inflata*	ref. 40	
PiS7-RNase	AF301168	*Petunia inflata*	ref. 40	
PiS8-RNase	AF301169	*Petunia inflata*	ref. 40	
PiS9-RNase	AF301170	*Petunia inflata*	ref. 40	
PiS10-RNase	AF301171	*Petunia inflata*	ref. 40	
PiS12-RNase	AF301173	*Petunia inflata*	ref. 40	
PiS13-RNase	AF301174	*Petunia inflata*	ref. 40	
PiS15-RNase	AF301175	*Petunia inflata*	ref. 40	
PiS16-RNase	AF301176	*Petunia inflata*	ref. 40	
PiS17-RNase	AF301177	*Petunia inflata*	ref. 40	
PiS19-RNase	AF301178	*Petunia inflata*	ref. 40	
PiS20-RNase	AF301179	*Petunia inflata*	ref. 40	
PiS21-RNase	AF301180	*Petunia inflata*	ref. 40	
PiSk-RNase	AB094600	*Petunia inflata*	ref. 85	
PiRNX2	M93418	*Petunia inflata*	ref. 86	non-S RNase
ScS11-RNase	S69589	*Solanum chacoense*	ref. 87	
ScS12-RNase	AF176533	*Solanum chacoense*	ref. 88	
ScS13-RNase	L36667	*Solanum chacoense*	ref. 89	
ScS14-RNase	AF232304	*Solanum chacoense*	ref. 90	
SchilS1-RNase	AB072469	*Solanum chilense*	ref. 91	
Sh_hab-1	GU361144	*Solanum habrochaites*	ref. 92	
Sh_hab-2	GU361145	*Solanum habrochaites*	ref. 92	
Sh_hab-3	GU361146	*Solanum habrochaites*	ref. 92	
Sh_hab-4	GU361147	*Solanum habrochaites*	ref. 92	
Sh_hab-5	GU361148	*Solanum habrochaites*	ref. 92	
Sh_hab-6	GU361149	*Solanum habrochaites*	ref. 92	
Sh_hgSRN1	AB072478	*Solanum habrochaites*	ref. 91	synonymous with LhgSRN-1
Sn_LpfSRN1	AB072475	*Solanum neorickii*	ref. 91	synonymous with LpfSRN-1
Spen_pen-1	GU361150	*Solanum pennellii*	ref. 92	
SpS6-RNase	Z26583	*Solanum peruvianum*	ref. 93	
SpS7-RNase	Z26582	*Solanum peruvianum*	ref. 93	
SpS11-RNase	U28795	*Solanum peruvianum*	ref. 94	
SpS12-RNase	U28796	*Solanum peruvianum*	ref. 94	

SpS13-RNase	D17325	*Solanum peruvianum*	ref. 95	
SpS15-RNase	AB072457	*Solanum peruvianum*	ref. 91	
SpS24-RNase	AB072466	*Solanum peruvianum*	ref. 91	
SpS25-RNase	AB072467	*Solanum peruvianum*	ref. 91	
Sp-nonS	Z26581	*Solanum peruvianum*	ref. 93	non-S RNase
StS2-RNase	X62727	*Solanum tuberosum*	ref. 96	
PGSC0003DMG400026738		*Solanum tuberosum*	ref. 12	
Solyc01g055200		*Solanum lycopersicum*	ref. 13	self-compatible allele
NaS2-RNase	X03803	*Nicotiana alata*	ref. 97	
NaS3-RNase	U66427	*Nicotiana alata*	ref. 98	
NaS6-RNase	U08861	*Nicotiana alata*	ref. 99	
NaS7-RNase	U13255	*Nicotiana alata*	ref. 100	
NaSA2-RNase	U45957	*Nicotiana alata*	ref. 101	
Na_D63887	D63887	*Nicotiana alata*	Norioka, S. Direct Submission	
Na_D63888	D63888	*Nicotiana alata*	Norioka, S. Direct Submission	
Ns_relicRNase	AJ002296	*Nicotiana sylvestris*	ref. 102	

Class-III: Antirrhinum S-RNases

AhS1-RNase	HE805271	*Antirrhinum hispanicum*	Liu, W. & Xue, Y. B. Direct Submission	
AhS2-RNase	X96465	*Antirrhinum hispanicum*	ref. 103	
AhS3-RNase	AJ315593	*Antirrhinum hispanicum*	Xue, Y. Direct Submission	
AhS4-RNase	X96466	*Antirrhinum hispanicum*	ref. 103	
AhS5-RNase	X96464	*Antirrhinum hispanicum*	ref. 103	

Class-III: Maloideae S-RNases

MdS2-RNase	U12199	*Malus x domestica*	ref. 104	
MdS3-RNase	U12200	*Malus x domestica*	ref. 104	
MdS4-RNase	AF327223	*Malus x domestica*	Van Nerum, I., et al. Direct Submission	
MdS9-RNase	U19793	*Malus x domestica*	ref. 104	
MdS10-RNase	AF327221	*Malus x domestica*	Van Nerum, I., et al. Direct Submission	
MdS27b-RNase	AF327222	*Malus x domestica*	Van Nerum, I., et al. Direct Submission	
PpS1-RNase	AB002139	*Pyrus pyrifolia*	ref. 105	
PpS3-RNase	AB002140	*Pyrus pyrifolia*	ref. 105	
PpS4-RNase	AB009385	*Pyrus pyrifolia*	ref. 106	
PpS5-RNase	AB002141	*Pyrus pyrifolia*	ref. 105	
PpS6-RNase	AB002142	*Pyrus pyrifolia*	ref. 105	
PpS7-RNase	AB002143	*Pyrus pyrifolia*	ref. 105	
PpS8-RNase	AB104908	*Pyrus pyrifolia*	ref. 107	
PpS9-RNase	AB104909	*Pyrus pyrifolia*	ref. 108	

Class-III: Prunus S-RNases

ParmS1-RNase	AY587561	*Prunus armeniaca*	ref. 109	
ParmS24-RNase	HQ615602	*Prunus armeniaca*	ref. 76	
PaviS1-RNase	AJ298310	*Prunus avium*	ref. 110	
PaviS4-RNase	AB028154	*Prunus avium*	ref. 111	
PdulSa-RNase	AB026836	*Prunus dulcis*	ref. 112	
PdulSb-RNase	AB011469	*Prunus dulcis*	ref. 113	
PdulSc-RNase	AB011470	*Prunus dulcis*	ref. 113	
PmS1-RNase	AB101438	*Prunus mume*	ref. 114	
PmS7-RNase	AB092644	*Prunus mume*	ref. 74	
PmS14-RNase	EU020121	*Prunus mume*	Zhang, S. L., et al., Direct Submission	
PmS15-RNase	EU020122	*Prunus mume*	Zhang, S. L., et al., Direct Submission	
PmS16-RNase	EU020123	*Prunus mume*	Zhang, S. L., et al., Direct Submission	
PmSf-RNase	AB101437	*Prunus mume*	ref. 114	
PsalSc-RNase	AB084102	*Prunus salicina*	ref. 115	
PsalSb-RNase	AB252413	*Prunus salicina*	ref. 116	

Class-III: S-clade non-S S-RNase-like, expressing in nectary

RNasePhy3	GQ465919	*Petunia hybrida*	ref. 62	expressing in nectary

RNasePhy4	GQ465918	*Petunia hybrida*	ref. 62	expressing in nectary
PGSC0003DMG400019997		*Solanum tuberosum*	ref. 12	
PGSC0003DMG400031503		*Solanum tuberosum*	ref. 12	
Solyc07g006570		*Solanum lycopersicum*	ref. 13	
Class-I				
RNasePhy1	GQ465920	*Petunia hybrida*	ref. 62	
RNasePhy5	GQ465917	*Petunia hybrida*	ref. 62	
RNaseNE	U13256	*Nicotiana alata*	ref. 117	
RNaseNGR1	AB112028	*Nicotiana glutinosa*	ref. 118	synonymous with RNaseNW
RNaseNGR3	AB032257	*Nicotiana glutinosa*	ref. 119	
RNaseNK1	AB034638	*Nicotiana tabacum*	ref. 120	
RNaseLE	X79337	*Solanum lycopersicum*	ref. 121	
RNaseLX	X79338	*Solanum lycopersicum*	ref. 121	
Solyc04g005640		*Solanum lycopersicum*	ref. 13	
Solyc05g007940		*Solanum lycopersicum*	ref. 13	
Solyc05g007950		*Solanum lycopersicum*	ref. 13	
PGSC0003DMG400002857		*Solanum tuberosum*	ref. 12	
Pp_non-S	D49529	*Pyrus pyrifolia*	ref. 122	non-*S-RNase* gene
RNasePD1	AF227522	*Prunus dulcis*	ref. 123	
RNasePD2	AF202030	*Prunus dulcis*	ref. 124	
Class-II				
RNasePhy2	GQ507487	*Petunia hybrida*	ref. 125	
RNaseNGR2	AB032256	*Nicotiana glutinosa*	ref. 119	
Solyc06g082890		*Solanum lycopersicum*	ref. 13	
Solyc09g020110		*Solanum lycopersicum*	ref. 13	
RNaseLER	AM408589	*Solanum lycopersicum*	ref. 126	
AhSL28	AJ489249	*Antirrhinum hispanicum*	ref. 127	S-like RNase 28
(Outgroup)				
RNase T2	NM_003730	*Homo sapiens*	ref. 63	
RNase Rh	D12476	*Rhizopus niveus*	ref. 64	

Classification is made according to refs. 61 and 62.

Supplementary Table 9 Summary of substitution rates among *SLF*s and *S-RNase*s

Group	No. of genes	*Ka*	*Ks*
Petunia Type-1 *SLF*s	20	0.037	0.107
Petunia Type-2 *SLF*s	8	0.090	0.303
Petunia Type-3 *SLF*s	12	0.059	0.166
Petunia Type-4 *SLF*s	11	0.027	0.090
Petunia Type-5 *SLF*s	14	0.021	0.074
Petunia Type-6 *SLF*s	11	0.023	0.081
Petunia Type-7 *SLF*s	9	0.038	0.086
Petunia Type-8 *SLF*s	14	0.031	0.113
Petunia Type-9 *SLF*s	13	0.021	0.097
Petunia Type-10 *SLF*s	14	0.014	0.022
Petunia Type-11 *SLF*s	10	0.029	0.133
Petunia Type-12 *SLF*s	11	0.018	0.054
Petunia Type-13 *SLF*s	10	0.023	0.078
Petunia Type-14 *SLF*s	9	0.027	0.058
Petunia Type-15 *SLF*s	7	0.016	0.025
Petunia Type-16 *SLF*s	11	0.031	0.078
Petunia Type-17 *SLF*s	6	0.000	0.001
*Petunia S-RNase*s	33	0.400	0.850
P. hybrida S5-haplotype *SLF*s	17	0.349	0.752
P. hybrida S7-haplotype *SLF*s	17	0.321	0.747
P. hybrida S9-haplotype *SLF*s	18	0.325	0.756
P. hybrida S11-haplotype *SLF*s	16	0.323	0.757
P. axillaris S17-haplotype *SLF*s	18	0.334	0.762
P. axillaris S19-haplotype *SLF*s	20	0.323	0.753
*Solanum S-RNase*s	26	0.410	0.785
S. tuberosum *SLF*s	14	0.405	0.950
S. lycopersicum *SLF*s	13	0.480	1.019

Supplementary Table 10 Results of the recombination analysis using LDhat

Dataset	$4N_er$	corr(r^2, d)	*P*corr(r^2, d)
All *SLF*s	49.721	-0.009	0.016
Type-3 *SLF*s	7.525	-0.023	0.047
Type-9 *SLF*s	2.975	-0.118	0.000
Type-9+10 *SLF*s + *FBX*s [a]	6.397	-0.094	0.000
Type-14+16+17 *SLF*s	8.776	-0.017	0.030

Recombination tests were carried out using the LDhat program[19]. Datasets analyzed were sequence alignments involving each type or some related types of *SLF*s. $4N_er$, population recombination rate; corr(r^2, d), correlations between r^2 and physical distance; *P*corr(r^2, d), simulated p values based on 1,000 permutations. Only statistically significant results ($p< 0.05$) are shown. [a] "*FBX*s" in this table indicates type 9– and type 10–related, ungrouped *FBX*s: S_{19}-*FBX1*, S_{19}-*FBX2*, S_{0m}-*FBX1*, and S_{0m}-*FBX2*.

Supplementary Table 11 Summary of the pairwise detection of the gene conversion in *SLF* genes using GENECONV

Dataset		Allele involved	Sim*P*	Begin	End	Length
only SI	all *SLF*s	*S7-SLF2; S19-SLF2*	0.0084	482	598	117
	Type-1 *SLF*s	n.d.				
	Type-2 *SLF*s	n.d.				
	Type-3 *SLF*s	*PiS2-SLF3; S17-SLF3*	0.0022	657	1233	577
		S10-SLF3; S22-SLF3	0.0315	732	1303	572
	Type-3+11+13 *SLF*s	*PiS2-SLF3; S17-SLF3*	0.0186	657	1233	577
	Type-4 *SLF*s	n.d.				
	Type-4+12 *SLF*s	n.d.				
	Type-5 *SLF*s	n.d.				
	Type-6 *SLF*s	n.d.				
	Type-8 *SLF*s	n.d.				
	Type-9+10 *SLF*s	*PiS1-SLF10; S10-SLF10*	0.0276	145	777	633
		PiS1-SLF10; S22-SLF10	0.0276	145	777	633
	Type-11 *SLF*s	n.d.				
	Type-11+13 *SLF*s	n.d.				
	Type-12 *SLF*s	n.d.				
	Type-13 *SLF*s	n.d.				
	Type-14+16+17 *SLF*s	n.d.				
SI + SC	all SLFs	*S7-SLF2; S19-SLF2*	0.0462	482	598	117
	Type-1 *SLF*s	*S10-SLF1; Sm-SLF1*	0.0120	1	659	659
	Type-2 *SLF*s	n.d.				
	Type-3 *SLF*s	*S0m-SLF3; S9-SLF3*	0.0066	507	831	325
		PiS2-SLF3; S17-SLF3	0.0037	601	1137	537
	Type-3+13 *SLF*s	*S0m-SLF3;S9-SLF3*	0.0263	510	834	325
		PiS2-SLF3;S17-SLF3	0.0143	604	1140	537
		S22-SLF13;Sm-SLF13	0.0035	1	535	535
		S19-SLF13;Sm-SLF13	0.0231	149	535	387
	Type-4 *SLF*s	n.d.				
	Type-5 *SLF*s	n.d.				
	Type-6 *SLF*s	n.d.				
	Type-7 *SLF*s	*S17-SLF7*ψ*; S19-SLF7*ψ	0.0243	493	651	159
	Type-8 *SLF*s	*S0m-SLF8; S5-SLF8*	0.0340	205	461	257
	Type-9 *SLF*s	*PiS3-SLF9; Sm-SLF9B*	0.0057	484	759	276
		S22-SLF9; Sm-SLF9A	0.0057	988	1188	201
	Type-10 *SLF*s	n.d.				
	Type-9+10 *SLF*s + *FBX*s [a]	*S0m-FBX1; S0m-FBX2*	0.0046	62	152	91
		S0m-FBX1; S19-FBX2	0.0379	79	147	69
		S19-FBX1; S19-FBX2	0.0120	162	233	72
		Sm-SLF9B; PiS3-SLF10	0.0215	670	792	123
		Sm-SLF9B; S5-SLF10	0.0340	670	792	123
		S17-SLF9A; PiS3-SLF10	0.0340	693	811	119
		S17-SLF9B; S0m-FBX1	0.0439	37	171	135
		S17-SLF9B; S0m-FBX2	0.0157	62	152	91
		Sm-SLF9A; S19-FBX2	0.0247	319	404	86
		PiS3-SLF9; S19-FBX2	0.0262	319	411	93
		S11-SLF9; S19-FBX2	0.0380	322	411	90
	Type-11 *SLF*s	*S11-SLF11; S19-SLF11*	0.0450	246	374	129
		S17-SLF11; S19-SLF11	0.0004	247	401	155
	Type-12 *SLF*s	n.d.				
	Type-13 *SLF*s	*S22-SLF13; Sm-SLF13*	0.0001	1	532	532
		S5-SLF13; Sm-SLF13	0.0029	1	287	287
		S5-SLF13; S22-SLF13	0.0119	1	287	287
		S19-SLF13; Sm-SLF13	0.0154	149	532	384
		S0m-SLF13; S7-SLF13	0.0317	952	1085	134
	Type-14 *SLF*s	n.d.				
	Type-14+16+17 *SLF*s	n.d.				
	Type-15 *SLF*s	n.d.				
	Type-16 *SLF*s	n.d.				
	Type-17 *SLF*s	n.d.				

Gene conversion events were detected by the GENECONV program[20]. Datasets analyzed were sequence alignments involving each type or some related types of SLFs. Sim*P*, simulated *p* values based on 1,000 permutations. Only statistically significant results ($p < 0.05$) are shown. Begin, first nucleotide of converted region; End, last nucleotide in converted region; Length, length of converted region. [a] "*FBX*s" in this table indicates type 9– and type 10–related, ungrouped *FBX*s: S_{19}-*FBX1*, S_{19}-*FBX2*, S_{0m}-*FBX1* and S_{0m}-*FBX2*. "n.d." indicates that no significant results was detected.

Supplementary Table 12 Summary of the interactions between S-RNase and SLF experimentally demonstrated in *Petunia*

	*SLF*s	S-RNase alleles positively interacted	Number	S-RNase alleles negatively interacted	Number	Number of tested interaction	Proportion
Type 1	S5-SLF1[a]	S9, S17	2	S5, S7, S11, S19	4	6	0.3333
	S7-SLF1[a]	S9, S17, (S22)[b, d]	2	S5, S7, S11, S19	4	6	0.3333
	S9-SLF1[a]	S17	1	S5, S7, S9, S11, S19	5	6	0.1667
	S11-SLF1[a]	S17	1	S5, S7, S9, S11, S19	5	6	0.1667
	*Pi*S2-SLF1[c]	*Pi*S1, *Pi*S3, *Pi*S7, *Pi*S13	4	*Pi*S2, *Pi*S5, *Pi*S11	3	7	0.5714
	*Pi*S3-SLF1[c]	-	0	*Pi*S2, *Pi*S3	2	2	0.0000
Type 2	S5-SLF2[a]	S9, S11	2	S5, S7, S17, S19	4	6	0.3333
	S7-SLF2[a]	S9, S11, S19	3	S5, S7, S17	3	6	0.5000
	S11-SLF2[a]	S9	1	S5, S7, S11, S17, S19	5	6	0.1667
Type 3	S5-SLF3[b]	S7	1	S5, S9, S11, S17, S19	5	6	0.1667
	S7-SLF3[b]	-	0	S5, S7, S9, S11, S17, S19	6	6	0.0000
	S11-SLF3[a]	S7	1	S5, S9, S11, S17, S19	5	6	0.1667
	S11-SLF3B[b]	-	0	S5, S7, S9, S11, S17, S19	6	6	0.0000
Type 4	*Pi*S2-SLF4[c]	*Pi*S5	1	*Pi*S2, *Pi*S3, *Pi*S6a, *Pi*S7, *Pi*S11, *Pi*S12, *Pi*S13	7	8	0.1250
Type 5	*Pi*S2-SLF5[c]	*Pi*S12	1	*Pi*S2, *Pi*S3, *Pi*S5, *Pi*S6a, *Pi*S7, *Pi*S11, *Pi*S13	7	8	0.1250
	*Pi*S3-SLF5[c]	-	0	*Pi*S2, *Pi*S3	2	2	0.0000
Type 6	*Pi*S2-SLF6[c]	-	0	*Pi*S2, *Pi*S3, *Pi*S5, *Pi*S6a, *Pi*S7, *Pi*S11, *Pi*S12, *Pi*S13	8	8	0.0000
	*Pi*S3-SLF6[c]	*Pi*S2	1	*Pi*S3	1	2	0.5000
Type 8	*Pi*S2-SLF8[c]	*Pi*S6a	1	*Pi*S2, *Pi*S3, *Pi*S5, *Pi*S7, *Pi*S11, *Pi*S12, *Pi*S13	7	8	0.1250
Type 9	S7-SLF9A[b]	S19	1	S5, S7, S9, S11, S17	5	6	0.1667
	S11-SLF9[b]	S19	1	S5, S7, S9, S11, S17	5	6	0.1667
Type 13	S7-SLF13[a]	-	0	S5, S7, S9, S11, S17, S19	6	6	0.0000
	total		24		105	129	

[a] Results cited from ref. 9. S_7-SLF13 is renamed from S_7-SLF3. (See caption of Supplementary Fig. 1.)

[b] Results from this work.

[c] Results cited from ref. 23. *Pi* indicates *Petunia inflata*.

[d] Interactuion between S_{22}-RNase and S_7-SLF1 eliminated from statistical analysis, because this results is based on the prediction and not random trial.

Supplementary Table 13 Statistical analyses of interactions between S-RNase and SLF

(**a**) Analysis for Bernouli simulation

	SLFs	S5	S7	S9	S11	S17	S19	PiS1	PiS2	PiS3	PiS5	PiS6	PiS7	PiS12	PiS13
Type 1	S5-SLF1	0	0	1	0	1	0								
	S7-SLF1	0	0	1	0	1	0								
	S9-SLF1	0	0	0	0	1	0								
	S11-SLF1	0	0	0	0	1	0								
	PiS2-SLF1				0			1	0	1	0		1		1
	PiS3-SLF1								0	0					
Type 2	S5-SLF2	0	0	1	1	0	0								
	S7-SLF2	0	0	1	1	0	1								
	S11-SLF2	0	0	1	0	0	0								
Type 3	S5-SLF3	0	1	0	0	0	0								
	S7-SLF3	0	0	0	0	0	0								
	S11-SLF3	0	1	0	0	0	0								
	S11-SLF3B	0	0	0	0	0	0								
Type 4	PiS2-SLF4				0				0	0	1	0	0	0	0
Type 5	PiS2-SLF5				0				0	0	0	0	0	1	0
	PiS3-SLF5								0	0					
Type 6	PiS2-SLF6				0				0	0	0	0	0	0	0
	PiS3-SLF6								1	0					
Type 8	PiS2-SLF8				0				0	0	0	1	0	0	0
Type 9	S7-SLF9	0	0	0	0	0	1								
	S11-SLF9	0	0	0	0	0	1								
Type 13	S7-SLF13	0	0	0	0	0	0								
	Resulting factors for Bernouli simulation														
	Average		0.1860												
	S.D.		0.3907												
	Count		129												
	S.E.		0.0344												
	T-value		1.9787												
	C.I.		0.0681												

(**b**) Analysis for Monte Carlo simulation

	S5	S7	S9	S11	S17	S19	PiS1	PiS2	PiS3	PiS5	PiS6	PiS7	PiS12	PiS13	Postive	Total	Proportion
Type 1	0	0	1	0	1	0	1	0	1	0		1		1	6	12	0.5000
Type 2	0	0	1	1	0	1									3	6	0.5000
Type 3	0	1	0	0	0	0									1	6	0.1667
Type 4				0				0	0	1	0	0	0	0	1	8	0.1250
Type 5				0				0	0	0	0	0	1	0	1	8	0.1250
Type 6				0				1	0	0	0	0	0	0	1	8	0.1250
Type 8				0				0	0	0	1	0	0	0	1	8	0.1250
Type 9	0	0	0	0	0	1									1	6	0.1667
Type 13	0	0	0	0	0	0									0	6	0.0000

Negative and positive interactions between S-RNase and SLF, which were summarized in Supplementary Table 12, were expressed as 0 and 1, respectively.

Supplementary Table 14 Summary of the sequenced reads

Haprotypes	Total number of reads (bp)	Read length (bp)[a]	Mean. read length (bp)	Mean. base quality
S5	590,953	40 - 722	355	32.7
S7	634,016	40 - 1196	288	32.3
S9	550,736	40 - 893	352	32.3
S11	545,880	40 - 764	344	32.2
S17	550,612	40 - 1118	347	32.3
S19	521,109	40 - 987	343	32.1
S0m	101,431	40 - 1118	410	29.2

Total number of reads, read length, mean of read length, and mean of base quality score are shown.

[a] The shortest and the longest lengths.

References list

51. Entani, T. *et al.* Relationship between polyploidy and pollen self-incompatibility phenotype in *Petunia hybrida* Vilm. *Biosci. Biotechnol. Biochem.* **63**, 1882–1888 (1999).
52. Tsukamoto, T. *et al.* Breakdown of self-incompatibility in a natural population of *Petunia axillaris* caused by loss of pollen function. *Plant Physiol.* **131**, 1903–1912 (2003).
53. Gerats, T. & Vandenbussche, M. A model system for comparative research: *Petunia*. *Trends Plant Sci.* **10**, 251–256 (2005).
54. Ai, Y., Kron, E. & Kao, T.-h. *S*-alleles are retained and expressed in a self-compatible cultivar of *Petunia hybrida*. *Mol. Gen. Genet.* **230**, 353–358 (1991).
55. Matsumoto, M. & Nishimura, T. Mersenne Twister: A 623-dimensionally equidistributed uniform pseudorandom number generator. *ACM Trans. Model. Comput. Simul.* **8**, 3–30 (1998).
56. Hua, Z., Meng, X. & Kao, T.-h. Comparison of *Petunia inflata S*-locus F-box protein (Pi SLF) with Pi SLF–like proteins reveals its unique function in S-RNase–based self-incompatibility. *Plant Cell* **19**, 3593–3609 (2007).
57. Twell, D., Yamaguchi, J. & McCormick, S. Pollen-specific gene expression in transgenic plants: coordinate regulation of two different tomato gene promoters during microsporogenesis. *Development* **109**, 705-713 (1990).
58. Kardailsky, I. *et al.* Activation tagging of the floral inducer *FT*. *Science* **286**, 1962-1965 (1999).
59. Nagai, T. *et al.* A variant of yellow fluorescent protein with fast and efficient maturation for cell-biological applications. *Nat Biotechnol.* **20**, 87-90 (2002).
60. Hua, Z. & Kao, T.-h. Identification and characterization of components of a putative petunia *S*-locus F-box-containing E3 ligase complex involved in S-RNase-based self-incompatibility. *Plant Cell* **18**, 2531–2553 (2006).
61. Igic, B. & Kohn, J.R. Evolutionary relationships among self-incompatibility RNases. *Proc. Natl. Acad. Sci. USA* **98**, 13167–133171 (2001).
62. Hillwig, M.S., Liu, X., Liu, G., Thornburg, R.W. & MacIntosh, G.C. *Petunia* nectar proteins have ribonuclease activity. *J. Exp. Bot.* **61**, 2951–2965 (2010).

63. Trubia, M., Sessa, L. & Taramelli, R. Mammalian Rh/T2/S-glycoprotein ribonuclease family genes: cloning of a human member located in a region of chromosome 6 (6q27) frequently deleted in human malignancies. *Genomics* **42**, 342–344 (1997).
64. Ohgi, K. *et al*. Expression of RNase Rh from *Rhizopus niveus* in yeast and characterization of the secreted proteins. *J. Biochem.* **109**, 776–785 (1991).
65. Sun, P. & Kao, T.-h. Self-incompatibility in *Petunia inflata*: the relationship between a self-incompatibility locus F-box protein and its non-self S-RNases. *Plant Cell* **25**, 470–485 (2013).
66. Wheeler, D. & Newbigin, E. Expression of 10 *S*-class *SLF-like* genes in *Nicotiana alata* pollen and its implications for understanding the pollen factor of the *S* locus. *Genetics* **177**, 2171–2180 (2007).
67. Lai, Z. *et al.* An F-box gene linked to the self-incompatibility (*S*) locus of *Antirrhinum* is expressed specifically in pollen and tapetum. *Plant Mol. Biol.* **50**, 29–42 (2002).
68. Zhou, J. *et al*. Structural and transcriptional analysis of *S*-locus F-box genes in *Antirrhinum*. *Sex. Plant Reprod.* **16**, 165–177 (2003).
69. Minamikawa, M. *et al.* Apple *S* locus region represents a large cluster of related, polymorphic and pollen-specific F-box genes. *Plant Mol. Biol.* **74**, 143–154 (2010).
70. Sassa, H. *et al. S locus F-box brothers*: multiple and pollen-specific F-box genes with *S* haplotype-specific polymorphisms in apple and Japanese pear. *Genetics* **175**, 1869–1881 (2007).
71. Okada, K. *et al.* Deletion of a 236 kb region around S_4-*RNase* in a stylar-part mutant S_4^{sm}-haplotype of Japanese pear. *Plant Mol. Biol.* **66**, 389–400 (2008).
72. Okada, K. *et al.* Related polymorphic F-box protein genes between haplotypes clustering in the BAC contig sequences around the *S-RNase* of Japanese pear. *J. Exp. Bot.* **62**, 1887–1892 (2011).
73. Kakui, H. *et al.* Sequence divergence and loss-of-function phenotypes of *S locus F-box brothers* (*SFBB*) genes are consistent with non-self recognition by multiple pollen determinants in self-incompatibility of Japanese pear (*Pyrus pyrifolia*). *Plant J.* **68**, 1028–1038 (2011).
74. Entani, T. *et al.* Comparative analysis of the self-incompatibility (*S*-) locus region

of *Prunus mume*: identification of a pollen-expressed F-box gene with allelic diversity. *Genes Cells* **8**, 203–213 (2003).

75. Ushijima, K. *et al.* The *S* haplotype-specific F-box protein gene, *SFB*, is defective in self-compatible haplotypes of *Prunus avium* and *P. mume*. *Plant J.* **39**, 573–586 (2004).
76. Gu, C., Wu, J., Du, Y.-H., Yang, Y.-N. & Zhang, S.-L. Two different *Prunus SFB* alleles have the same function in the self-incompatibility reaction. *Plant Mol. Biol. Rep.* **31**, 425–434 (2013).
77. Ikeda, K. *et al*. Primary structural features of the *S* haplotype-specific F-box protein, *SFB*, in *Prunus*. *Sex. Plant Reprod.* **16**, 235–243 (2004).
78. Zhang, S.-L., Huang, S.-X., Kitashiba, H. & Nishio, T. Identification of *S*-haplotype-specific F-box in Japanese plum (*Prunus salicina* Lindl.) *Sex. Plant Reprod.* **20**:1–8 (2007).
79. Matsumoto, D., Yamane, H., Abe, K. & Tao, R. Identification of a Skp1-Like protein interacting with SFB, the pollen S determinant of the gametophytic self-incompatibility in *Prunus. Plant Physiol.* **159**, 1252–1262 (2012).
80. Wang, P.-P., Gao, Z.-H., Ni, Z.-J., Zhang, Z. & Cai, B.-H. Self-compatibility in 'Zaohong' Japanese apricot is associated with the loss of function of pollen *S* genes. *Mol. Biol. Rep.* **40**, 6485–6493 (2013).
81. Tsukamoto, T. *et al.* Breakdown of self-incompatibility in a natural population of *Petunia axillaris* caused by a modifier locus that suppresses the expression of an S-RNase gene. *Sex. Plant Reprod.* **15**, 255–263 (2003).
82. Clark, K.R., Okuley, J.J., Collins, P.D. & Sims, T.L. Sequence variability and developmental expression of *S*-alleles in self-incompatible and pseudo-self-compatible petunia. *Plant Cell* **2**, 815–826 (1990).
83. Coleman, C.E. & Kao, T.-h. The flanking regions of two *Petunia inflata S* alleles are heterogeneous and contain repetitive sequences. *Plant Mol. Biol.* **18**, 725–737 (1992).
84. Ai, Y. *et al.* Self-incompatibility in *Petunia inflata*: Isolation and characterization of cDNAs encoding three *S*-allele associated proteins. *Sex. Plant Reprod.* **3**, 130–138 (1990).

85. Sassa, H. & Hirano, H. Identification of a new class of pistil-specific proteins of *Petunia inflata* that is structurally similar to, but functionally distinct from, the self-incompatibility factor HT. *Mol. Genet. Genomics* **275**, 97–104 (2006).
86. Lee, H.S., Singh, A. & Kao, T.-h. RNase X2, a pistil-specific ribonuclease from *Petunia inflata*, shares sequence similarity with solanaceous S proteins. *Plant Mol. Biol.* **20**, 1131–1141 (1992).
87. Saba-el-Leil, M.K., Rivard, S., Morse, D. & Cappadocia, M. The S_{11} and S_{13} selfincompatibility alleles in *Solanum chacoense* Bitt. are remarkably similar. *Plant Mol. Biol.* **24**, 571–583 (1994).
88. Qi, X. *et al.* Genotype-dependent differences in S_{12}-*RNase* expression lead to sporadic self-compatibility. *Plant Mol. Biol.* **45**, 295–305 (2001).
89. Despres, C., Saba-El-Leil, M.K., Rivard, S.R., Morse, D. & Cappadocia, M. Molecular cloning of two *Solanum chacoense S*-alleles and a hypothesis concerning their evolution. *Sexual Plant Reprod.* **7**, 169–176 (1994).
90. O'Brien, M. *et al.* Molecular analysis of the stylar-expressed *Solanum chacoense* small asparagine-rich protein family related to the HT modifier of gametophytic self-incompatibility in *Nicotiana. Plant J.* **32**, 985–996 (2002).
91. Kondo, K. *et al.* Insights into the evolution of self-compatibility in *Lycopersicon* from a study of stylar factors. *Plant J.* **30**, 143–153 (2002).
92. Covey, P.A. *et al.* Multiple features that distinguish unilateral incongruity and self-incompatibility in the tomato clade. *Plant J.* **64**, 367–378 (2010).
93. Royo, J. *et al.* Loss of a histidine residue at the active site of *S*-locus ribonuclease is associated with self-compatibility in *Lycopersicon peruvianum*. *Proc. Natl. Acad. Sci. USA* **91**, 6511–6514 (1994).
94. Chung, I.K. *et al.* The 5′ flanking sequences of two *S* alleles in *Lycopersicon peruvianum* are highly heterogeneous but contain short blocks of homologous sequences. *Plant Cell Physiol.* **36,** 1621–1927 (1995).
95. Chung, I.K. *et al.* Molecular diversity of three *S*-allele cDNAs associated with gametophytic self-incompatibility in *Lycopersicon peruvianum. Plant Mol. Biol.* **26**, 757–762 (1994).
96. Kaufmann, H., Salamini, F. & Thompson, R.D. Sequence variability and gene structure at the self-incompatibility locus of *Solanum tuberosum. Mol. Gen. Genet.* **226**, 457–466 (1991).

97. Anderson, M.A. *et al.* Cloning of cDNA for a stylar glycoprotein associated with expression of self-incompatibility in *Nicotiana alata. Nature* **321**, 38–44 (1986).

98. Anderson, M.A. *et al.* Sequence variability of three alleles of the self-incompatibility gene of *Nicotiana alata. Plant Cell* **1**, 483–491 (1989).

99. Matton, D.P., Mau, S.L., Okamoto, S., Clarke, A.E. & Newbigin, E. The *S*-locus of *Nicotiana alata*: genomic organization and sequence analysis of two *S-RNase* alleles. *Plant Mol. Biol.* **28**, 847–858 (1995).

100. Vissers, A., Dodds, P., Golz, J.F. & Clarke, A.E. Cloning and nucleotide sequence of the S_7*-RNase* from *Nicotiana alata* Link and Otto. *Plant Physiol.* **108**, 427–428 (1995).

101. Murfett, J., Bourque, J.E. & McClure, B.A. Antisense suppression of *S-RNase* expression in *Nicotiana* using RNA polymerase II- and III-transcribed gene constructs. *Plant Mol. Biol.* **29**, 201–212 (1995).

102. Golz, J.F., Clarke, A.E., Newbigin, E. & Anderson, M. A relic *S-RNase* is expressed in the styles of self-compatible *Nicotiana sylvestris. Plant J.* **16**, 591–599 (1998).

103. Xue, Y., Carpenter, R., Dickinson, H.G. & Coen, E.S. Origin of allelic diversity in *Antirrhinum S* locus RNases. *Plant Cell* **8**, 805–814 (1996).

104. Broothaerts, W., Janssens, G.A., Proost, P. & Broekaert, W.F. cDNA cloning and molecular analysis of two self-incompatibility alleles from apple. *Plant Mol. Biol.* **27**, 499–511 (1995).

105. Ishimizu, T., Shinkawa, T., Sakiyama, F. & Norioka, S. Primary structural features of rosaceous S-RNases associated with gametophytic self-incompatibility. *Plant Mol. Biol.* **37**, 931–941 (1998).

106. Ushijima, K., Sassa, H. & Hirano, H. Characterization of the flanking regions of the *S-RNase* genes of Japanese pear (*Pyrus serotina*) and apple (*Malus* × *domestica*). *Gene* **211**, 159–167 (1998).

107. Castillo, C. *et al.* Reconsideration of *S*-genotypes assignments, and discovery of a new allele based on *S-RNase* PCR-RFLPs in Japanese pear cultivars. *Breed. Sci.* **51**, 5–11 (2001).

108. Castillo, C. *et al.* *S-RNase* based PCR-RFLP system for *S*-genotype assignment in Japanese pear. *Acta Hortic.* **587**, 449–458 (2002).

109. Romero, C. *et al*. Analysis of the *S*-locus structure in *Prunus armeniaca* L. Identification of *S*-haplotype specific *S-RNase* and *F-box* genes. *Plant Mol. Biol.* **56**, 145–157 (2004).
110. Sonneveld, T., Robbins, T.P., Boskovic, R. & Tobutt, K.R. Cloning of sex cherry self-incompatibility alleles and development of allele-specific PCR detection. *Theor. Appl. Genet.* **102**, 1046–1055 (2001).
111. Tao, R., Yamane, H. & Sugiura, A. Cloning and nucleotide sequences of cDNAs encoding S_1- and S_4-*RNase* from sweet cherry (*Prunus avium* L.). *Plant Physiol.* **120**, 1207 (1999).
112. Tamura, M. *et al*. Identification of self-incompatibility genotypes of almond by allele-specific PCR analysis. *Theor. Appl. Genet.* **101**, 344–349 (2000).
113. Ushijima, K. *et al*. Cloning and characterization of cDNAs encoding *S-RNase*s from almond (*Prunus dulcis*): primary structural features and sequence diversity of the *S-RNase*s in Rosaceae. *Mol. Gen. Genet.* **260**, 261–268 (1998).
114. Tao, R., Habu, T., Yamane, H. & Sugiura, A. Characterization and cDNA cloning for S_f-*RNase*, a molecular marker for self-compatibility, in Japanese apricot (*Prunus mume*). *J. Jpn. Soc. Hort. Sci.* **71**, 595–600 (2002).
115. Beppu, K. *et al*. Diversity of *S-RNase* genes and *S*-haplotypes in Japanese plum (*Prunus salicina* Lindl.). *J. Hortic. Sci. Biotechnol.* **77**, 658–664 (2002).
116. Tao, R. *et al*. Self-compatible peach (*Prunus persica*) has mutant versions of the *S* haplotypes found in self-incompatible *Prunus* species. *Plant Mol. Biol.* **63**, 109–123 (2007).
117. Dodds, P.N., Clarke, A.E. & Newbigin, E. Molecular characterisation of an S-like RNase of *Nicotiana alata* that is induced by phosphate starvation. *Plant Mol. Biol.* **31**, 227–238 (1996).
118. Hayashi, T. *et al.* Genomic cloning of ribonucleases in *Nicotiana glutinosa* leaves, as induced in response to wounding or to TMV-infection, and characterization of their promoters. *Biosci. Biotechnol. Biochem.* **67**, 2574–2583 (2003).
119. Kurata, N., Kariu, T., Kawano, S. & Kimura, M. Molecular cloning of cDNAs encoding ribonuclease-related proteinsin *Nicotiana glutinosa* leaves, as induced in response to woundingor to TMV-infection. *Biosci. Biotechnol. Biochem*. **66**, 391–397 (2002).

120. Ohno, H. & Ehara, Y. Expression of ribonuclease gene in mechanically injured or virus-inoculated *Nicotiana tabacum* leaves. *Tohoku J. Agric. Res.* **55**, 99–109 (2005).

121. Kock, M., Loffler, A., Abel, S. & Glund, K. cDNA structure and regulatory properties of a family of starvation-induced ribonucleases from tomato. *Plant Mol. Biol.* **27**, 477–485 (1995).

122. Norioka, N. *et al*. Molecular cloning and nucleotide sequences of cDNAs encoding *S*-allele specific stylar RNases in a self-incompatible cultivar and its self-compatible mutant of Japanese pear, *Pyrus pyrifolia* Nakai. *J. Biochem.* **120**, 335–345 (1996).

123. Van Nerum, I., Certal, A.C., Oliveira, M.M., Keulemans, J. & Broothaerts, W. *PD1*, an *S-like RNase* gene from a self-incompatible cultivar of almond. *Plant Cell Rep.* **19**, 1108–1114 (2000).

124. Ma, R.C. & Oliveira, M.M. The *RNase PD2* gene of almond (*Prunus dulcis*) represents anevolutionarily distinct class of *S-like RNase* genes. *Mol. Gen. Genet.* **263**, 925–933 (2000).

125. MacIntosh, G.C., Hillwig, M.S., Meyer, A. & Flagel, L. RNase T2 genes from rice and the evolution of secretory ribonucleases in plants. *Mol. Genet. Genomics* **283**, 381–396 (2010).

126. Kothke, S. & Kock, M. The *Solanum lycopersicum RNaseLER* is a class II enzyme of the RNase T2 family and shows preferential expression in guard cells. *J. Plant Physiol.* **168**, 840–847 (2011).

127. Liang, L., Lai, Z., Ma, W., Zhang, Y. & Xue,Y. *AhSL28*, a senescence- and phosphate starvation-induced *S-like RNase* gene in *Antirrhinum*. *Biochim. Biophys. Acta* **1579**, 64–71 (2002).