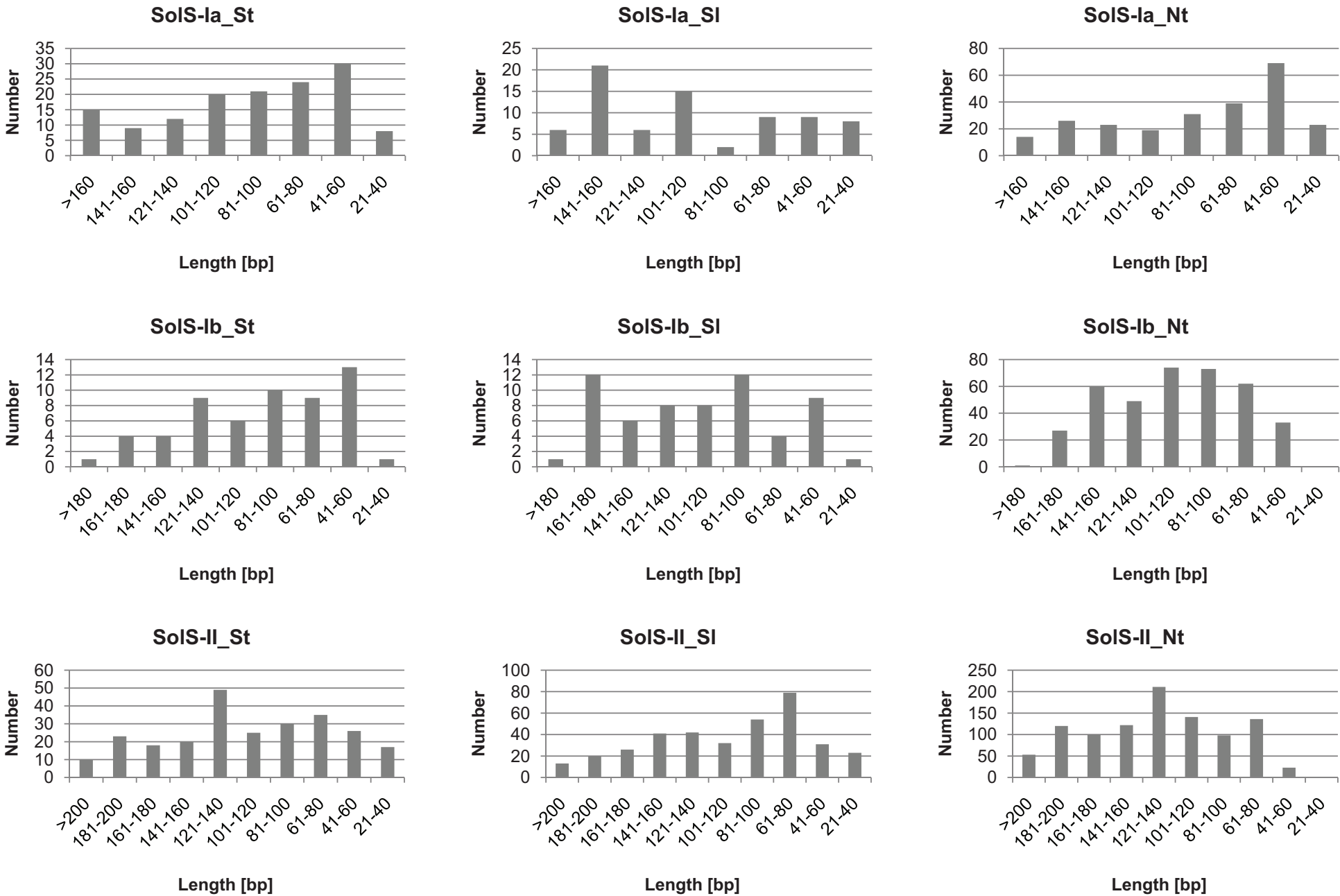
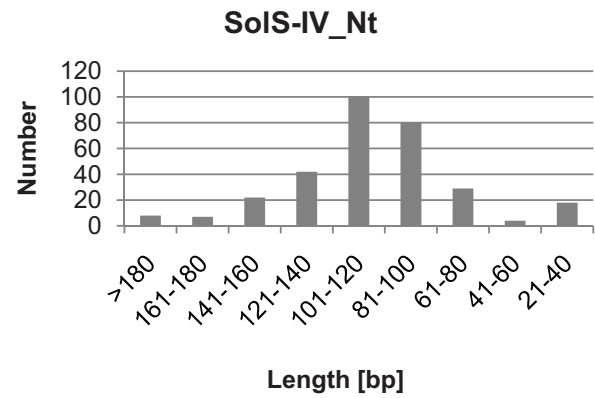
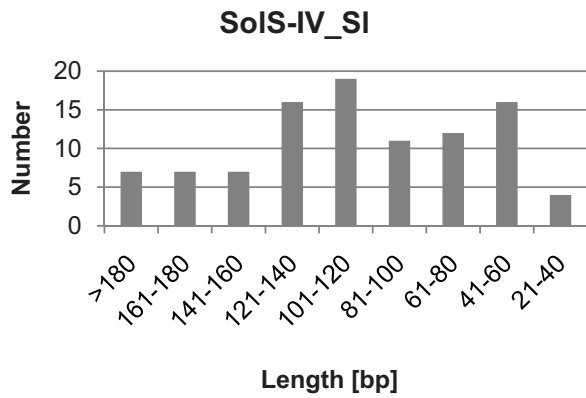
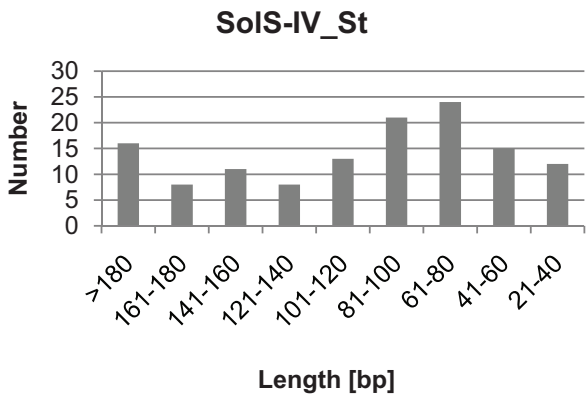
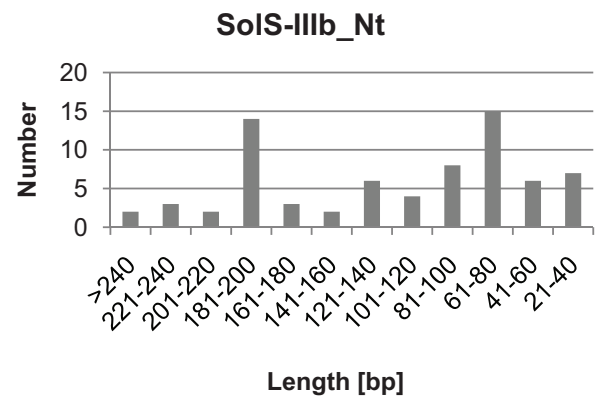
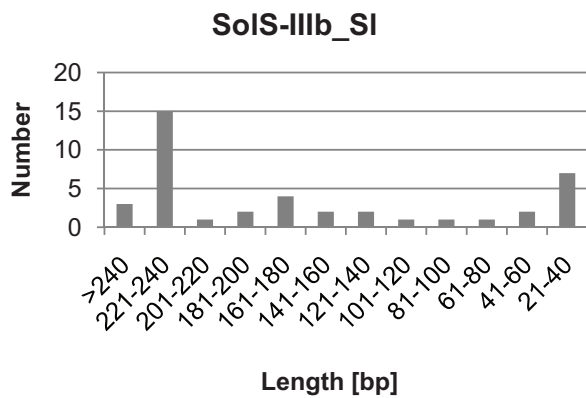
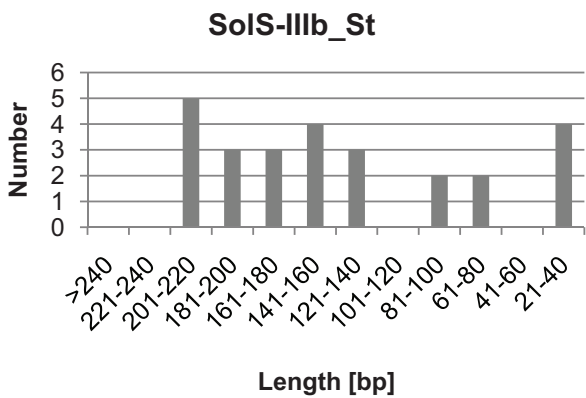
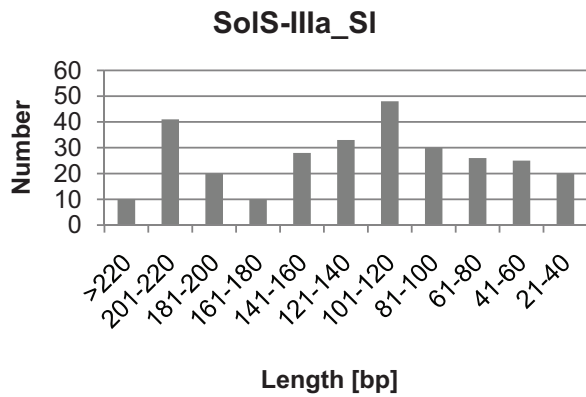
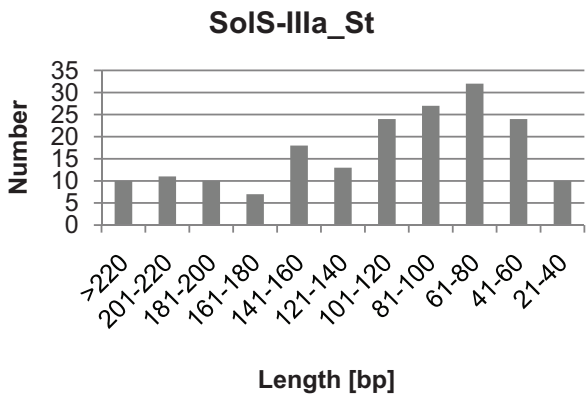
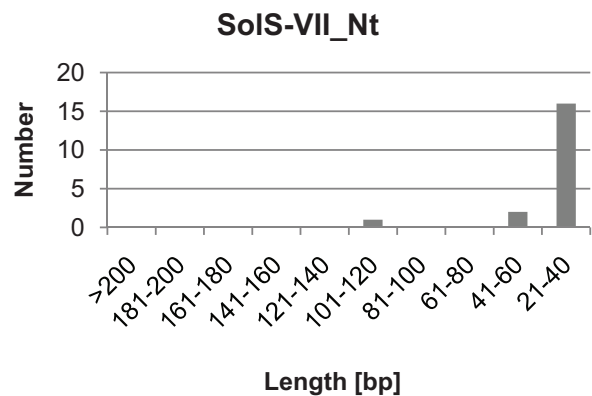
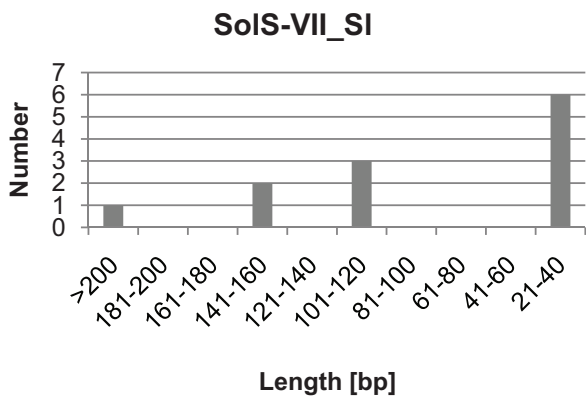
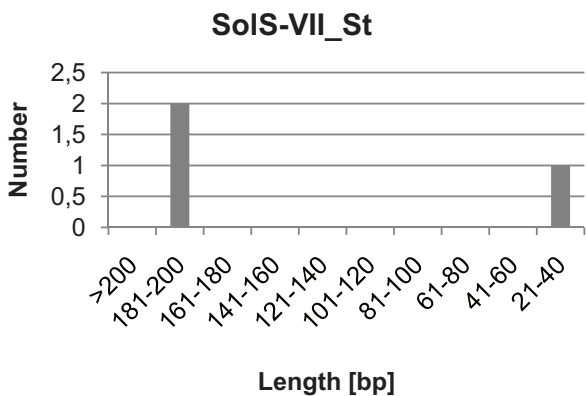
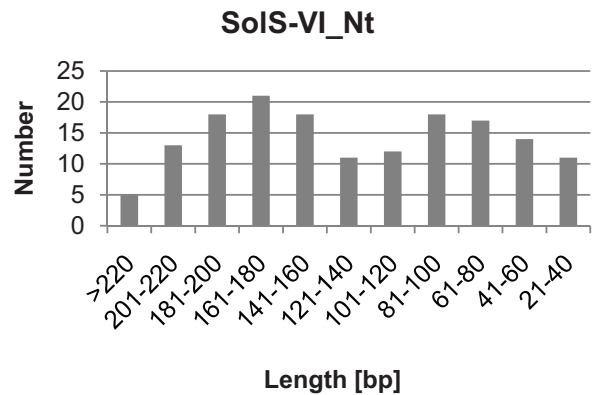
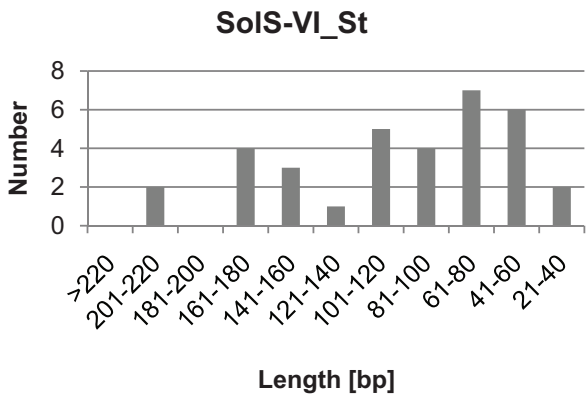
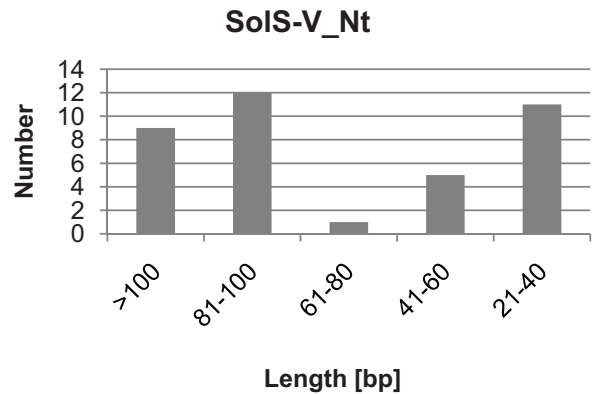
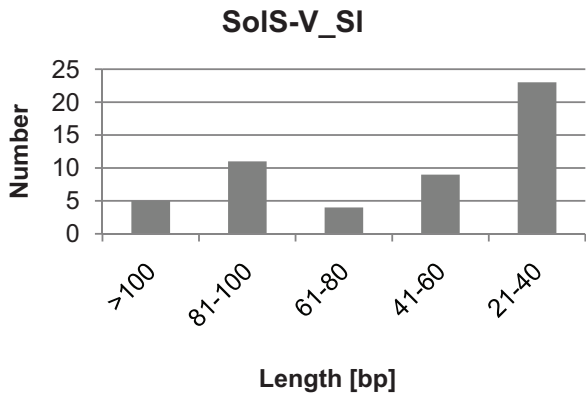
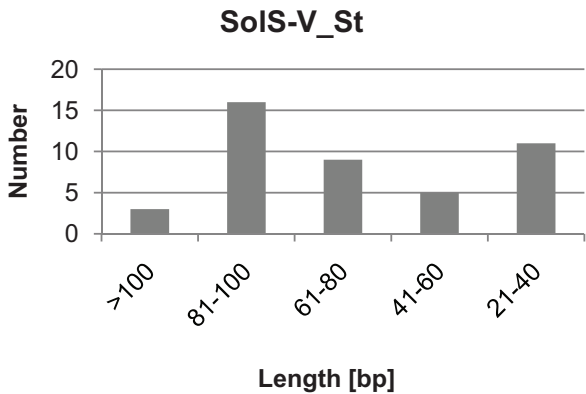
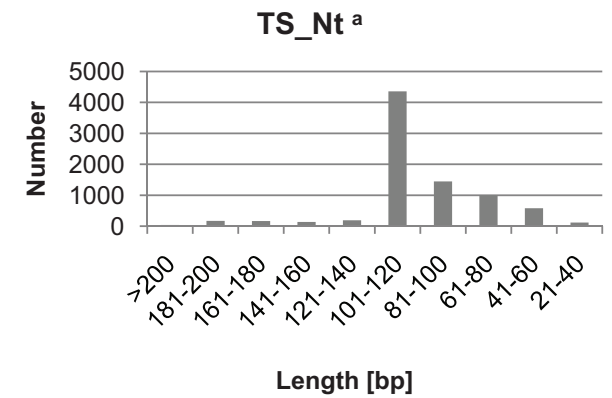
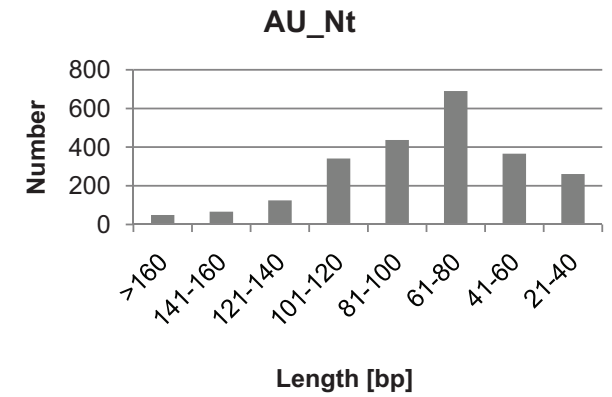
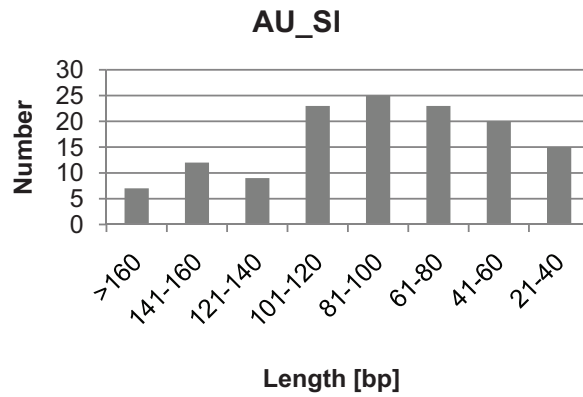
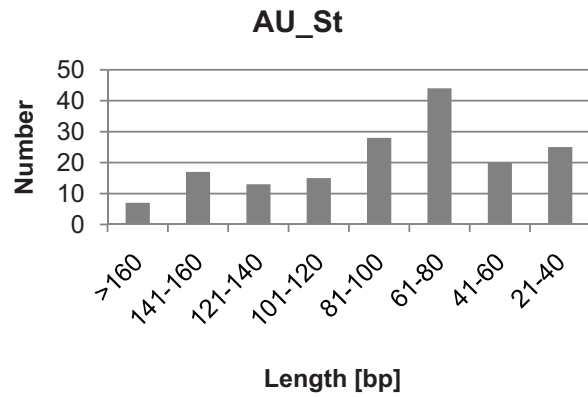


Supplemental Figure 1. Frequency and length of 5' truncated SINES (SoIS, AU, TS) detected in the data sets of potato, tomato and tobacco.



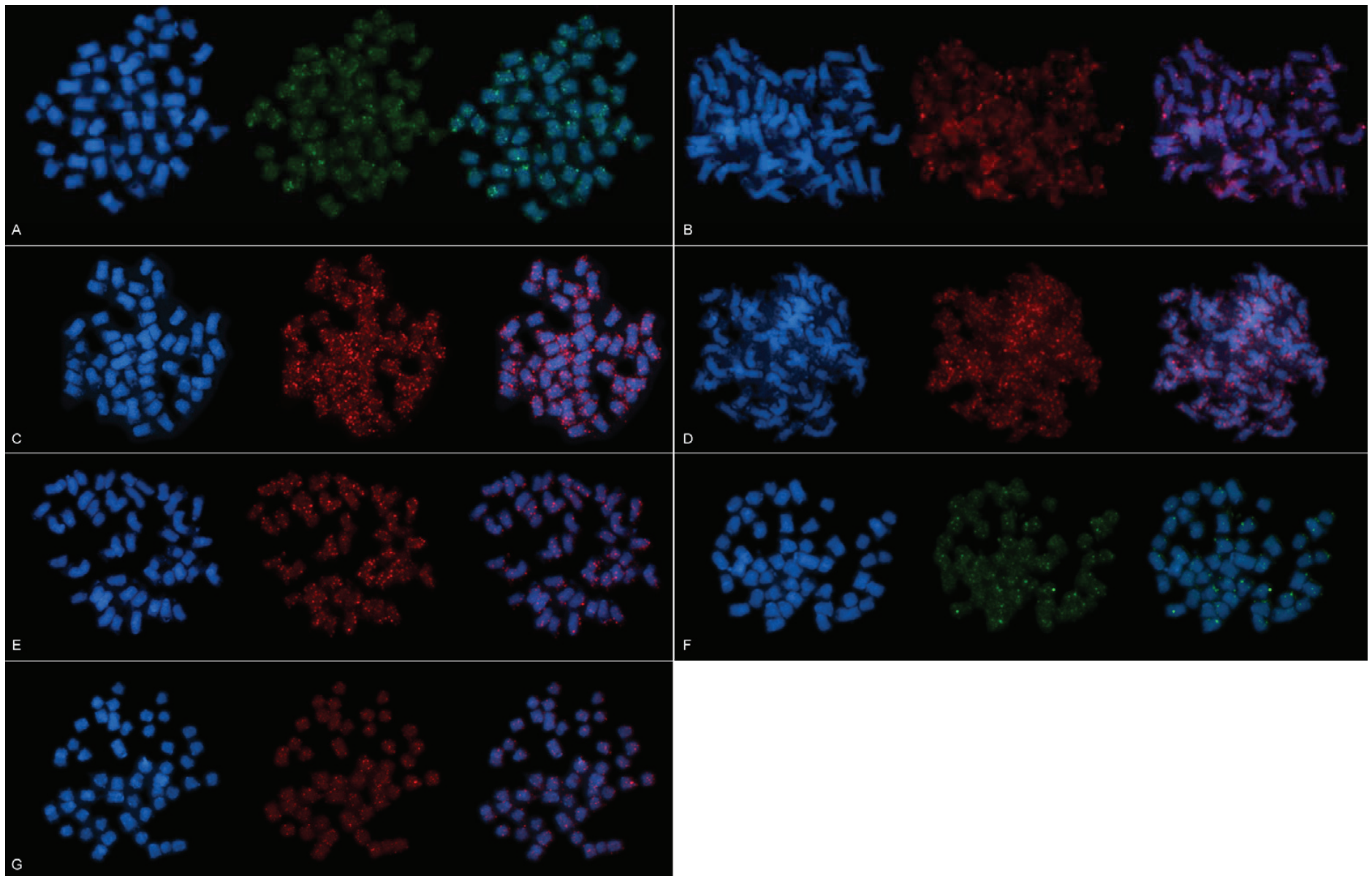






^a The 3' end of TS (102 bp upstream of the poly(GTT) tail) is highly similar to the 3' end of the SolRTE-I family (see Figure 6), and the differentiation between both retroelements is not possible. The detection of the very high number of 5' truncated copies which are shorter than 120 bp is most likely due to highly abundant SolRTE-I LINE sequences in tobacco.

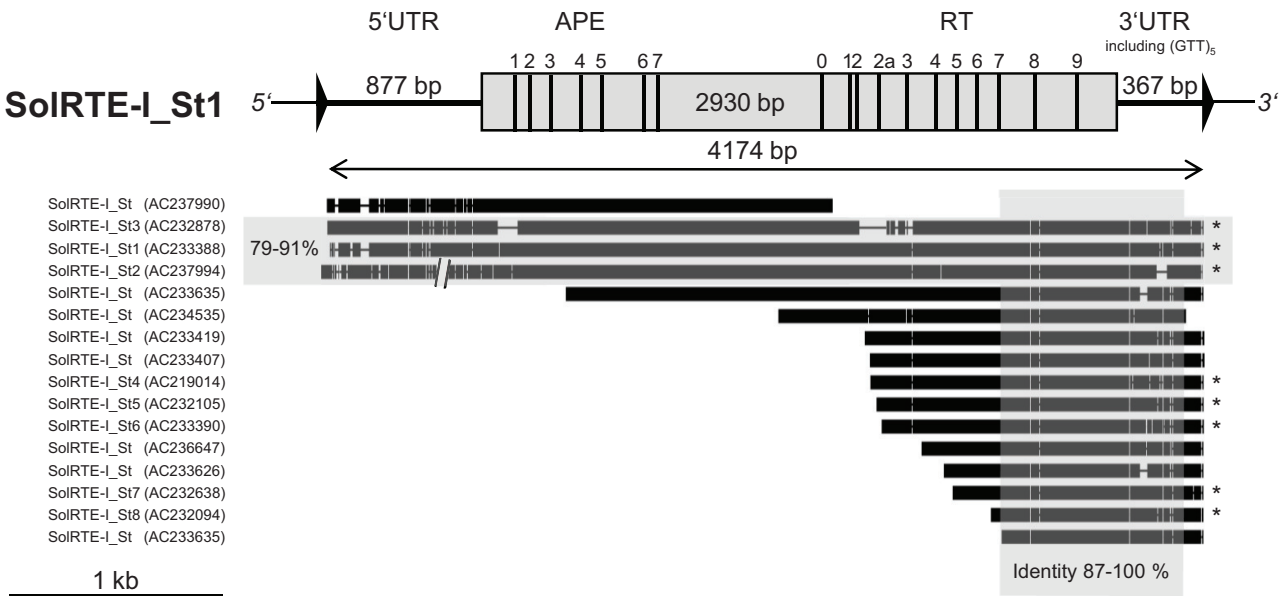
Supplemental Figure 2. Physical mapping of SolS SINE families by FISH.



SINEs of SolS-Ia (A), SolS-II (B), SolS-IIIa (C), SolS-IV (D), SolS-V (E), SolS-VI (F) and SolS-VII (G) were localized on potato metaphase chromosomes. Red and green signals are sites of hybridization while blue fluorescence shows DAPI stained DNA.

Supplemental Figure 3. Structure and amino acid alignments of SolRTE-I sequences.

A



The structure of the potato SolRTE-I_St1 LINE (above, drawn to scale). The grey rectangle represents the single ORF. UTR, APE and RT refer to the untranslated regions, apurinic/apyrimidinic endonuclease and reverse transcriptase, respectively. Black vertical lines and numbers show positions of conserved APE and RT domains. Triangles indicate target site duplications (TSD).

The schematic alignment of potato SolRTE-I sequences are arranged to the structure of SolRTE-I_St1 (below). Thick black bars indicate similar sequences, thin lines parts without similarity. Identity values are given for SolRTE-I_St1, St2 and St3 (highlighted as horizontal grey rectangle) and for SolRTE-I 3' end regions (highlighted as vertical grey rectangle). Asterisks indicate LINEs delimited by TSDs. SolRTE-I_St2 is interrupted in the 5' UTR by a L1-like LINE which is flanked by TSDs.

B

1 2 3

SolRTE-I_St1_ (AC233388) LRVGPNIGSLTGK-SLELVKILKKK-INIACVPTRWVGSKARDVDGFKLWYSGG---SRDRNGVGIIVGGDLREQVVEVRINDELIM
 SolRTE-I_St2_ (AC237994) LRVGSWNIGSLTGK-SLELVKILKKK-INIACVPTRWVGSKARDVDGFKLWYSGG---SRDRNGVGIIVGGDLREQVVEVRINDELIM
 SolRTE-I_St3_ (AC232878) LRVGSWNIGSLTGK-SLELVKILKKK-INIACVPTRWVGSKAREVDGFKLWYSGG---SRDRNGVGIIVGGDLREQVVEVRINDELIM
 SolRTE-I_St_ (AC237990) LRVGSWNIGSLTGK-SLELVKILKKK-INIACVPTRWVGSKARDVDGFKLWYSGG---SRDRNGVGIIVGGDLREQVVEVRINDELIM
 YCIGTNVVRMNPFG-KIDVVKQEMDINIDILGISLKWITGMGLNSDDHYIYCCQQ--SLRRNGVGIIVKKVQNAIIGCNLKNMDSMI
 RTE1_ (AF025462) YRVCTFNCRSSDDRRLAELLEETREIQDFVIGLCETKRAAEHLIHHDGTGVLEKRNESVSGSGVFIIVRSTLLPKLIEVFLSHSIRIG

4 5

SolRTE-I_St1_ (AC233388) LKILVV-GGGTSLVISAYAPQVGLGEEAKKLFYEDLDEVVRGIPSTEKIVIGGDFNGHIGATSNGFNDVGGGFGGERNGGCTSLDRAK
 SIKLVI-GGCTLSVISAYAPQVGLGEEAKKLFYEDLDEVVRGIPSTEKIVIGGDFNGHIGATSNGFDDIHGGCGFGERNGGCTSLDRAK
 SolRTE-I_St2_ (AC237994) LKILVV-GGCTLSVISAYAPQVGLGEEAKKLFYEDLDEVVRGIPSTEKIVIGGDFNGHIGATSNGFDDIHGGCGFGERNGGCTSLDRAK
 TIKIVI-GGCTLSVISAYAPQVGLGEEAKKLFYEDLDEVVRGIPSTEKIVIGGDFNGHIGATSSGGCDVHGGGFGGERNGGCTSLDRAK
 SolRTE-I_St3_ (AC232878) LKILVV-GGCTLSVISAYAPQVGLGEEAKKLFYEDLDEVVRGIPSTEKIVIGGDFNGHIGATSNGFDDVHGGGFGGERNGGCTSLDRAK
 SLRFQG-KPFNLTIVIQVAPTPYAEAGEVYRFYEDLQHLLEITPKIDVLFHIGGNNAKVGSGE--IPGITGFRGLMCGEACRRILDSCH
 BCNT_ (AB191483) LLTFKVSRRKFNCTVIVQVAPTADSDLEICFVDSVEDVFECCRKYKLVIG--ENARMSCRON-NERYIGPHAMEPRNDTSELATACE
 RTE1_ (AF025462)

6 7

SolRTE-I_St1_ (AC233388) AFELVIANSGEPKKNHLMVFRSS--VAKTQIDYLLLRKGDRLVKDCKVISENLTTOHKLIVMDLEIK
 SolRTE-I_St2_ (AC237994) AFELVIANSGEPKKNHLMVFRSS--VAKTQIDYLLLRKGDRLVKDCKVISENLTTOHKLIVMDLEIK
 SolRTE-I_St3_ (AC232878) AFELVIANSGEPKKNHLMVFRSS--IAKTQIDYLLLRKGDRLVKDCKVISENLTTOHKLIVMDLEIK
 SolRTE-I_St_ (AC237990) AFELVIANSGEPKKNHLMVFRSS--VAKTQIDYLLLRKGDRLVKDCKVISENLTTOHKLIVMDLEIK
 HNRLVIANITLQPPSRRLYNTSPDGRFRDQIYICQRWRSSVQSAKTRSGADCGSDHLLIAKFRLK
 BCNT_ (AB191483) TNRWHTNSMKGKPMHKRWIVSPDGNHRRHDIHILANG---KFTITTTVLSTFTNGSDHLLIRCNLHFN
 RTE1_ (AF025462)

C

0 1 2

SolRTEI_St1_ (AC233388) RCFRIEIVIRAI SRMSRGRAGGDEPVDVFKSTDKAGLEWLTGLFN-VIFKTAKMPDEMRWSTMVPLYNAGDIQNCNRYRGKILSHT
 SolRTEI_St2_ (AC237994) RCFRIEIVIRAI SRMSRGRAGGDEPVDVFKSTDKAGLEWLTGLFN-VIFKTTKMSDEMRWSTMVPLYNAGDIQNCNRYRGKILSHT
 SolRTE-I_St_ (AC233635) RCFRIEIVIRAI SRMSRGRAGGDEPVDVFKSTDKAGLEWLTGLFN-VIFKTTKMPDEMRWSTMVPLYNAGDIQNCNRYRGKILSHT
 SolRTE-I_St_ (AC234535) RCFRIEIVIRAI SRMSRGRAGGDEPVDVFKSTDKAGLEWLTGLFN-VILKTAKMPDEMRWSTMVPLYNAGDIQNCNRYRGKILSHT
 RTE1_ (AF025462) PPELPBEIRHVLRSFPNGKAAADKSADEFKSCNDNVLDITDREN-RYLHSRNVKPKTKSTTLTIFRK--GRENLENRYRPHCLPVL
 JAM1_ (Z86117) PAPTMCEVKDAIQQLKNNRAGGKSGAELIRMGPDRLAACLHRSDSQSGKSEQLPBEMKQGVICETPKK--GKLECNRYRPHCLPVLNAA

2a 3

SolRTEI_St1_ (AC233388) MLIWERVVMVRREVSISE--NCGGMPGRSTTEATHLMRRLVEKYRERKRDHL-MVIFIDLEKAMDVPRNVLRCLKAGIPIPIYIRA
 SolRTEI_St2_ (AC237994) MLIWETVVEIVRRGVSISE--NCGGMPGP-STTEATHLMRRLVEKYRERKRDHL-MVIFIDLEKAMDVPRNVLRCLKAGIPIPIYIRA
 SolRTE-I_St_ (AC233635) MLIWERVVMVRREVSISE--NCGGMPGRSTTEATHLMRRLVEKYRERKRDHL-MVIFIDLEKAMDVPRNVLRCLKAGIPIPIYIRA
 SolRTE-I_St_ (AC234535) MLIWERVVMVRREVSISE--NCGGMPGRSTTEATHLMRRLVEKYRERKRDHL-MVIFIDLEKAMDVPRNVLRCLKAGIPIPIYIRA
 YRVFTKCLLNMRSLDEAOPVEAGERRSFIDHLSLQRLLEVGRBYQIPIT-LVIFIDFKKAFDSVHQAIWKSLEQAGADGAYIDL
 RTE1_ (AF025462) YRVLSQILFRLLPIANEFVGSYNTSIDGRSITMYVFSVRQILOKCRBYQVPT-HLIFIDFKKAFDSIDRIELWKIMDENSTFGKLTSL
 JAM1_ (Z86117)

4 5

SolRTEI_St1_ (AC233388) IKDMYGGAKTRVRTVGGDSEHFPVEMGLHQSGLSPFLFALVMDELTR-----SIQERVPWCMLFADDIVLIDET
 SolRTEI_St2_ (AC237994) IKDMYGGAKTR-RTVGGDSEHFPVEMGLHQSGLSPFLFALVMDELTR-----SIQEKVPWCMLFADDIVLIDET
 SolRTE-I_St_ (AC233635) IKDMYGGAKIRVRTVGGDSEHFPVEMGLHQSGLSPFLFALVMDELTR-----SIQEKVPWCMLFADDIVLIDER
 SolRTE-I_St_ (AC234535) IKDMYGGAKTRVRTVGGDSEHFPVEMGLHQSGLSPFLFALVIDELTQ-----SIQEKVPWCMLFADDIVLIDET
 RTE1_ (AF025462) LKCYKNCITNFTPFHR-PVAVPVTKSVRQGDPISENLFSACLEHVFRKLWIELKGEAEDYDIPGMVRNGRLNLTNLFADDIVLIDANH
 JAM1_ (Z86117) ITRATMDGVQNCVKISSEHSSESRRGRLRQDGLSCMSCGEPVLNSRG-----TIFTRSVQFVSEFADMDVIGEN

6 7

SolRTEI_St1_ (AC233388) RDRADARLEVWRQTLSEKCFKLSRTKDEYLCK-FSDALDEADGVRLATQIIPKKEFKYIGFVIQSGSDIDDDVTHRIGVAMMKWRLA
 SolRTEI_St2_ (AC237994) RDRVNARLEVWRQTLSEKCFKLSRTKDEYLCK-FSDALDEADMEVKLATQIIPKKEFKYIGSVIQSGSDIDDDVTHRIGVAMMKWRLA
 SolRTE-I_St_ (AC233635) RDRVNARLEVWRQTLSEKCFKLSRTKDEYLCK-FSDVVDDETDEVRLLAQIIPKKEFKYINAVIQSGSDIDDDVTHRIGVAMMKWRLV
 SolRTE-I_St_ (AC234535) RDRVNARLEVWRQTLSEKCFKLSRTKDEYLCK-FSDALDEADVEVRLATQIIPKKEFKYIGSVIQSGSDIDDDVTHRIGVAMMKWRLA
 PNIAKMLQELVQKCEVGLINTGKKVLRNR-EADPS-KVYFGSPSPITQLDVDEYIYLRQINQANILMPEIHRARRAANAFAFNGI
 RTE1_ (AF025462) LKQNSDLFTRLKREATRVGLMNVNSKKKMLVGGTECDRLRGSSVITDGTTFEVDEEVYLSGLLTADNNVSREIRRSITSGSRAYYGL
 JAM1_ (Z86117)

8

SolRTEI_St1_ (AC233388) SGVLCDKKIPRLKGFYRVVVRBALLYGACQWPVKNSHVQKMHVAEMRMLWMCSHTRSDKIRNEVIREKVGVASVVDK----LREARL
 SolRTEI_St2_ (AC237994) SRVLCDKKIPRLKGFYRVVVRBALLYGACQWPVKNSHVQKMHVAEMRMLWMCSHTRSDKIRNEVIREKVGVASVVDK----LREARL
 SolRTE-I_St_ (AC233635) SGVLCDKKIPRLKGFYRVVVRBALLYGACQWPVKNAHVQKMHVAEMRMLWMCSHTRSDMIRNEVIREKVGVAIVVDK----LREARL
 SolRTE-I_St_ (AC234535) SVVLCDKKIPRLKGFYRVVVRBALLYGACQWPVKNSHVQKMHVAEMRMLWMCSHTRSDKMRNEVIREKVGVASVVDK----LREARL
 RTE1_ (AF025462) KN-TTSDITDKKIRANLFDISIVLPALTYSSAWFTFKALSERVRITHASLEIRLVITLTQQRERDLHRRDITRTMSLRDPLNFVKRKL
 JAM1_ (Z86117) QKKIRSRKIQRTKCTMKTLIRLEVVLVSHBATMLEEDLQALGFERRVLTIFESVQENGWRRRNHLEALQLYGEPIS-IVKVLKGR

9

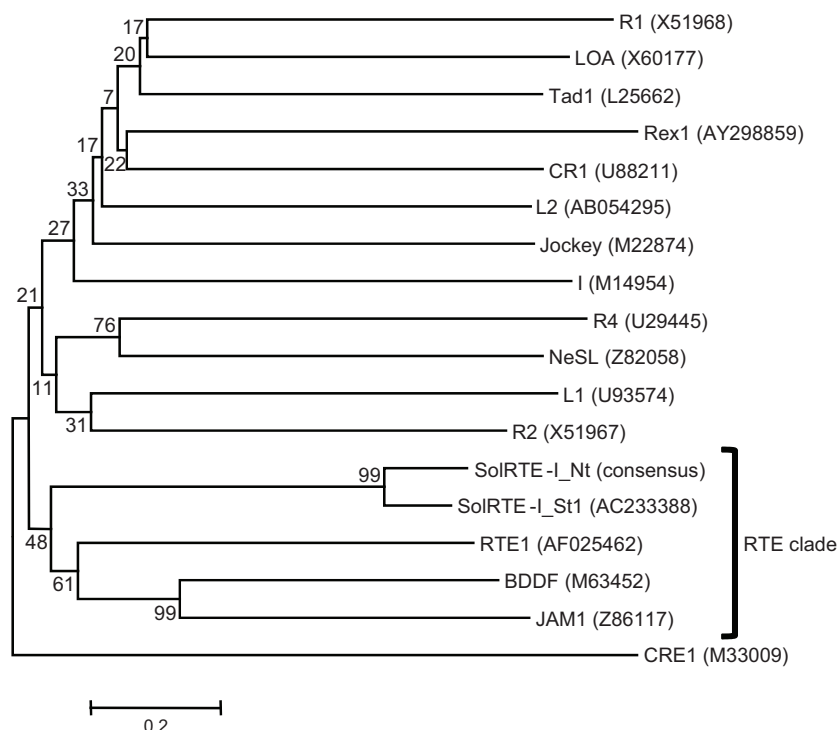
SolRTEI_St1_ (AC233388) RRGSHYRRCRCA--
 SolRTEI_St2_ (AC237994) RRGSHYRRCRCT--
 SolRTE-I_St_ (AC233635) RRGSHYRRCRSA--
 SolRTE-I_St_ (AC234535) RRGSHYRRCRCA--
 RTE1_ (AF025462) RRGSHYARRKDGR
 JAM1_ (Z86117) RRGSHYARRMPDNN

The amino acid alignments show the apurinic/apyrimidinic endonuclease (B) and reverse transcriptase (C) region of SolRTE-I LINES compared to LINES of the RTE clade. Characteristic domains of the APE and RT are indicated according to Malik and Eickbush (1998) and Malik et al. (1999), respectively. Black boxes designate residues conserved in all and gray boxes designate residues conserved in four of six sequences depicted.

References

- Malik, H.S. and Eickbush, T.H.** (1998). The RTE class of non-LTR retrotransposons is widely distributed in animals and is the origin of many SINEs. *Mol. Biol. Evol.* **15**: 1123-1134.
- Malik, H.S., Burke, W.D. and Eickbush, T.H.** (1999). The age and evolution of non-LTR retrotransposable elements. *Mol. Biol. Evol.* **16**: 793-805.

Supplemental Figure 4. Assignment of the SolRTE-I family to the RTE clade of LINEs.



The dendrogram shows the grouping of potato and tobacco SolRTE-I to RTE1, BDDF and JAM1 of the RTE clade (Szemraj et al., 1995; Youngman et al., 1996; Warren et al., 1997; Malik and Eickbush, 1998). The Neighbor-Joining tree (substitution model: Poisson, bootstrap values: 1000 replicates) was constructed using the computational translated reverse transcriptase domains 1-7 (see Supplemental Figure 3) assigned to 14 different LINE clades. The following clades were included: R1 (R1, *Drosophila melanogaster*), LOA (LOA, *Drosophila silvestris*), Tad1 (Tad1, *Neurospora crassa*), Rex1 (Rex1, *Xiphophorus maculatus*), CR1 (CR1, *Gallus gallus*), L2 (L2, *Oryzias latipes*), Jockey (Jockey, *D. melanogaster*), I (I, *D. melanogaster*), R4 (R4, *Ascaris lumbricoides*), NeSL (NeSL, *Caenorhabditis elegans*), L1 (L1, *Homo sapiens*), R2 (R2, *D. melanogaster*), RTE (SolRTE-I_Nt, *Nicotiana tabacum*; SolRTE-I_St1, *Solanum tuberosum*; RTE1, *C. elegans*; BDDF, *Bos taurus*; JAM1, *Aedes aegypti*), CRE1 (CRE1, *Crithidia fasciculata*). EMBL accessions are indicated. SolRTE-I_Nt is a consensus of 1640 tobacco sequences (see Supplemental Data Set 6).

References

- Szemraj, J., Plucienniczak, G., Jaworski, J. and Plucienniczak, A.** (1995). Bovine Alu-like sequences mediate transposition of a new site-specific retroelement. *Gene* **152**: 261-264.
- Youngman, S., van Luenen, H.G. and Plasterk, R.H.** (1996). Rte-1, a retrotransposon-like element in *Caenorhabditis elegans*. *FEBS Lett.* **380**: 1-7.
- Warren, A.M., Hughes, M.A. and Crampton, J.M.** (1997). Zebedee: a novel copia-Ty1 family of transposable elements in the genome of the medically important mosquito *Aedes aegypti*. *Mol. Gen. Genet.* **254**: 505-513.
- Malik, H.S. and Eickbush, T.H.** (1998). The RTE class of non-LTR retrotransposons is widely distributed in animals and is the origin of many SINEs. *Mol. Biol. Evol.* **15**: 1123-1134.

Supplemental Table 1. Number of SINEs in large sequence accessions of potato.

Sequence accession number (EMBL)	Length [bp]	SINE families (SoIS, AU)										Number of SINEs per sequence accession
		Ia	Ib	II	IIIa	IIIb	IV	V	VI	VII	AU	
AC233633	142953	2	1	2	1		2				1	9
AC233628	102676	1	2	3			2				1	9
AC236712	139508	2		1	2		1	1			2	9
AC233609	141570	2		2	1		2				1	8
EF514212	417445	2			2			2			1	7
AC233636	147623				1	1	1	1	1		2	7
AC213585	117020	3	1	2			1					7
AC206931	163599	1		2			1	2			1	7
AC231998	176590	1	1	2	2		1					7
AC233605	141262	2		2	1			1			1	7
AC215773	160546	1	2	1	1		1	1				7
AC233407	165359		1	1	1			1	1		1	6
AC235660	174813	1	2	1		1		1				6
AC235976	171039	1	1	1			1	1			1	6
AC235978	165818	1	1	2	1			1				6
AC233353	119301		1	1			2	1			1	6
AC233616	136335	1		1	2			1			1	6
AC206935	136627		1		1	1	1	1			1	6
AC233618	144807	1		3			1				1	6
AC232032	111567	1	1	2			1	1				6
AC232055	160074	1		3			1				1	6
AC234539	141772	1		1	2		1				1	6
AC209519	131657	1	1	1	1		1	1				6
AC233489	139205	1		2	1				1		1	6
AC231673	116204	1		2	1						2	6
Total number		28	16	38	21	3	21	17	3	0	21	

Supplemental Table 2. Number of SINEs in large sequence accessions of tomato.

Sequence accession number (EMBL)	Length [bp]	SINE families (SolS, AU)										Number of SINEs per sequence accession
		Ia	Ib	II	IIIa	IIIb	IV	V	VI	VII	AU	
AC215403	123184	2		1	2		1	1				7
AC215362	134651	1		1	2		1	1				6
AC232636	93617	1	1	2	1						1	6
AC212274	93265	1	1	1	2						1	6
AC217334	150975		1	2		1	1				1	6
EF647600	88227		2	2							2	6
AC216365	166562	1			2			1			2	6
AC238478	138572	1	1	1	2							5
AC212304	129165	3		2								5
EU180575	140448	1			1		1	1			1	5
AC211034	168476		1	2	1			1				5
AC234405	130648	1	1		1		1	1				5
AP010939	147816			2	1		1				1	5
AC209584	138883			1			1	1			2	5
AC211071	148371		1	1	1		1				1	5
EF647602	132378	1		1	1	1		1				5
AC205681	109367	2					1	2				5
AC234402	136545		2	1			1				1	5
EU124739	117727	1	1		1		1	1				5
AC196876	145193	1		1	1		1				1	5
AC216401	148650	2	1	1	1							5
AP009398	82278	1		1	2		1					5
AP009520	142029		1	2	2							5
AC212623	97158		1	1	1					1	1	5
AC215426	159752		1	1	1			1		1		5
Total number		20	16	27	26	2	13	12	0	2	15	

Supplemental Table 3. Number of SINEs (SoIS, AU, TS) per sequence accession detected in the sequence data sets of potato, tomato and tobacco.

Total number of SINEs per sequence accession	Number of sequence accessions		
	potato	tomato	tobacco
9	3		
8	1		
7	7	1	
6	17	6	
5	30	21	
4	52	53	
3	64	133	
2	115	263	149
1	1633	1604	9792

Supplemental Table 4. Genome data sets analyzed in this study.

Analyzed species	URLs, Source	Sequence data [Mbp]
<i>Arabidopsis lyrata</i>	ftp://ftp.jgi-psf.org/pub/JGI_data/phytozome/v5.0/Alyrata/	210
<i>Arabidopsis thaliana</i>	ftp://ftp.arabidopsis.org/Sequences/whole_chromosomes/	124
<i>Brachypodium distachyon</i>	ftp://ftp.jgi-psf.org/pub/JGI_data/phytozome/v5.0/Bdistachyon/assembly/sequences/	275
<i>Cucumis sativus</i>	ftp://ftp.jgi-psf.org/pub/JGI_data/phytozome/v5.0/Csativus/assembly/	207
<i>Glycine max</i>	ftp://ftp.jgi-psf.org/pub/JGI_data/phytozome/v5.0/Gmax/assembly/sequences/	986
<i>Manihot esculenta</i>	ftp://ftp.jgi-psf.org/pub/JGI_data/phytozome/v5.0/Mesculenta/	424
<i>Medicago truncatula</i>	http://www.medicago.org/genome/downloads/Mt3/	313
<i>Mimulus guttatus</i>	ftp://ftp.jgi-psf.org/pub/JGI_data/phytozome/v5.0/Mguttatus/assembly/	326
<i>Nicotiana tabacum</i>	http://srs.ebi.ac.uk/srsbin/cgi-bin/wgetz?-page+srsq2+-noSession	1420
<i>Nuphar adveana</i> (Nymphaeales)	http://srs.ebi.ac.uk/srsbin/cgi-bin/wgetz?-page+srsq2+-noSession	27
<i>Pinus taeda</i> , <i>Pinus sitchensis</i> , <i>Picea glauca</i> (Pinaceae)	http://srs.ebi.ac.uk/srsbin/cgi-bin/wgetz?-page+srsq2+-noSession	843
<i>Populus trichocarpa</i>	ftp://ftp.jgi-psf.org/pub/JGI_data/phytozome/v5.0/Ptrichocarpa/assembly/	422
<i>Solanum lycopersicum</i>	http://srs.ebi.ac.uk/srsbin/cgi-bin/wgetz?-page+srsq2+-noSession	722
<i>Solanum tuberosum</i>	http://srs.ebi.ac.uk/srsbin/cgi-bin/wgetz?-page+srsq2+-noSession	350
<i>Vitis vinifera</i>	ftp://ftp.jgi-psf.org/pub/JGI_data/phytozome/v5.0/Vvinifera/assembly/	506
<i>Zea mays</i>	http://zoneannfu.gdcb.iastate.edu/XGDB/phplib/download.php?GDB=Zm	2087
<i>Danio rerio</i>	http://hgdownload.cse.ucsc.edu/goldenPath/danRer6/bigZips/	1543

Supplemental Table 5. Primers used for the generation of SolS SINE probes for Southern blot and fluorescent *in situ* hybridization.

SINE family		Primer	Amplicon [bp]	Position within the SINE
SolS-Ia	for	AAATCCTGTTGGGAGCGCCAC	99	downstream of boxes A and B
	rev	TTGGTTTCCACCCGGTGTC		
SolS-II	for	GTGATTTCTTCCCATCTGTC	122	downstream of boxes A and B
	rev	ACCGTGGTGTCCGGGCCAGC		
SolS-IIIa	for	AAACCCCTTGCCAGCGAAAG	170	downstream of boxes A and B
	rev	ATGACAAGGGAAACCCGCAG		
SolS-IIIb	for	AGTCGAGCCTGTGCGAT	148	downstream of boxes A and B
	rev	AACCCGCAGCCGCTACA		
SolS-IV	for	AGCCCGGTATTTAAGTGGAG	103	downstream of boxes A and B
	rev	CGAGAAATCCGTCTGTGAC		
SolS-V	for	ATGGTAAGCACCCCTCACTTC	90	complete SINE
	rev	TTTACCCTCCCTAGGAGCTC		
SolS-VI	for	ACAATTTCTGAGGGCCATCG	123	downstream of boxes A and B
	rev	GTGTCCGAGTCTCTTTGAG		
SolS-VII	for	CACTGGCATTACAAACC	106	downstream of boxes A and B
	rev	GAACCCGACTAGCTGTAC		
SolRTE-I	for	AGATGAGGATGTTGAGGTGG	235	ORF 3' end
	rev	TCTCCCAATACTTCTTAGG		