Supplemental Data – Additional file 5

Pietzenuk et al., Recurrent evolution of heat-responsiveness in Brassicaceae COPIA elements.

Figure S1. Number of transposable element families in A. thaliana (n = 364) and A. lyrata (n = 376) as identified by RepeatMasker. The overlap shows number of families common to both species and not overlapping parts the numbers of speciesspecific families.



Figure S2. Unrooted phylogenetic tree of heat-responsive and -non-responsive COPIA TEs. The tree is based on the reverse transcriptase amino acid sequences (Additional file 10) of the following heat-responsive (ONSEN, TERESTRA, COPIA37 and ROMANIAT5) and -nonresponsive (COPIA19, COPIA23, COPIA35, COPIA45, COPIA66, COPIA75) COPIA TEs.



Table S1. List of *ONSEN* elements in *A. thaliana* Col-0 genome. *Heat responsiveness is based on the RNA-sequencing data of this study. **Names of *ONSEN1* to *ONSEN8* are based on Cavrak et al., 2014; HRE - Heat responsive element. RT - reverse transcriptase. ***Additional sequence insertion between 5' LTR and gag polyplotein domain.

	Element**	AGI code	Chr	Start	End	Size	Туре	HRE
	AtONSEN1	AT1TE12295	1	3780765	3785720	4956	full-length	4P
	AtONSEN2	AT3TE92525	3	22695566	22700521	4956	full-length	4P
/e*	AtONSEN3	AT5TE15240	5	4208083	4213084	5002	full-length	4P
nsi	AtONSEN4	AT1TE71045	1	21524995	21529850	4855	full-length	3P
spc	AtONSEN5	AT1TE59755	1	18013162	18018117	5273	full-length	4P
at re	AtONSEN6	AT3TE89830	3	22059535	22064329	4795	full-length	4P
He		AT1TE240E0	1	7714708	7715145	438	full longth***	40
	ALONSEN7	ATT1E24850	T	7717356	7722547	5191	Tull-length	42
	AtONSEN8	AT3TE54550	3	13369174	13374107	4934	full-length	4P
				17201388	17201573	185	truncated solo	
	AtONSEN9	AI11E57015	1	17201917	17202175	258	LTR	none
	AtONSEN10	AT1TE10935	1	3360540	3361316	776	pre-Integrase region	none
	AtONSEN11	AT2TE45420	2	10582288	10582517	229	fragmented solo LTR	none
nsive*	AtONSEN12	AT2TE26505	2	6483643	6483961	318	fragmented solo LTR	none
ods								
ion re	AtONSEN13	AT2TE12265	2	2780086	2781859	1773	fragment - RT & Rnase_H1	none
at-r	AtONSEN14	AT2TE62740	2	14190558	14191027	469	RT fragment	none
He	AtONSEN15	AT3TE59075	3	14401313	14403971	2658	RT & Rnase_H1+3'LTR	none
	AtONSEN16	AT3TE59080	3	14403653	14403946	293	fragment of 5′LTR and gag- polyprotein	none
	AtONSEN17	AT3TE31680	3	7539914	7540288	274	solo LTR	none
	AtONSEN18	AT4TE42010	4	9320200	9320565	265	truncated solo LTR	none

Figure S3. Heat responsive elements (HREs) found in 5' long terminal repeats of *ONSEN* elements. Only heat-responsive elements are shown for *A. lyrata* and *A. thaliana*. All elements are displayed for *other species*. HRE types: red – 4P, orange – 3P, yellow – gap, green – step.

		80	90	100	110	120	130	140	150	160	170	180
R stricta	BsONSEN1	caaattcta-					gaa	gtttataagaaa	atatctag	gagaaatc		
D. Sincia	BsONSEN2	aaattctag-					cctaaa		- ttctag	gaaacttg		
	AIONSEN10	- aaatacac -					ccccttaaa	a a g <mark>titctagaaa</mark>	TTTTCTAG	GAAtcatt	t t c	cacctcc
	AIONSEN14	caaatccaa-	- gTTCTAGA	GT TTTCTCTA	<mark>GAA</mark> atatcat	aattacc	acctccttaaa	atgTTCTAGAAA	ГСТТСТА	GAAtcatc	t t c	cacctcc
	AIONSEN6	aaaatccaa-	- gTTCTAAA	GT TTTCTCTA	<mark>GAA</mark> atatcat	aattacc	acctccttaaa	atg <mark>TTCTAGAAA</mark>	TTTTCTAG	GAAtcatc	ttc	cacctcc
	AIONSEN7	- aaatccaa-	- aTTCTAGA	GT TTTCTCTA	GAA <mark>atatcat</mark>	aattacc	acctccttaaa	atgTTCTAGAAA	TTTTCTAG	GAAtcatc	t t c	cacctcc
	AIONSEN9	-aaatccaa-	- gTTCTAGA	GT TTTCTCTA	<mark>GAA</mark> atatcat	aattacc	acctccttaaa	atgTTCTAGAAA	TTTTCTAG	GAAtcatc	t t c	cacctcc
	AIONSEN11	- aaatccaa-	- gTTCTAGA	GT TTTCTCTA	GAA <mark>atatcat</mark>	aattacc	acctccttaaa	atgTTCTAGAAA	TTTTCTAG	GAAtcatc	t t c	cacctcc
	AIONSEN15	- aaatccaa-	- gTTCTAGA	GT TTTCTCTA	GAA <mark>atatcat</mark>	aattacc	accttcttaaa	atg <mark>TTCTAGAAA</mark>	TTTTCTA	GAAtcatc	t t c	cacctcc
A lurata	AIONSEN8	- aaatccaa-	- gTTCTAGA	GT TTTCTCTA	<mark>GAA</mark> atatcat	aattacc	acctccttaaa	a	t t TTCTA	GAATCATC	<mark>TTC</mark>	cacctcc
A. Iyrala	AIONSEN13	- aaatccaa-	-gttctagag	gt-tttttcta	gaaatatcat	aattacc	acctccttaaa	<u> a</u>	t t TTCTA	GAATCATC	TTC	cacctcc
	AIONSEN3	- aaatccaa-	-gctctagag	gt-tttctcta	gaaatatcat	catcttc	acctccttaaa	a a g TTCTAGAAG		GAA <mark>tgatc</mark>	ttccat	cacctcc
	AIONSEN16	- aaatccaag	ggctctagag	gtatttctcta	gaaatatcat	catcttc	acctccttaaa	a a g TTCTAGAAG.		GAAtgatc	ttccat	cacctcc
	AIONSEN17	- aaatccaag	ggctctagag	gtatttctcta	gaaatatcat	catcttc	acctccttaaa	a a g TTCTAGAAG	ATCTCTA	GAAtgatc	<u>ttc</u> cat	cacctcc
	AIONSEN4	- aaatccaa-	-gttctagag	gt-tttctcta	caaatatcat	catctcc	acctccttaaa	aagttctagaaa	TTCTCTAG	GAATGATC	TTCcat	cacctcc
	AIONSEN5	- aaatccaa-	-gttctagag	gt-tttctcta	caaatatcat	catctcc	acctccttaaa	aagttctagaaa	TTCTCTAG	GAATGATC	TTCcat	cacctcc
	AIONSEN1	- aaatccaa-	-gttctagag	gt-tttctcta	caaatatcat	catctcc	acctccttaaa	aagttctagaaa	TTCTCTA	GAATGATC	TTCcat	cacctcc
	AIONSEN12	- aaatccaa-	- gTTCTAGA/	AT-TTTCtcta	caaatatcat	catctcc	acctccttaaa	aagttctagaaa	TTCTCTA	GAATGATC	TTCcat	cacctcc
	AIONSEN2	- aaatccaa-	- gTTCTAGA	JT TTTCTCTA	GAAatatcat	catct-c	acctccttaaa	aaattctagaaa	ttctctag	gaaccatc	t c	cacctcc
	AtONSEN1	- aaatccaa-	- gTTCTAGAG	GT TTTCTCTA	GAAatatcat	catttcc	acctccttaaa	a g a TTCTAGAAA	TTTTCTAG	GAAtcatc	t t c	cacctcc
	AtONSEN2	- aaatccaa-	- gTTCTAGA	GT TTTCTCTA	GAA <mark>atatcat</mark>	catttcc	acctccttaaa	aga <mark>TTCTAGAAA</mark>	TTTTCTAG	GAAtcatc	t t c	cacctcc
	AtONSEN3	- aaatccaa-	- gTTCTAGA	GT TTTCTCTA	<mark>GAA</mark> atatcat	catttcc	acctccttaaa	aga <mark>TTCTAGAAA</mark>	TTTTCTAG	GAAtcatc	t t c	cacctcc
A thaliana	AtONSEN4	- aaatctaa-	- gTTCTAAA	ST TTTCTTTA	<mark>GAA</mark> atatcat	catttcc	atctccttaaa	agattctagaaa	ttttctad	caatcatc	t t c	cacctcc
n. thununu	AtONSEN5	- aaatccaa-	- gTTCTAGA	JT TTTCTCTA	GAA atatcat	catttcc	acctccttaaa	agaTTCTAGAAA	TTTTCTAG	GAAtcatc	t t c	cacctcc
	AtONSEN6	- aaatccaa-	- gTTCTAGA	GT TTTCTCTA	<mark>GAA</mark> atatcat	catttcc	acctccttaaa	g g a TTCTAGAAA	TTTTCTAG	GAAtcatc	t t c	cacctcc
	AtONSEN7	- aaatccaa-	- gTTCTAGA	JT TTTCTCTA	GAAatatcat	catttcc	acctccttaaa	aga <mark>TTCTAGAAA</mark>	TTTTCTA	GAAtcatc	t t c	cacctcc
	AtONSEN8	- aaatccaa-	- TTCTAGA	GT TTTCTCTA	GAA <mark>atatcat</mark>	catttcc	acctccttaaa	aga <mark>TTCTAGAAA</mark>	TTTTCTA	GAAtcatc	t t c	cacctcc
	BaONSEN1	- aaatccaa-			aatatga-		tccaaa	TTCTAGAAT	ATTTCTA	GAA too to to a	agatctcta	cacctcc
B. antipoda	BaONSEN3	- aaatccaa-			gatatgt		ttcaa-	gTTCTAGAAC	TTTTCTAG	GAAttctc	ta	cacctca
	BaONSEN2	- aaatccaa-			gaaatga		cccaag		- ttctag	gaatcctctct	agatttcta	cacctct
	BrONSEN3	caacattaa-					cccaaa		- TTCTA	GAACAATC	<mark>TTC</mark>	cac-tcc
	BrONSEN1	caaagttaa-					cctaaa		- ttctag	gaattatc	ctc	cacctct
R rana	BrONSEN4								- ttctag	gaattatc	c t c	cacctct
D. Tapa	BrONSEN5	caaacttag-					cccaat		- atctag	gaattatc	cta	cacctcc
	BrONSEN6	caaacttaa-					ctcaat		- atctag	gaattatc	c t c	cacctcc
	BrONSEN2								gtgg	gaggtatt	tat	agcctcc
—	EsONSEN	taacttcta-						gaaa	ctctcta	GAATCATCTTC	ATATTTTC	cacttcc
E. salsu-												

gineum

Table S2. List of COPIA78/ONSEN elements in Arabidopsis lyrata MN47 genome.

*Heat responsiveness is based on RNA-sequencing data of this study. HRE - Heat responsive element; contig end - the element is at the edge of particular genome assembly contig; n.a. - not analyzed; **Heat responsiveness based only on multiply mapping RNA-seq reads; ***Not heat responsive in RNA-sequencing, possibly due to small size. RT - reverse transcriptase.

	Element	Scaffold	Start	End	Size	Туре	HRE	Ito et al.
								(2013)
	AIONSEN1	1	11268872	11273881	5010	full-length	gap/step	5
	AIONSEN2	1	24919344	24919772	429	solo LTR	gap	n.a.
	AIONSEN3	2	1120762	1121196	440	solo LTR	none**	n.a.
	AIONSEN4	2	4268383	4273330	4978	full-length	gap/step	3
	AIONSEN5	2	12788861	12789817	956	solo LTR	gap/step	n.a.
	AIONSEN6	3	13033504	13038475	4972	full-length	gap + 4P	2
	AIONSEN7	3	14350695	14355704	5010	full-length	gap + 4P	1
_{e^*	AIONSEN8	3	23055604	23059108	3504	contig end	gap	n.a.
nsi	AIONSEN9	4	16304811	16309766	4956	full-length	gap + 4P	10
od	AIONSEN10	5	4327023	4327410	388	solo LTR	4P	17
res	AIONSEN11	5	9883484	9888427	4944	full-length	gap + 4P	7
eat	AIONSEN12	6	22653438	22658398	4961	full-length	gap	4
Ť	AIONSEN13	7	23781774	23786710	4937	full-length	gap	7
	AIONSEN14	8	15966326	15970217	3892	full-length	gap + 4P	n.a.
	AIONSEN15	247	3711	8654	4944	full-length	gap + 4P	8
	AIONSEN16	1007	2411	3818	1408	contig end	none**	n.a.
	AIONSEN17	638	3577	4818	1242	contig end	gap + 4P	12
						fragmented		
	AIONSEN18	7	8283764	8284127	363	solo LTR	none	n.a.
	AIONSEN19	1007	42	1686	1645	RT	none	n.a.
						truncated		
						5 L I R &		
	AIONSEN20	3	14003080	14004319	1239	polypeptide	none	na
	/		11000000		.200	RT & RNase		mai
	AIONSEN21	3	14016614	14019627	3013	H1 & 3'LTR	none	n.a.
						31 TR		
	AIONSEN22	1	10332397	10332510	113	fragment	none	n.a.
						fragmented		
,e	AIONSEN23	1	13615947	13616317	370	solo LTR	none	n.a.
Jsiv						solo LTR		
por	AIONSEN24	1	24919900	24920073	173	fragment	none	n.a.
res	AIONSEN25	1	25691749	25692168	419	RT fragment	none	n.a.
uo						RNase H1		
t-ne	AIONSEN26	1	25692678	25692869	191	fragment	none	n.a.
lea						solo LTR		
<u> </u>	AIONSEN27	2	11661689	11661997	308	fragment	none	n.a.
	AIONSEN28	2	10259067	10259437	370	fragment	none	n.a.
						LTR		
	AIONSEN29	2	10974958	10975001	43	fragment	none	n.a.
						LTR		
	AIONSEN30	2	11911062	11911137	75	fragment	none	n.a.
	AIONSEN31	3	9491471	9491721	250	fragment	none	n.a.
						truncated		
	AIONSEN32	3	14002611	14002810	199	solo LTR	4P***	n.a.

AIONSEN30 Construct Construct Construct Construct Construct Inter Inter <t< th=""><th>AIONSEN33</th><th>3</th><th>23040531</th><th>23040611</th><th>80</th><th>solo LTR fragment</th><th>none</th><th>na</th></t<>	AIONSEN33	3	23040531	23040611	80	solo LTR fragment	none	na
AIONSEN34 4 15133412 15133767 355 fragment solo none n.a. AIONSEN35 4 15138010 15138365 355 LTRfragment none n.a. AIONSEN36 5 18806876 18807231 355 fragments none n.a. AIONSEN37 5 9649982 9650265 283 fragment none n.a. AIONSEN37 5 9649982 9650265 283 fragment fragment none n.a. AIONSEN38 5 9943036 9943399 363 fragment fragment none n.a. AIONSEN38 5 9943036 9943399 363 fragment none n.a. AIONSEN40 5 12394243 12394562 319 fragment none n.a. AIONSEN41 5 12398029 12398350 321 fragment none n.a. AIONSEN42 5 12560877 12561493 616 polypeptide none n.a. AIONSEN43 5	/		20040001	20040011		solo LTR	TIONE	n.a.
AIONSEN35 4 15138010 15138365 355 LTRfragment solo LTR & solo LTR & AIONSEN36 none n.a. AIONSEN36 5 18806876 18807231 355 solo LTR & fragments none n.a. AIONSEN37 5 9649982 9650265 283 fragments none n.a. AIONSEN38 5 9943036 9943399 363 fragment none n.a. AIONSEN38 5 9943036 9943399 363 fragment none n.a. AIONSEN39 5 11358443 11358638 195 fragment none n.a. AIONSEN40 5 12394243 12394562 319 fragment none n.a. AIONSEN41 5 123608077 12561493 616 polypeptide none n.a. AIONSEN43 5 13036269 13036319 50 fragmented AIONSEN44 5 18802278 8802633 355 solo LTR none n	AIONSEN34	4	15133412	15133767	355	fragment	none	n.a.
AIONSEN35 4 15138010 15138365 355 LTRfragment none n.a. AIONSEN36 5 18806876 18807231 355 fragments none n.a. AIONSEN37 5 9649982 9650265 283 fragment none n.a. AIONSEN38 5 9943036 9943399 363 fragment none n.a. AIONSEN38 5 9943036 9943399 363 fragment none n.a. AIONSEN38 5 9943036 9943399 363 fragment none n.a. AIONSEN40 5 12394243 12394562 319 fragment none n.a. AIONSEN41 5 12398029 12398350 321 fragment none n.a. AIONSEN42 5 12560877 12561493 616 polypeptide none n.a. AIONSEN43 5 13036269 13036319 50 fragmented AIONSE						solo		
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AIONSEN36 5 18800876 18807231 335 Hagilieftis Hole H.a. AIONSEN37 5 9649982 9650265 283 fragment none none n.a. AIONSEN38 5 9943036 9943399 363 fragment none none n.a. AIONSEN38 5 9943036 9943399 363 fragment none none n.a. AIONSEN39 5 11358443 11358638 195 fragment none n.a. AIONSEN40 5 12394243 12394562 319 fragment none n.a. AIONSEN41 5 12398029 12398350 321 fragment none n.a. AIONSEN42 5 12560877 12561493 616 polypeptide none n.a. AIONSEN43 5 13036269 13036319 50 fragmented solo LTR none n.a. AIONSEN44 5 18802233 3055 solo LTR none n.a. AIONSEN44 </td <td></td> <td>F</td> <td>10006076</td> <td>10007001</td> <td>255</td> <td>solo LTR &</td> <td>2020</td> <td>n 0</td>		F	10006076	10007001	255	solo LTR &	2020	n 0
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AIONSENIA 5 000000 0000000 0000000 0000000 none n.a. AIONSEN38 5 9943036 9943399 363 fragment none n.a. AIONSEN39 5 11358443 11358638 195 fragment none n.a. AIONSEN40 5 12394243 12394562 319 fragment none n.a. AIONSEN41 5 12398029 12398350 321 fragment none n.a. AIONSEN42 5 12560877 12561493 616 polypeptide none n.a. AIONSEN43 5 13036269 13036319 50 fragment none n.a. AIONSEN43 5 13036269 13036319 50 LTR none n.a. AIONSEN44 5 18802278 18802633 355 solo LTR none n.a. AIONSEN44 5 18802278 18802633 363 solo LTR none	AIONSEN37	5	9649982	9650265	283	fragment	none	n.a.
AIONSEN38 5 9943036 9943399 363 fragment fragment none n.a. AIONSEN39 5 11358443 11358638 195 fragment none n.a. AIONSEN40 5 12394243 12394562 319 fragment none n.a. AIONSEN41 5 12398029 12398350 321 fragment none n.a. AIONSEN41 5 12560877 12561493 616 polypeptide none n.a. AIONSEN43 5 13036269 13036319 50 fragment none n.a. AIONSEN43 5 13036269 13036319 50 fragmented none n.a. AIONSEN43 5 18802278 18802633 355 solo LTR none n.a. AIONSEN44 5 18802278 18802633 363 solo LTR none n.a. AIONSEN44 7 3003523 3003877 354 solo LTR <t< td=""><td></td><td></td><td></td><td></td><td></td><td>solo LTR</td><td></td><td></td></t<>						solo LTR		
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AIONSEN39 5 11358443 11358638 195 fragment none n.a. AIONSEN40 5 12394243 12394562 319 fragment none n.a. AIONSEN41 5 12398029 12398350 321 fragment none n.a. AIONSEN42 5 12560877 12561493 616 polypeptide none n.a. AIONSEN43 5 13036269 13036319 50 fragment none n.a. AIONSEN43 5 18802278 18802633 355 solo LTR none n.a. AIONSEN44 5 18802278 18802633 355 solo LTR none n.a. AIONSEN45 7 3003523 3003877 354 solo LTR none n.a. AIONSEN45 7 3003523 3003872 363 solo LTR none n.a. AIONSEN45 7 10045372 10046134 762 solo LTR none <td></td> <td></td> <td></td> <td></td> <td></td> <td>solo LTR</td> <td></td> <td></td>						solo LTR		
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AIONSEN41 5 12398029 12398350 321 fragment none n.a. AIONSEN42 5 12560877 12561493 616 polypeptide none n.a. AIONSEN42 5 12560877 12561493 616 polypeptide none n.a. AIONSEN43 5 13036269 13036319 50 fragmented none n.a. AIONSEN44 5 18802278 18802633 355 solo LTR none n.a. AIONSEN44 5 18802278 18802633 355 solo LTR none n.a. AIONSEN44 5 18802278 18802633 355 solo LTR none n.a. AIONSEN45 7 3003523 3003877 354 solo LTR none n.a. AIONSEN46 7 8288370 8288733 363 solo LTR none n.a. AIONSEN47 7 14850284 14850721 437 solo LTR non	AIONSEN40	5	12394243	12394562	319	fragment	none	n.a.
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AIONSEN42 3 12360877 12361493 616 polypeptide florie fl.a. AIONSEN43 5 13036269 13036319 50 fragment none n.a. AIONSEN44 5 18802278 18802633 355 solo LTR none n.a. AIONSEN44 5 18802278 18802633 355 solo LTR none n.a. AIONSEN44 5 18802278 18802633 355 solo LTR none n.a. AIONSEN45 7 3003523 3003877 354 solo LTR none n.a. AIONSEN46 7 8288370 8288733 363 solo LTR none n.a. AIONSEN47 7 14850284 14850721 437 solo LTR none n.a. AIONSEN47 7 10045372 10046134 762 solo LTR none n.a. AIONSEN49 7 13857185 13857510 325 fragment none<		F	10560077	10561402	616	gag-	2020	n 0
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Alonsenso Biologicoli 1000000 1000000 1000000 1000000 1000000	AIONSEN53	<u>ہ</u>	15685300	15685663	363	fragment	none	n.a.
	AIONSEN55	8	17245916	17246222	306	fragment	none	n.a.

Figure S4. Percentage identity matrix of reverse transcriptase nucleotide sequences of *ONSEN* elements from different species. LTR identity: Pink = >80%. All elements for which the full reverse transcriptase sequence was available are shown. None of the *B. antipoda* contigs contained *ONSEN* reverse transcriptase sequence and therefore it is not presented here.

	BrONSEN3	BsONSEN1	BsONSEN2	Esonsen	AtONSEN8	<i>AtONSEN7</i>	AtONSEN5	<i>AtONSEN3</i>	<i>AtONSEN6</i>	AtONSEN4	<i>AtONSEN1</i>	AtONSEN2	AIONSEN 7	AIONSEN9	AIONSEN6	AIONSEN 14	AIONSEN4	AIONSEN 11	AIONSEN 15	AIONSEN 12	<i>AIONSEN8</i>	AIONSEN 13
BrONSEN3	100.0	84.1	84.6	84.1	84.3	84.0	84.4	84.2	84.2	84.5	84.5	84.4	82.5	85.1	84.4	85.1	84.4	84.5	84.5	84.7	84.8	84.8
BsONSEN1	84.1	100.0	95.1	85.5	86.6	86.7	86.9	86.9	87.0	87.0	86.7	86.6	84.2	86.6	87.0	87.1	86.5	86.6	86.6	86.9	87.0	87.0
BsONSEN2	84.6	95.1	100.0	85.8	87.0	86.9	87.0	87.3	87.1	87.4	87.1	87.0	81.7	86.6	87.0	87.1	86.5	86.6	86.6	86.9	87.0	87.0
EsONSEN	84.1	85.5	85.8	100.0	87.8	87.3	87.3	87.3	87.3	87.5	87.3	87.3	86.7	88.7	88.0	88.5	88.0	87.8	87.8	88.2	88.5	88.7
AtONSEN8	84.3	86.6	87.0	87.8	100.0	97.8	98.0	98.1	98.1	98.4	98.1	98.0	90.8	93.7	93.6	94.1	93.6	93.7	93.7	93.7	93.9	94.1
AtONSEN7	84.0	86.7	86.9	87.3	97.8	100.0	99.1	98.9	99.2	99.2	98.9	98.8	91.7	94.2	94.2	94.7	93.9	94.3	94.3	94.0	94.2	94.2
AtONSEN5	84.4	86.9	87.0	87.3	98.0	99.1	100.0	99.1	99.3	99.3	99.1	98.9	90.8	94.4	94.3	94.9	94.0	94.4	94.4	94.2	94.3	94.3
AtONSEN3	84.2	86.9	87.3	87.3	98.1	98.9	99.1	100.0	99.2	99.5	99.5	99.3	91.7	94.3	94.6	95.0	94.2	94.6	94.6	94.3	94.4	94.4
AtONSEN6	84.2	87.0	87.1	87.3	98.1	99.2	99.3	99.2	100.0	99.5	99.5	99.3	91.7	94.3	94.4	95.0	94.2	94.6	94.6	94.3	94.4	94.4
AtONSEN4	84.5	87.0	87.4	87.5	98.4	99.2	99.3	99.5	99.5	100.0	99.5	99.3	91.7	94.6	94.7	95.3	94.4	94.9	94.9	94.6	94.7	94.7
AtONSEN1	84.5	86.7	87.1	87.3	98.1	98.9	99.1	99.5	99.5	99.5	100.0	99.9	91.7	94.3	94.4	95.0	94.2	94.6	94.6	94.3	94.4	94.4
AtONSEN2	84.4	86.6	87.0	87.3	98.0	98.8	98.9	99.3	99.3	99.3	99.9	100.0	91.7	94.2	94.3	94.9	94.0	94.4	94.4	94.2	94.3	94.3
AIONSEN7	82.5	84.2	81.7	86.7	90.8	91.7	90.8	91.7	91.7	91.7	91.7	91.7	100.0	95.8	97.5	97.5	96.7	97.5	97.5	96.7	96.7	96.7
AIONSEN9	85.1	86.6	86.6	88.7	93.7	94.2	94.4	94.3	94.3	94.6	94.3	94.2	95.8	100.0	97.2	97.7	98.0	98.1	98.1	98.1	98.0	98.0
AIONSEN6	84.4	87.0	87.0	88.0	93.6	94.2	94.3	94.6	94.4	94.7	94.4	94.3	97.5	97.2	100.0	99.2	98.4	98.5	98.5	98.2	98.4	98.4
AlONSEN14	85.1	87.1	87.1	88.5	94.1	94.7	94.9	95.0	95.0	95.3	95.0	94.9	97.5	97.7	99.2	100.0	98.6	99.1	99.1	98.8	98.9	98.9
AIONSEN4	84.4	86.5	86.5	88.0	93.6	93.9	94.0	94.2	94.2	94.4	94.2	94.0	96.7	98.0	98.4	98.6	100.0	99.1	99.1	99.1	98.9	98.9
AIONSEN11	84.5	86.6	86.6	87.8	93.7	94.3	94.4	94.6	94.6	94.9	94.6	94.4	97.5	98.1	98.5	99.1	99.1	100.0	100.0	99.2	99.1	99.1
AIONSEN15	84.5	86.6	86.6	87.8	93.7	94.3	94.4	94.6	94.6	94.9	94.6	94.4	97.5	98.1	98.5	99.1	99.1	100.0	100.0	99.2	99.1	99.1
AIONSEN12	84.7	86.9	86.9	88.2	93.7	94.0	94.2	94.3	94.3	94.6	94.3	94.2	96.7	98.1	98.2	98.8	99.1	99.2	99.2	100.0	99.1	99.1
AIONSEN8	84.8	87.0	87.0	88.5	93.9	94.2	94.3	94.4	94.4	94.7	94.4	94.3	96.7	98.0	98.4	98.9	98.9	99.1	99.1	99.1	100.0	99.7
AIONSEN13	84.8	87.0	87.0	88.7	94.1	94.2	94.3	94.4	94.4	94.7	94.4	94.3	96.7	98.0	98.4	98.9	98.9	99.1	99.1	99.1	99.7	100.0

Figure S5. Percentage identity matrix of LTR nucleotide sequences of *ONSEN* elements from different species. LTR identity: Pink = >80%, yellow = 70-80%, green = 60-70%, no color = <60%. LTRs were clustered according to their similarity.

	RONSEN2	<i>sonsen1</i>	sonsen2	SONSEN	VONSEN2	aONSEN1	aONSEN2	aONSEN3	It ONSEN4	<i>AtONSEN8</i>	It ONSEN7	<i>ItONSEN6</i>	<i>tonsens</i>	<i>ItONSEN2</i>	<i>NTONSEN1</i>	<i>tonsen3</i>	VONSEN10	NONSEN14	VONSEN6	VONSEN7	NONSEN9	NONSEN11	VONSEN15	NONSEN8	NONSEN13	NONSEN3	NONSEN16	VONSEN17	NONSEN4	NONSENS	NONSEN1	VONSEN12	<i>RONSEN3</i>	<i>RONSEN1</i>	RONSEN4	Ironsenos	<i>rONSEN6</i>
BrONSEN2	100.0	60.8	64.3	64.9	60.1	64.1	61.5	61.4	63.5	62.4	62.3	62.4	62.4	62.4	62.4	62.0	64.5	64.7	64.7	62.4	63.5	64.1	63.5	64.1	64.7	65.9	67.5	67.5	64.7	64.7	65.9	65.9	63.6	61.5	64.1	59.6	62.3
BsONSEN1	60.8	100.0	84.1	57.3	59.9	67.5	63.7	63.8	68.0	66.4	67.1	68.3	66.9	67.5	67.5	67.5	68.0	69.4	67.7	69.0	69.0	68.4	68.4	68.3	68.6	68.1	65.7	65.7	67.4	67.4	67.6	68.1	63.3	65.1	75.7	66.9	67.7
BsONSEN2	64.3	84.1	100.0	61.5	64.6	72.7	70.0	70.1	74.5	72.7	73.3	73.9	73.0	73.6	73.6	73.6	73.9	74.1	75.7	76.0	75.7	76.0	75.7	75.1	75.1	75.7	73.0	73.0	74.5	74.5	73.9	73.6	71.6	69.9	76.6	73.9	70.6
EsONSEN	64.9	57.3	61.5	100.0	66.8	73.7	72.1	69.9	72.4	72.7	72.4	73.3	73.0	73.0	73.0	73.1	73.3	72.9	73.2	74.0	74.7	74.3	73.7	73.5	74.1	73.6	72.5	72.5	75.2	75.2	73.7	73.7	69.7	67.5	78.6	67.3	69.3
AIONSEN2	60.1	59.9	64.6	66.8	100.0	65.7	66.9	77.2	75.8	75.4	76.0	76.5	76.5	76.7	76.7	76.8	74.3	74.9	78.2	79.0	79.0	78.8	78.5	78.4	78.7	80.6	77.9	77.9	81.9	81.9	80.3	80.3	66.1	64.7	76.5	67.5	65.1
BaONSEN1	64.1	67.5	72.7	73.7	65.7	100.0	79.2	82.8	76.5	76.5	76.8	76.5	76.2	76.8	76.8	76.5	75.9	77.0	78.0	78.6	78.6	79.3	78.6	77.1	77.8	78.5	78.4	78.4	77.5	77.5	77.0	77.0	71.8	74.3	85.4	72.4	74.8
BaONSEN2	61.5	63.7	70.0	72.1	66.9	79.2	100.0	82.0	74.7	73.1	73.4	74.7	73.4	74.0	74.0	74.0	73.2	76.5	75.1	77.9	75.7	76.6	76.6	75.7	76.3	77.2	77.6	77.6	74.9	74.9	75.6	75.6	71.1	70.7	79.5	68.2	70.8
BaONSEN3	61.4	63.8	70.1	69.9	77.2	82.8	82.0	100.0	78.7	77.2	79.4	79.4	78.7	79.4	79.4	79.4	78.3	80.0	81.8	81.8	81.0	82.5	81.8	81.3	81.3	81.0	81.9	81.9	78.8	78.8	79.6	78.8	69.0	73.9	82.2	72.2	75.9
AtONSEN4	63.5	68.0	74.5	72.4	75.8	76.5	74.7	78.7	100.0	95.3	95.8	96.5	96.3	96.8	96.8	96.8	86.6	90.3	89.1	90.1	89.9	90.4	90.1	89.6	89.3	88.6	88.3	88.3	86.2	86.2	87.1	86.6	72.3	73.3	83.8	73.1	76.0
AtONSEN8	62.4	66.4	72.7	72.7	75.4	76.5	73.1	77.2	95.3	100.0	97.7	98.0	98.2	98.2	98.2	98.2	88.6	92.9	91.1	92.3	91.8	92.7	92.5	92.1	91.8	89.0	90.0	90.0	88.8	88.8	89.5	89.1	71.0	71.1	83.8	73.1	75.7
AtONSEN7	62.3	67.1	73.3	72.4	76.0	76.8	73.4	79.4	95.8	97.7	100.0	98.4	98.6	99.1	99.1	99.1	88.2	92.0	91.5	92.4	92.6	92.6	92.4	92.2	92.0	88.9	89.4	89.4	88.7	88.7	89.2	88.7	71.0	71.4	83.1	72.8	76.0
AtONSEN6	62.4	68.3	73.9	73.3	76.5	76.5	74.7	79.4	96.5	98.0	98.4	100.0	98.9	99.3	99.3	99.3	88.1	92.6	91.3	92.7	92.5	92.9	92.7	92.5	92.3	89.2	89.7	89.7	88.8	88.8	89.5	89.1	71.0	71.4	83.1	73.4	76.0
AtONSEN5	62.4	66.9	73.0	73.0	76.5	76.2	73.4	78.7	96.3	98.2	98.6	98.9	100.0	99.6	99.6	99.6	88.1	92.9	91.3	92.5	92.3	92.7	92.5	92.1	91.8	89.0	89.4	89.4	88.5	88.5	89.3	88.8	71.0	71.1	83.1	72.8	75.4
AtONSEN2	62.4	67.5	73.6	73.0	76.7	76.8	74.0	79.4	96.8	98.2	99.1	99.3	99.6	100.0	100.0	100.0	88.6	92.6	91.8	92.9	92.7	93.2	92.9	92.5	92.3	89.4	90.0	90.0	89.0	89.0	89.8	89.3	71.3	71.6	83.8	73.4	76.0
AtONSEN1	62.4	67.5	73.6	73.0	76.7	76.8	74.0	79.4	96.8	98.2	99.1	99.3	99.6	100.0	100.0	100.0	88.6	92.6	91.8	92.9	92.7	93.2	92.9	92.5	92.3	89.4	90.0	90.0	89.0	89.0	89.8	89.3	71.3	71.6	83.8	73.4	76.0
AtONSEN3	62.0	67.5	73.6	73.1	76.8	76.5	74.0	79.4	96.8	98.2	99.1	99.3	99.6	100.0	100.0	100.0	88.6	92.6	91.8	92.9	92.7	93.2	92.9	92.5	92.3	89.4	90.0	90.0	89.0	89.0	89.8	89.3	71.3	71.6	83.8	73.4	76.0
AIONSEN10	64.5	68.0	73.9	73.3	74.3	75.9	73.2	78.3	86.6	88.6	88.2	88.1	88.1	88.6	88.6	88.6	100.0	91.8	93.3	92.3	92.8	93.0	92.3	93.1	93.1	90.1	90.0	90.0	90.0	90.0	89.9	89.9	72.4	74.3	85.5	73.1	74.2
AIONSEN14	64.7	69.4	74.1	72.9	74.9	77.0	76.5	80.0	90.3	92.9	92.0	92.6	92.9	92.6	92.6	92.6	91.8	100.0	94.9	96.4	96.5	97.5	97.0	96.3	96.1	91.0	92.5	92.5	92.2	92.2	92.9	92.4	73.8	74.6	85.6	75.4	77.4
AIONSEN6	64.7	67.7	75.7	73.2	78.2	78.0	75.1	81.8	89.1	91.1	91.5	91.3	91.3	91.8	91.8	91.8	93.3	94.9	100.0	96.2	96.4	97.3	96.6	97.7	97.5	90.9	91.8	91.8	93.6	93.6	93.0	92.7	72.4	72.7	85.6	/3.6	75.2
AIONSEN7	62.4	69.0	76.0	74.0	79.0	78.6	77.9	81.8	90.1	92.3	92.4	92.7	92.5	92.9	92.9	92.9	92.3	96.4	96.2	100.0	97.7	98.2	98.0	97.2	97.0	91.5	92.6	92.6	92.9	92.9	92.7	92.5	72.8	/3.5	84.4	75.0	77.0
AIONSEN9	63.5	69.0	75.7	74.7	79.0	78.6	75.7	81.0	89.9	91.8	92.6	92.5	92.3	92.7	92.7	92.7	92.8	96.5	96.4	97.7	100.0	98.2	97.5	97.5	97.2	91.5	92.6	92.6	92.9	92.9	92.7	92.5	73.4	74.1	86.3	74.4	76.2
AIONSEN11	64.1	68.4	76.0	74.3	78.8	79.3	76.6	82.5	90.4	92.7	92.6	92.9	92.7	93.2	93.2	93.2	93.0	97.5	97.3	98.2	98.2	100.0	99.3	98.6	98.4	92.5	93.7	93.7	94.1	94.1	94.1	93.9	74.0	74.4	85.0	75.3	77.0
AIONSENIS	64.1	60.4 60.2	75.7	/ 3. / 72 E	70.5	70.0	70.0	01.0	90.1	92.5	92.4	92.7	92.5	92.9	92.9	92.9	92.5	97.0	90.0	98.0	97.5	99.5	100.0	97.9	97.7	91.8	92.9	92.9	95.4	95.4	95.4	95.2	/3./ 72 /	74.1	05.U	75.0	76.0
AIONSEN0	64.1	68.6	75.1	75.5	70.4	77.1	76.2	01.5 01.2	89.0	92.1	92.2	92.5	01.0	92.5	92.5	92.5	02.1	90.5	97.7	97.2	97.5	90.0	97.9	100.0	100.0	91.0	92.7	92.7	94.2	94.Z	92.0	92.0	73.4	73.0	05.0 96.2	75.0	76.0
AIONSEN3	65.9	68.1	75.7	73.6	80.6	78.5	77.2	81.0	88.6	89.0	88.9	89.2	89.0	89.4	89.4	89.4	90.1	91.0	90.9	91.5	91.5	92.5	91.8	91.6	91.8	100.0	98.2	98.2	93.8	93.8	94.6	94.3	72.5	72.1	84.4	72.9	74.0
AIONSEN16	67.5	65.7	73.0	72.5	77.9	78.4	77.6	81.0	88.3	90.0	89.4	89.7	89.4	90.0	90.0	90.0	90.0	92.5	91.8	92.6	92.6	93.7	92.9	92.7	93.0	98.2	100.0	100.0	95.9	95.0	96.6	96.1	73.8	73.0	85.0	72.5	75.0
AIONSEN17	67.5	65.7	73.0	72.5	77.9	78.4	77.6	81.9	88.3	90.0	89.4	89.7	89.4	90.0	90.0	90.0	90.0	92.5	91.8	92.6	92.6	93.7	92.9	92.7	93.0	98.2	100.0	100.0	95.9	95.9	96.6	96.1	73.8	73.0	85.0	72.7	75.0
AIONSEN4	64.7	67.4	74.5	75.2	81.9	77.5	74.9	78.8	86.2	88.8	88.7	88.8	88.5	89.0	89.0	89.0	90.0	92.2	93.6	92.9	92.9	94.1	93.4	94.2	94.2	93.8	95.9	95.9	100.0	100.0	97.4	97.2	74.4	73.9	83.8	74.0	76.0
AIONSEN5	64.7	67.4	74.5	75.2	81.9	77.5	74.9	78.8	86.2	88.8	88.7	88.8	88.5	89.0	89.0	89.0	90.0	92.2	93.6	92.9	92.9	94.1	93.4	94.2	94.2	93.8	95.9	95.9	100.0	100.0	97.4	97.2	74.4	73.9	83.8	74.0	76.0
AIONSEN1	65.9	67.6	73.9	73.7	80.3	77.0	75.6	79.6	87.1	89.5	89.2	89.5	89.3	89.8	89.8	89.8	89.9	92.9	93.0	92.7	92.7	94.1	93.4	92.8	93.0	94.6	96.6	96.6	97.4	97.4	100.0	99.3	72.8	72.9	83.1	72.4	74.6
AIONSEN12	65.9	68.1	73.6	73.7	80.3	77.0	75.6	78.8	86.6	89.1	88.7	89.1	88.8	89.3	89.3	89.3	89.9	92.4	92.7	92.5	92.5	93.9	93.2	92.6	92.8	94.3	96.1	96.1	97.2	97.2	99.3	100.0	72.8	72.9	82.5	72.4	74.6
BrONSEN3	63.6	63.3	71.6	69.7	66.1	71.8	71.1	69.0	72.3	71.0	71.0	71.0	71.0	71.3	71.3	71.3	72.4	73.8	72.4	72.8	73.4	74.0	73.7	73.4	73.4	72.5	73.8	73.8	74.4	74.4	72.8	72.8	100.0	81.4	84.8	79.4	75.3
BrONSEN1	61.5	65.1	69.9	67.5	64.7	74.3	70.7	73.9	73.3	71.1	71.4	71.4	71.1	71.6	71.6	71.6	74.3	74.6	72.7	73.5	74.1	74.4	74.1	73.8	73.8	72.1	73.0	73.0	73.9	73.9	72.9	72.9	81.4	100.0	100.0	83.8	81.0
BrONSEN4	64.1	75.7	76.6	78.6	76.5	85.4	79.5	82.2	83.8	83.8	83.1	83.1	83.1	83.8	83.8	83.8	85.5	85.6	85.6	84.4	86.3	85.6	85.0	85.6	86.3	84.4	85.0	85.0	83.8	83.8	83.1	82.5	84.8	100.0	100.0	86.9	88.7
BrONSEN05	59.6	66.9	73.9	67.3	67.5	72.4	68.2	72.2	73.1	73.1	72.8	73.4	72.8	73.4	73.4	73.4	73.1	75.4	73.6	75.0	74.4	75.3	75.0	75.0	74.4	72.9	72.7	72.7	74.0	74.0	72.4	72.4	79.4	83.8	86.9	100.0	86.8
BrONSEN6	62.3	67.7	70.6	69.3	65.1	74.8	70.8	75.9	76.0	75.7	76.0	76.0	75.4	76.0	76.0	76.0	74.2	77.4	75.2	77.0	76.2	77.3	76.8	76.0	76.0	74.0	75.0	75.0	76.0	76.0	74.6	74.6	75.3	81.0	88.7	86.8	100.0

Figure S6. Heat responsive elements (HREs) found in the 5' long terminal repeats of *COPIA37* elements. Only heat-responsive elements are shown for *A. lyrata* and *A. thaliana*. All elements are displayed for *C. rubella* and *E. salsugineum*. HRE types: orange – 3P, yellow – gap, green – step.

		220	230	240	250	260	270	280	290	300	310	320	330	340
C ruballa	Crubella_a	AGAG	TCTA			GAGAA	AGTGAGAG	- AACGTTGGA	GTT T	CAAGCAAGCT	TCTCCTCTTT	GTT-CTTT-	GTCTTTTGAT	CTTTGTTCT
C. Tubella	Crubella_b	GAGAG	TCTA			GAGAA		- CGTTGGAG-	TTT	CAAGCAAGCT	TTCTCCTCTTT	GTT-CTTT-	- GTCTTTGAT	CTTTGTTCT
A lurata	Alyrata_a	AGGG	<u>ТСТА</u>			GAGAA	AG - AGAGAA	- AACGTTAG-	AG	TCAAGAAGCT	TCTCCCTGTT	GTTCTTTTG	TGTCTTTGAT	C- TTGTTCT
A. Iyrala	Alyrata_b	AGAG	ТСТА			GAGAA	AGGAAAAAAA	AAAAAAAAAA	GGTTCTTCT	TCAACAAGCT	TTCTCCTTCTT	TGT-TCTT-	TGTCTTTGAT	CTTTGTTCT
	Athaliana_h	AGAGT1	ГСТА			GAGA-	AGAGAG	- ATAAAAAG-	CTTCC	AAAGCAAGCT	TTCTTCTTCCT	CTT-TGTT-	GTTCTTGAAT	C-TTGTTCT
	Athaliana_f	AGAGTT	TCTA			GAGA-	AGAGAG	- ATAAAGAG-	CTTCC	AAAGCAAGCT	TTTTTCTTTCT	CTT-TGTT-	ATTTTTGCAT	C-TTGTTCT
	Athaliana_g	AGAGTT	TCAA			GAGA-	AGATAG	- ATAAAGAG-	CTTCC	GAAGCAAGCT	TTCTTCTTCCT	CTT-TGTT-	GTTCTTGAAT	C-TTGTTCT
	Athaliana_c	CACCGAAGTO	CCCACCTATTO	CAAAAAAAT	GGTGCCTGAAC	CGACGGGAA	GCAAAGAGAT	- AAAAAAAA	CTTCC	TAAGCAAGCT	TTCTTCTTCCT	CTT- TATT-	GTTCTTGAAT	CTTTGTTTT
A thaliana	Athaliana_a	AGAGT1	TCTA			GAGA-	AGAGAG	ATAAAAGAG-	CTTCC	TAAACAAGCT	TTCTTCTTCCT	CTT-TGTT-	GTTCTTGAAT	CTTTGTTCT
/ II thanana	Athaliana_b	AGTGT1	ГСТА			GAGAA	GAGAGAT	AAAAAGAG-	CTTCC	TAAGCAAGCT	TCTTCTTCT	ATT-TGTT-	GTTCTTAAAT	CTTTGTTCT
	Athaliana_d	AGAGT	ГСТА			GAGAA	G AGAGAT	- AAAAAGAG-	CTTCC	TAAGCAAGCT	TTCTTCTTCCT	CTT-TGTT-	GTTCTTAAAT	ATTTGTTCT
	Athaliana_j	AGAG	ГСТА			GAGAG	AAAGAGAA	- GAAACGAGA	GTTTATTT	TCAAGAAGCT	TCTCCTTCTT	TGT-TCTT-	TATCTTTGAT	CTTTGTTCT
	Athaliana_e	GGAG	TCTA			GAGAG	AA AGAGAA	- GAAACGAGA	GTTTATTC	TCAAGAAGCT	TTTCCTTCTT	TGT-TCTT-	TGTCTTTGAT	CTTTGTTCT
	Athaliana i	AGAGT	ГСТА			GAGAG	AAAGAGAA	- GAAACGAGA	GTTTATTC	TCAAGAAGCT	TCTCCTTCTT	TGT-TCTT-	TGTGTTTGAT	CTTTGTTCT
E salsu	Esalsugineum_b	AGAG	TCTA			GAGAA	AC AAAGAA	- ATCAAGGG-	TT	TCAAGGGGTT	ICTTGTTCTTT.	ATT - TGTTG	TGTCTTTGAT	CCTTGTTCT
L. Saisu-	Esalsugineum_a	ACAC	GTTCTA			GAG	AAAC - AAAG	AA- ATCAAGO	3G	TCTCAAGGGG	TTTCTTGTTCT	TTCTT- TGT	TGTGTCTTTG	ATCCTTGTT
gineum														

Figure S7. Consensus DNA sequence of *A. lyrata TERESTRAs.* Specific regions were indicated in different colors according to Fig. 3c: 5' LTR (grey), PBS (underlined), **GAG polyprotein (green)**, **integrase (violet)**, reverse transcriptase (yellow), **RNAse H1 (blue)**, **PPT (red)**, 3' LTR (grey). CG dinucleotides within 5' LTR were underlined and bold.

TGAAGTTAAACTTGATTTTGGTTTAAGCTTAATTATGGGTTTATAATTCAATATTCTATATTGGATAAAACCCAAAGTTAAGCC TAAGTTCTAGATTTCTCTAGAGCATCATAGAAAAATCATCACCTCCTTAAATGTTCTAGAGAATTYTATTAGATAGATAGATATTTAG AWAATTATGTAGAATAATCTAGAAGTTTGTAAGATAAAATCATGATATTTTAGTAGAGATTATAGAGATGGTAGAATAATCT ACAACTTTCTAACCTAAC
TGAATAAAAGAAGTTCAAATAAAAGAACACTCTTTAAAGTCCCCCCCMTCATTGTAATWTGTGAGGAGAGTGAACAAG TGAATAAAAAGAAAGTTCAAATAAAAAGAACACTCTTTAAAGTTCTTCAAGTCTCTCCAAAAGTCTTTCAAGTAGTCTCTAATT GTTCTTCCAAATTTTCTATCATACTTAGAGGGTTTCTTTATCTTGATTATAT <u>CG</u> AGTTTCT <u>CG</u> GGTATTA <u>CG</u> GGTATTACGGGTATTCTGGGCTAGT GCTAAGCACTATCGGGTTTCTTTACATGGTATCACTCGAGGAGCCATTCTAATCTTGGCTCTCCAAGAGTCGCGGATT
ATAGGAGAACTCGGATCTACTCTAAGTATGGAATCTATGGGTCGTGTTGTTGGATTGGGAATGGAGATC
ACTACCGGTTATGGAAGTCATGTATGGAGTCATACTTGGTTAGTGAGGACTTATGGGATGTCGTCGGCGGAAGTAATACTT
CACCACCTACCGGAGATGCTGCAACCGCGGAAGCGACAAAGGAGTGGACACGTAAAAATGCCAAGGCGGARTTTRCTTTA
AAGAGGTCAATATCCTCAGGAGTATTTGAGCATGTCTCAAGGTGCACATCCGCTAGTTCAATTTGGCAAGCGTTAGATCGAC
TGTTCAACAAGAARAAYGAAGCTCGTCTACAATTGTTAGAAAACGAGTTGGCRAATGCGAAGCAGGGGGGGGGG
CGGAGTITITCATCAAGGTAAAGAACCTITGCTCTGAGTMAATAGTCTTAATCCGGAGGAATCAATCTCGGATGCTCGGT
GGRAGCGCYTTTGTAGCTAGGAGGCAACAMAACTTYAAAGCCAAATCYAATGAYGGTGGTCCAAGAAATAATGATGGACAT
GAAGGATCTTCTAAGGGAGATAAGAAAAAATTCAAGTGCTATCGGTGTGGAAAACTWGGGCATTTTAAAAARGATTGCCGA
GTCAAGCTGAAGGAAACAAACATGGCRGAATCAAAAGGTCATAATGAAGACGAAGAATGGGGAAAATGTTTTACGRTGGAG
GCTGCATCTTCAAGTACATCTACACCTAAGAARGTGGAAAATAATTGGATCGTAGATTCTGGTTGTAGCCATCATATYACYG
GAGACGAGAAATTATTTTCTAGTCTTCAACGCCATGAAGGAAAAGAAGCAATCATTACCGCGGGATAATTCAATCCATCACGT
IGAGAAGGAACGGIGGICAICAAAGGAGAIGAIGGAAGCCCAAICACTCIYRAGAACGIIIACCAIGIICCIGGAG
AAAAAAGAATCTTCTCCCGTGGTAAATGCGGTGGACTCAGGTAACTATGTYTTATTGCCCCAAGAGATGTTAAATTCTAA
GTIATGGTRAATAAAGAYTTGGTKAACGGGCTCCCAAAGTTGAAGATCCAAGATGAAGACACTTTGGAAGATGTCAAT
ATGGAAAGTCTCATAGACTTCCATTTGACTATTCCACTTCAAGGTGCAGTGTCCGTTGGARAGGGTCCAYAGTGACTTGAT
GGGTCCGACAAGAACACCCTCATATTYCGGGTATCRCTACATGTTGTTGTTGTTGAYGACTTCTCWCGGTACACTTGGGT
ATACTTTGTGAAGGAAAAATCTGAAGTATTCTCCAAGTTTCTAGAATTCAAGGTTACCGTGGAAGGGGAGTTAGGTCAGAAG
ATCAAGACCTTAAGGACGGATAATGGAGGGGAGTTCATGTCTAAGGAGTTTCTCTCTTTTTGTAGAGATAATGGTATCAAGA
GAGAATTTACATGTCCGCATACACCTCAACAAAATGGAGTAGCAGAGAGGAAGATCAGACATCTAAGTGAGACGTGTAGAA
G I I GGC I CCA I GGC I AAGGAG I I A I GGCG GGAGGGMA I GAGA I GI GCA CAACCGGA I G
GATCAGIC IGCIACGOTICATIGIGITIGATCACAAAGAACIAGGIGGAGGGCAAAGAAGAAGAAGAAGAATIGCCAATTGTCGCGAGAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA
GTTTCTTCATACTACGGGCCACCTCAAGTCTTGGTTGAAAAAGATGGTGCRAGTTCCTCCAAGATCGATGAATCAACTCTCC
AAGTACCATGTGAGARTGGAAGTCCTGGAAATAAAATTCAAGGTCAAAGGGGGAGCACTAACCAAGAAGAAGAAGAAGAACAAG
ATCATGGTTCGATGGTCAATCAACGGCCGAAAAGAAACATTGTCAAGCCTGCAAGATATAGAGATGAAGAATTCATCACTAC
TTATTCATGCTTCTTCGCAGCTCCGTTAGATGATGATGAGCCATCTTCTTATGATGAAGCTAAAGGAGTCCAAGAATGGGAA
GCTGCAATGAAKGAGGAGATGATGCTCTMAAGAAAAATGAAACTTGGGATCTGGTTCCAAAACCCCAAGGATGTTGAGCCC
GCATTECCACCAWCATTECCTECACATTATCCCACCTECACACCTCCACATTATCCCCCCTTCCTATATCCTCCACCA
CTTCATGGAGCAACCACCTGGTTTCGAATCACGAGAGCATCYTGATCATGTGTGCAAGCTGAAAAAGGCCTTGTACGGAT
AAAACAAGCTCCACGAGCTTGGTATGGAAAGGTTGCTCARTTCCTTCAATTTTGCGGCTATGAGGCATCAAATTCTGACCCG
AGTCTATTCTTCAAGAAGAAAGGAGGAGTYCACGTAGTAGTTCTTCTTTACGTGGATGATATGAT
ATGCAGAAATTGCTCGCTTACAAGAAGAYATGTCGATAAGGTTCGAGATGAAGAAGTTGGGTGAGCTGAATAACTTTCTTGG
CCTAGAGGTTGAAAGAGKAAAKGATGGAATATTCGTTGGTCAACAAGGTTATGCAAGAAGGATTGTTGAGAAGTTCGGGGT
GCACGAAGGAAAGAYGCGCACIACICCGAIGGAIGIGAACAICAAAGCICAAACCGIGAIGAAGGIICAIIGIIACCIGAICC
AUTOGOLITATOCAAOCAACTACAAAGAAACCAACTAAAGAGOCAAAGAAOATOLIGATGACTATOCAAAACTACTAACTA
GAAAATCAACTTCGGGCTATGTGTTCTTATGTGGAGACACAAGCATTTCGTGGTGTAGCAAGAAACAACCAAC
ATCTACCACTGAAGCGGAGTATAAAGCTTCCACACTCGCTGCTCAAGAGTGTATATGGCTTCGAAGACTCTTTGAAGATTTG
TTCGAGCCCATAAATAAACCGGTGGCTATCTACGGAGATAATCAAAGTGCTATCAAGTTAGCTAACAATCCGGTGTTTCATG
CAAGGACAAARCATATTGAGTTAGAACATCACTTCATAAGGGAGAAGGTTCTTCTTGATGGAACAATTGAAGCCTTGGAAGT
TCGAAGTGAGGACAACGTTGCAGACATCTTCACCAAGTCATTACCAAAAGGCCAATTCGAGTTACTTCGCTYGAAGCTCGG
ΑΤΑΤΙΟΤΑΤΑΓΙΟΟΑΤΑΛΑΑΟΟΟΑΛΑΘΤΙΑΑΟΟΟΤΑΑΟΤΙΟΤΑΟΑΤΙΟΤΟΤΑΟΑΟΟΑΤΟΑΤΑΟΑΑΑΑΑΤΟΑΤΟΑΟΟΟΟΤΟ
TTAGTAGAGTTATAGAGATGATGGTAGAATAATCTAGAGAGACTTTGTAAGCTAGAAGTTGTAGATAAAATCTAGATAAT
CCMTCATTTGTAATTWTGTGAGGAAGTTGAACAAGTGAATAAAAGGAAAGTTCAAATAAAAGAACACTCTTTAAAAGTTCTCT
AAGTCTCTCCAAAAGTCTTTCAAGTAGTCTCTAATTGTTCTTCCAAATTTTCTATCATACTTAGAGGRTTTCWTATCTTGATTA
TATCGAGTTTCTCGGGTATTACGGTCTTGGGCTAGTGCTAAGCACTATCGADYTCGGDTTCTTTAACCGAATCA

Table S3. List of *Arabidopsis thaliana* accessions negatively tested for presence of *TERESTRA* elements. *Arabidopsis lyrata* MN47 genomic DNA was used as positive control.

			Arabidanaia
Line	Arabidopsis Biological Resource Centre ID	Line	Biological Resource
Bay-0	CS76094	Se-0	CS76226
Bor-4	CS76100	Shahdara	CS76227
Bur-1	CS76105	Sq-8	CS76230
C24	CS76106	Uod-7	CS76296
Ct-1	CS76114	Van-0	CS76297
Oy-0	CS76203	Wei-0	CS76301
Kin-0	CS76153	Ws-0	CS76303
Kno-18	CS76154	Yo-0	CS76305
Ga-0	CS76133	Zdr-6	CS76306
Got7	CS76136	Hod	CS76141
Gy-0	CS76139	Kbs-Mac- 8	CS76151
Hr-5	CS76144	Köln	CS76155
LL-0	CS76172	LAC-3	CS76157
Lp2-2	CS76176	LDV-58	CS76163
Lp2-6	CS76177	Liarum	CS76166
Lz-0	CS76179	Krot-2	CS28420
Mr-0	CS76190	Li-7	CS28461
Mt-0	CS76192	Mc-0	CS28490
Nd-1	CS76197	Mh-0	CS28492
Pna-17	CS76213	Nc-1	CS28527
Pro-0	CS76214	No-0	CS28564
Pu2-23	CS76215	Udul	CS76269
Ra-0	CS76216	UKID101	CS76270
Ren-1	CS76218	UKNW06- 436	CS76278
Rsch-4	CS76222	UII2-3	CS76293

Figure S8. The fragment of *TERESTRA* from *A. cebennensis* clone 44. This sequence was identified by BLASTs in NCBI sequence database using *A. lyrata TERESTRA* consensus sequence. Domains were indicated in different colors according to Figure 4A: 5' LTR (grey), PBS (underlined) and GAG polyprotein (green).

TGAATAATACTGAACGGGTAAACAGAATTATGGTTAAGCTTAATTATGGGTTTATAATTCAATATCCTATATTGA
ACAAAACCCAAAGTTAAGCCAAAGTTCTAGATTTCTCTAGAGCATCATAGAAAAATCATCACCTCCTTAAGTGT
TCTAGAAAATTTTATTAAATAGATATTTAGATAATTATGTAGAATAAT
ATTTTAGTAGAGTTATAGAGATGATTTTAGAATAATCTAGAGACTTTGTAAGCTAACTTTGGAGGCTATAAATA
CCTCCTCACCCCCTCATTTGTAATCAAGTTGAACAAGTGAATAAAAAGAAAG
ATAAATTCTCTAAGTCTCTCTAAAAGTCTTTCAAGTAATCTCTAGTTGTTCTTCCAAATTTTCTATCATACTTAGA
GGATTTCTTATCTTGGTTATATCGAGTTTCTCGGGTATTACGGTCTTGGGCTAGTGCTAAGCACTATCGAGTC
GGTTTCTTTACATGA <u>TATCA</u> GAGCCATTCTAATCTTGTGCTCATCAAGATCAAGGTTATAGAGAACTCGGGTTT
ACTCTAAGTATGGAATCTATGGGTCGTGTTGTTGGATTGGGAATGGAGATC <mark>TTAAACCAATCTAACTACCGGT</mark>
TATGGAAGTCATGTATGGAGTCATACTTGGTTAGTGAGGACTTATGGGATGTCGTCGGCGGAAGTAGTACTT
CACCACCTACCGGAGATGCTGCTACTGCGGAAGCGACAAAGGAGTGGACACGTAAAAATGCCAAGGCGGAG
TTTGCTTTAAAGAGGTCAATATCCTCGGGAGTATTTGAGCATGTCTCAAGGTGTACATCCGCTAGTTCAATTT
GGCAAGCTTTAGATCTACTGTTCAACAAGAAGAACGAAGCTCGTCTATAATTGTTAGAAAACGAGTTGGCGAA
TGCGAAGCTGGGGGAGTCTTCAATCTCGGAGTTTTTCATCAAAGTCAAGAACCTTTGCTCTGAGATCAATAGT
CTTAATCCGGAGGAATCAATCTCGGATGCTCGGTTGAAGCGGTTTATTATTCGAGGTCTTAGACCCGAGTATA
CACCGTTTGTGACTTCGGTTCAAGGATGGGCTACACAACCTTCCTT
GCAAGAATCACTAGCGGTACAAATGGCGGGAGTCAAAATTCATGATGACTCGGGGGAGCGCTTTTGTAGCTAG
GAGGCAACACAACTTCAAAGCCAAATCCAATGATGGTGGTCCAAGAAAAAATGATGGACATGAAGGATCTTC
TAAGGGAGATAAGAAAAATTCAAGTGCTATCGGTGTGGAAAACTTGGGCATTTTAAAAAAGATTGCCGAGTC
AAGCTGAAGGAAACAAAGATGGCAAAATCAAAAGGTCATAATGAAGACGAAGAATGGGGAAAATGTTTTATG
GTGGAGGCTGCATCTTCAAGTACATCTACACCTAAGAAGGTGGAAAATAATTGGATCGTAGATTCTGGTTGTA
GCCATCATATCACCGGAGACGAGGAATTATTTTCTAGTCTTCAACGCCATGAAGGAAAAGAAGCAATCATTAC
CGCGAATAATTCAATCCATCACGTTGAGAAGGAAAGAACGGTGGTCATCAAAGGAGATGATGGAAGCCCAAT
CACTCTCGAGAACGTTTACCATGTTCCTGGAGTAAAAAAGAATCTTCTCTCCGTGGTAAATGCGGTGGAGTCA
GGTAACTATGTTTTATTTGGCCCAAGAGATGTTAAATTCTTAAAGAATATTCAAGAGTTAAAGGCGGACATGGT
TCACACTGGAGCACAGGTTAAAGATCTGTACGTTTTATCGGCGTTAAACTCTTATGTAGAGAAGAT

Figure S9. *A. halleri TERESTRA* reconstructed based on NCBI BLASTs using *A. lyrata TERESTRA* consensus sequence. Domains were indicated in different colors according to Figure 4A: 5' LTR (grey), PBS (underlined), GAG polyprotein (green), integrase (violet), reverse transcriptase (yellow), RNAse H1 (blue), PPT (red), 3' LTR (grey). Note that LTRs could not be reconstructed to a full length.

GGGTTTCTTATCTTGGTTATATCGAGTTTCTCGGATATTACGGTCTTGGGCTAGTGCTAAGCACTATCGAGTC GGTTTCTTTACATGG<u>TATCAGAGCCATTC</u>TAATCTTGTGCTCTTCAAGATCGGGGTTATAGAGAACTCGGGTT TACTCTAAGTATGGAATCTATGGGTCGTGTTGTTGGATTGGGAATGGAGATCTTAAACCAA GAAAGTCATGTATAGAGTCATACTTGGTTAGTGAGGACTTATGGGATGTCGTCGGCGGAAGTAATACT ACCACCTACCGGAGATGCTGCAACCGCGGAAGCGACAAAGGAGTGGACACGTAAAAATGCCAAGGCGGA GTTTGCTTTAAAGAGGTCAATATCTTCGGGAGTATTTGAGCATGTCTCAAGGTGCACATCCGCTAGTTCTAT GGCAAGCGTTAGATCGACTGTTCAACAAGAAGAACGAAGCTCGTCTACAATTGTTAGAAAACGAGTTGGC ATGCGAAGCAGGGGGGGGTCTTCAATCTCAGAGTTTTTCATCAAGGTAAAAAACCTTTGCTCTGAGATCAATA GTCTTAATCCGGAGGAATCAATCTCGGATGCTCGGTTGAAGCAGTTTATTATTCGAGGTCTACGACCCGAG TTCGCAAGAATCACTAGCGGTACAAATGGCGGGGGGTCAAAATTCATGATGACTCGGGGGGGCGCTTTTGTAGC TAGGAGGCAACACAACTTCAAAGCCAAATCTAATGATGGTGGTCCAAGAAATAATGATGGACATGAAGGATCT TCTAAGGGAGATAAGAAAAAATTCAAGTGTTATCGGTGTGGAAAACTTGGGCATTTTAAAAAGGATTGCCGAG TCAAGCTGAAGGAAACAAACATGGCGGAATCAAAAGGTCATAATGAAGACGAAGAATGAGGAAAATGTTTTA CGGTGGAGGCTGCATCTTCAAGTACATCTACACCTAAGAAAGTGGAAAATAATTGGATCGTAGATTCTGGTTG TAGCCATCATATCACTGGAGAGAGAGAAATTATTTTCTAGTCTTCAACGCCATGAAGGAAAAGAAGCAATCATT ATCACTCTCGAAAACGTTTACCATGTTCCTGGAGTAAAAAAGAATCTTCTCCCGTGGTGAATGTGGTGGACT CAGGTAACTATGTTTTATTTGGCCCAAGGGATGTTAAATTCTTAAAGAATATCCAAGAGTTAAAGGCGGACGC GCTTCACACTGGAGCACGGGTTAAAGATTTATACGTTTTATCGGCGTCAAACTCTTATGTGGAAAAGATGAGT TAAAGATTTGGTGAACGGGCTCCCAAAGTTGAAGATCCAAGATGGAGGCACAATTTGTGAAGGATGTCAATA TGGAAAATCTCATAGGCTTCCATTTGACTATTCCATTTCAAGGTGCAGTTTTCCGTTGGAGAGGGTCCACAGT GACTTGATGGGTCCGACAAGAACACCCTCATATTCCGGGTATCTCTACATGTTGTTGTTCGTTGACGACTTCT CTCGGTACACTTGGGTATACTTTGTGAAGGAAAAATCTGAAGTATTCTCCAAGTTTCTAGAATTCAAGGTTACC GTGGAAGGGGAGTTAGGTCAGAAGATCAAGACTTTAAGGACGGATAATGGAGGGGAGTTCATGTCTAAGGA GTTTCTCTCTTTTTGTCGAGATAATGGTATCAAGAGAGAATTTACATGTCCGCATACACCTCAACAAAATGGAG TAGCAGAGAGAGAAGATCAGACATCTAAGTGAGACGTGTAGAAGTTGGCTCCATGGAAAAGATTTGCCTAAGG CGTTATGGGCGGAAGGCATGAGATGTGCAGCTTATGTCATCAACCGGATGCCACTTAGTCCAAACAATATGA AGTCTCCTTATGAGATGGTTCATGGGAAGAAGCCAACGGTGAAACATCTCAGGATATTTGGATCAGTCTGCTT CGTCCATGTGTTTGATTCACAAAGAACCAAGTTGGAGGCAAAGGCGAAAAATGCATATTTGTCGGCTACGAT GAACAAAGGAAGGGTTGGAGGTGTATGGATTCCGAGACACAAGTATGTTGTGTCTCGTGATGTTGTCTTT GATGAAGTTTCTTCATACTACGGGTCACCTCAAGTCTTGGTTGAGAAAGATGGTGCTAATTCCTCTAAGAACG ATGAATCAACTCTCCAAGTACCATGTGAGAGTGGAAGTCCTGAAAATAAAATTCAAGGTGAAAAGGGGAGCA AGCCTGCAAGATATAGAGATGAAGTATTCATCACTACTTATTCATGCTTCTTCACAGCTCCTCTAGATGATGAT GAGCCATCTTCTTATGATGAAGCTAAAGGAGTTCAAGAATGGGAAGTTGCAATGAAGGAGGAGATGAGTGCT CTCAAGAAAAATGAAACTTGGCATCTGGTTCCAAAACCCCAAGGATGTTGAGCCCGTTTCTTGCAAATGGGTGT AAAAATATGGAGAAGATTATGATGAGACATTTAGTCCTGTGGCGAAGATGACAACTTGATGTGAAGAATGCTT TTCTATATGGTGAGCTTGATAAAAGTATCTTCATGGAGCAACCACCTGGTTTCGAATCGCGAGAGCATCCTGA TCATGTGTGCAAGCTGAAAAAGGCCTTGTACGGATTAAAACAAGCTCCACAAGCTTGGTATGGAAAGGTTGC TCAATTCCTTCAATTTTGTGGCTATGAGGCATCAAATTCTGACCCGAGTCTATTCTTCAAGAAGAAGGAGGAGGA TACAAGAAGACATGTCGATAAGGTTCGAGATGAAGAAGTTGGGTGAGCTGAATAACTTTCTTGGCCTAGAGG TTGAAAGAAGAAAGGATGGAATATTCGTTGGTCAACAAGGTTATGCAAGAAGGATTGTTGAGAAATTCAGGGT GCACGAAGGAAAGACGCGCACTACTCCGATGGATGTGACCATCAAGCTCAAACGTGATGAAGGTTCATTGTT ACCTGATCCTCGACCTTATCGCGCTCTTGTGGGAAGTCTTCTATACTTAACCATTACAAGACCTGATATTGCC TTCGCAGTAGGTCTGGTAAGTCGGTTTATGCAAGCACCAAGGAAACCACACTTAGAAGCGGCAAAGAAGATC TTGAAGTATGTCAAGACAACTCTTGACATGGGCTTGGTGTACAAGTACAATGCAAAGATTTCTCTTATT<mark>GGTTT</mark> TACGGATGCTGACTTTGGTGGAGATCTAGATGACCGAAAATCAACTTCGGGCAATGTGTTCTTATGTGGAGA CACAAGCATTTCGTGGTGTAGCAAGAAACAACCAACGGTATCGCTATCTACCACTGAAGCGGAGTATAAAGC AGCATATTGAGTTAGAACATCACTTCATAAGGGAGAAGGTTCTTGATGGAACAATTGAAGCCTTAGAAGTTCG AAGTGAGGACAACGTTGCGGACATCTTCACCAAGTCATTACCAAAAGGCCAATTCGAGTTACTTCGCTCGAA GCTCGGGATGGTTGACAAAATCAAGTTT<mark>AAGGGGGGAG</mark>TATTGAAGTTAAACTTGATTTTGGTTTAAGCTTAAT TATGGGTTTATAATTCAATATTCTATATTGGACAAAACCCAAAGTTAAGCCTAAGTTCTAGATTTCTCTAGAGC ACTCTTTAAAAGTTCTCTAAGTCTCTCCAAAAGTCTTTCAAGTAATCTCTAATTGTTCTTCCAAATTTTCTATCAT ACTTAGA

Figure S10. Heat responsive elements (HREs) found in 5' long terminal repeats of *TERESTRA* elements. All identified *TERESTRA* elements (irrespective of their heat-responsiveness) are shown. HRE types: red - 4P, yellow – gap, green – step.

		200	210	220	230	240	250	260	270
	BSTERESTRA 1	anaatttet	inceett	atcataaaaa.	- atratrar	ctettetaa	- tottotan	etatteene	taaat.t.
	BSTERESTRA 2	agaatttct	trtanaaata	attataaaa	attatcat	teteetetaa	a-tottotao	agaattata	ttaat-t-
	BSTERESTRA 8	aaaatttri	totagaaatt	- rataaaaaa	- atratrar	ctcttctaa	n-totoatao	anaattrta	ttaat-ta
	BSTERESTRA 9	agaatttci	trtaaaaari	ttraraaatr-	- atratrar	ttrtttaa	aantttan	agaattett	ttaat-t-
	BSTERESTRA 3	agaat	CTAGAAACI	Teacaa-atr	- atcatcac	ctctttgaa	naanttatan	aaaattett	ttaat-t-
	BSTERESTRA 4	agaatTTC	CTAGAAACI	TTCacaa-atc	atcatcac	ctctttGAA	AAGTTCTAG	AGAAttett	taat-t-
	BSTERESTRA 5	agaatTTC	CAAGAAAA	TTCacaaatc-	- atcatcac	ctctttGAA	GAAGTTCTAG	AGAAttett	ttaat-t-
B. stricta	BSTERESTRA 6	agaatTTC	CTAGAAACI	TTCacaa-atc	atcatcac	ctctttGAA	GAAGTTCTAG	AGAAttett	ttaat-t-
	BSTERESTRA 7	agaatTTC	CTAGAAACI	TTCacaa-atc	atcatcat	tctctttGAA	BAAGTTCTAG	AGAAttett	ttaat-t-
	BSTERESTRA 10	agaatTTC	CTAGAAACI	TTCacaaatc-	atcatcad	ttctttGAAG	BAAATTCTAG	AGAAttett	ttaat-t-
	BSTERESTRA 11	agaatTTCT	CTAGAAACI	TTCacaaatc-	atcatcad	ctctttGAA	AAGTTCTAG	AGAAttett	ttaat-t-
	BSTERESTRA 12	aaaa t TTC1	CTAGAAACI	TTCacaa-atc	atcatcad	ctctttGAA	GAAGTTCTAG	AGAAttett	ttaat-t-
	BsTERESTRA_13	agaa t <mark>TTC</mark> I	CTAGAAAC	TTCacaa-atc	atcatcad	ctctttgaa	BAAATTATAG	AAAATTCtt	ttaat-t-
	BsTERESTRA_14	agaa t <mark>TTC</mark> T	CTAGAAAC	TTCacaaatc-	atcatcad	ctcttt <mark>GAA</mark>	BAAGTTCTAG	AGAAttctt	ttaat-t-
	AITERESTRA_1	aga-tttc1	tctag-agca	atcatagaaaa	atcatcad	ctccttaaa	-tgttctag	agaattcta	ttaga-t-
	AITERESTRA_2	aga-tttc1	tctag-agca	atcatagaaaa	atcatcad	ctccttaaa	-tgttctag	agaattcta	ttaga-t-
A lyrata	AITERESTRA_3	aga-tttc1	tctag-agca	atcatagaaaa	atcatcad	ctccttaaa	- tgttctag	agaattcta	ttaga-t-
n. iyraid	AITERESTRA_4	aga-tttc1	tctag-agca	atcatagaaaa	atcatcad	ctccttaaa.	-tgttctag	agaatttta	ttaga-t-
	AITERESTRA_5	aga-tttc	tctag-agca	atcatagacaa	atcatcad	ctccttaaa.	-tgttctag	agaatteta	ttaga-t-
	AITERESTRA_6	aga-tttc1	to tag-agoa	atcatagaaaa	atcatcac	ctccttaaa.	- tgttctag	agaatttta	ttaga-t-
B rapa	Brierestra_1	agaatttt	CIAGAAata	attttaa-att	ttcgccad	ctcatcaaa	a-agticiag	agaatt	
Dirapa	BITERESTRA_2	agaatctct	ctagaaaaa	accataaaaga	tcaccaccac	ciccicaag	- igiiciag	agaicicci	tigga-t-
	ESTERESTRA_2	agaaattetet		ACICIAGAAGG	ligalcad	tteestaaa	g-lgilciag	agaaalttt	taagigi-
E salsu	ESTERESTRA_S	ayayıaıcı	to tagaaac.	- totanaaan	allillat	teteettaaay	- catttaa	addalltia	taayall-
L. Saisu-	ESTERESTRA 1	anagatttt	trtagtaar	actotattana	- ttaattar	cttcttaaa	- tottotag	agaagiiii	taage-t-
gineum	ESTERESTRA 4	agagattt	totataaaca	antitanaann	ttgatcac	atcottaaa	n-tottctag	aaaaatrta	taact-t-
	ESTERESTRA 5	agagattt	t c t a d a a a a c a	attttaaaadd	ttgatcad	ctccttata	- tottatao	aaaaaccta	taadt-t-
		170				51.5	500	500	5.10
		470	480	490	500	510	520	530	540
	BsTERESTRA_1	470 a t	480	490 caacttgaat:	500 aagtgaaata	510 taaaaataa	520 cttcaa	530 agaaaaag	540 -tgtttt
	BsTERESTRA_1 BsTERESTRA_2	470 at at	480	490 caacttgaata taacttgaata	500 aagtgaaata aagtgaa-at	510 taaaaaataa aaaaa	520 cttcaa	530 agaaaaag	540 -tgtttt
	BsTERESTRA_1 BsTERESTRA_2 BsTERESTRA_8	470 a t	480	490 caacttgaata taacttgaata caatttaaata	500 aagtgaaata aagtgaa-at aagtgaagt-	510 taaaaataa aaaaa aaaaagcaag	520 cttcaa ttcaaa	530 agaaaaag- agaaagac	540 -tgtttt -ggtttt
	BsTERESTRA_1 BsTERESTRA_2 BsTERESTRA_8 BsTERESTRA_9	470 at at at actatccaa	480 g	490 caacttgaata taacttgaata caatttaaata aaga	500 aagtgaaata aagtgaa-at aagtgaagt- aagtgaa-at	510 taaaaaataa aaaaa aaaaagcaag aaaaagagag	520 cttcaa ttcaaa ttta	530 agaaaaag agaaagac agaaagag	540 - tgtttt - ggtttt - tgttct
	BSTERESTRA_1 BSTERESTRA_2 BSTERESTRA_8 BSTERESTRA_9 BSTERESTRA_3 D=TFFFERTA_4	470 at at at	480 g	490 caacttgaat taacttgaat caatttaaat aag	500 aagtgaaata agtgaa-at agtgaagt- agtgaa-at agtgaa-at	510 taaaaaataa aaaaa aaaaagcaag aaaaagagag	520 c t t c a a t t c a a a t t t a t t t a	530 agaaaaaga agaaagac agaaagag acaaagag	540 - tgtttt - ggtttt - tgttct - tgttct
	BSTERESTRA_1 BSTERESTRA_2 BSTERESTRA_8 BSTERESTRA_9 BSTERESTRA_3 BSTERESTRA_4 DSTERESTRA_4	470 at at actatccaa actatcaaa accatccaa	480 g	490 caacttgaat taacttgaat caatttaaat aag 	500 aagtgaaata aagtgaa-at aagtgaagt- aagtgaa-at aagtgaaata aagtgaaata	510 taaaaaataa aaaaagcaag aaaaagagag aaaaagagag	520 c t t c a a t t c a a a t t t a t t t a t t t a	530 agaaagac agaaagac agaaagag acaaagag agaaagag	540 - tgtttt - ggtttt - tgttct - tgttct - tgttct
B. stricta	BSTERESTRA_1 BSTERESTRA_2 BSTERESTRA_8 BSTERESTRA_9 BSTERESTRA_3 BSTERESTRA_3 BSTERESTRA_4 BSTERESTRA_5 BSTERESTRA_5	470 a t	480 g	490 caacttgaat caatttaatt aag aag	500 aagtgaaata aagtgaa-at aagtgaa-at aagtgaa-at aagtgaa-at aagtgaa-at		520 c t t c a a t t c a a t t t a t t t a t t t a	530 agaaagag agaaagag agaaagag agaaagag agaaagag agaaagag	540 - tgtttt - ggtttt - tgttct - tgttct - tgttct - tgttct - tgttct
B. stricta	BSTERESTRA_1 BSTERESTRA_2 BSTERESTRA_8 BSTERESTRA_8 BSTERESTRA_3 BSTERESTRA_4 BSTERESTRA_6 BSTERESTRA_6 BSTERESTRA_6	470 at at actatccaa actatccaa accatccaa accatccaa actatccaa	480 9	490 caacttgaat taacttgaat caatttaaat aag aag aag	500 aagtgaaata aagtgaaata aagtgaaata aagtgaaata aagtgaaata aagtgaaata aagtgaaata	510 taaaaataa aaaagcaag aaaaggagg aaaagagagg aaaagagagg	520 t t t c a a a t t c a a a t t t a t t t a t t t a t t t a	530 agaaaaagag - agaaagagag - agaaagagag - agaaagag - agaaagag - agaaagag - agaaagag -	540 - tgtttt - ggttt - tgttct - tgttct - tgttct - tgttct - tgttct - tgttct
B. stricta	BSTERESTRA_1 BSTERESTRA_2 BSTERESTRA_8 BSTERESTRA_9 BSTERESTRA_3 BSTERESTRA_3 BSTERESTRA_5 BSTERESTRA_6 BSTERESTRA_7 BSTERESTRA_7	470 at at actatccaa actatccaa accatccaa actatccaa actatccaa actatccaa	480 9 9 9 9 9 9 9 9 9 9 9 9 9 9	490 caacttgaat taacttgaat caatttaaat caatttaaat aag aag aag	500 aagtgaaata aagtgaaata aagtgaaata aagtgaaata aagtgaaata aagtgaaata aagtgaaata		520 tttaa ttta ttta ttta ttta ttta	530 agaaagag agaaagag agaaagag agaaagag agaaagag agaaagag agaaagag agaaagag	540 - tgtttt - ggtttt - tgttct - tgttct - tgttct - tgttct - tgttct - tgttct - tgttct
B. stricta	BSTERESTRA_1 BSTERESTRA_2 BSTERESTRA_2 BSTERESTRA_9 BSTERESTRA_3 BSTERESTRA_4 BSTERESTRA_4 BSTERESTRA_6 BSTERESTRA_7 BSTERESTRA_10 BSTERESTRA_10 BSTERESTRA_110	470 atat atat at.t.caa actatccaa actatccaa actatccaa actatccaa actatccaa	480 , 9	490 c aac t t gaa t t aac t t gaa t c aa t t t aaa t aag aag aag aag	500 aagtgaaata aagtgaa-at aagtgaa-at aagtgaa-at aagtgaa-at aagtgaa-at aagtgaa-at aagtgaa-at		520 t t t c a a t t c a a a t t t a t t a t t a t a t a t a t a t a t a t a t	530 agaaagag agaaagag agaaagag agaaagag agaaggag - agaaggag - agaaggag - agaaggag - agaaggag	540 - tgtttt - tgtttt - tgttct - tgttct - tgttct - tgttct - tgttct - tgttct - tgttct - tgttct
B. stricta	BSTERESTRA_1 BSTERESTRA_2 BSTERESTRA_9 BSTERESTRA_9 BSTERESTRA_3 BSTERESTRA_4 BSTERESTRA_4 BSTERESTRA_6 BSTERESTRA_7 BSTERESTRA_10 BSTERESTRA_12	470 at at actatccaa actatccaa actatccaa actatccaa actatccaa actatccaa actatccaa	480	490 caacttgaat caacttgaat caatttaaat aag aag aag 	500 aagtgaaata aagtgaaata aagtgaaata aagtgaaata aagtgaaata aagtgaaata aagtgaaat aagtgaaat aagtgaaata		520 t t c c a a t t c a a a t t t	530 a g a a a a g a c - a g a a a g a c - a g a a a g a c - a g a a a g a g - a g - a g a a g a g - a	540 - tgtttt - tgtttt - tgttct - tgttct - tgttct - tgttct - tgttct - tgttct - tgttct - tgttct - tgttct - tgttct
B. stricta	BSTERESTRA_1 BSTERESTRA_2 BSTERESTRA_8 BSTERESTRA_9 BSTERESTRA_3 BSTERESTRA_4 BSTERESTRA_4 BSTERESTRA_5 BSTERESTRA_7 BSTERESTRA_10 BSTERESTRA_11 BSTERESTRA_12 BSTERESTRA_12 BSTERESTRA_13	470 at	480	490 caacttgaat taacttgaat caatttaaat aag aag 	500 aagtgaaata aagtgaaata aagtgaaata aagtgaaata aagtgaaata aagtgaaata aagtgaaata aagtgaaata aagtgaaata		520 ttcaaa ttcaaa ttta ttta ttta ttta ttta ttta ttta ttta ttta ttta ttt	530 a g a a a a g a c - a g a a a g a g a c - a g a a a g a g a - a g a a a g a g a - a g a a a g a g a - a g a a a g a g a - a g a a a g a g - a g - a g a g - a g -	540 - tgtttt - tgttt - tgttct - tgttct
B. stricta	BSTERESTRA_1 BSTERESTRA_2 BSTERESTRA_3 BSTERESTRA_3 BSTERESTRA_3 BSTERESTRA_4 BSTERESTRA_4 BSTERESTRA_6 BSTERESTRA_7 BSTERESTRA_10 BSTERESTRA_11 BSTERESTRA_12 BSTERESTRA_13 BSTERESTRA_13	470 at at actatccaa actatccaa actatccaa actatccaa actatccaa actatccaa actatccaa actatccaa actatccaa actatccaa actatccaa actatccaa	480 , 9	490 caact t gaa t caact t gaa t caatt t aact aag aag aag aag aag aag aag aag aag aag	500 aagtgaaata aagtgaaata aagtgaaata aagtgaaata aagtgaaata aagtgaaata aagtgaaata aagtgaaata aagtgaaata aagtgaaata		520 t t c a a a t t c a a a t t t	530 a g a a a g a c a g a a a g a g a c a g a a a g a g a a g a a a g a g a a g a a a g a g a g a a a g a g	540 - tgitit - tgitct - tgitct
B. stricta	BSTERESTRA_1 BSTERESTRA_2 BSTERESTRA_9 BSTERESTRA_3 BSTERESTRA_4 BSTERESTRA_4 BSTERESTRA_6 BSTERESTRA_16 BSTERESTRA_11 BSTERESTRA_11 BSTERESTRA_12 BSTERESTRA_13 BSTERESTRA_14 ATTERESTRA_14	470 atat atat at.at.caa actat.caa	480 9	490 c a a c t t g a t t t a a c t t g a t t c a a t t t a a t t a a g a a g 	500 aagtgaaata aagtgaa-at aagtgaa-at aagtgaa-at aagtgaa-at aagtgaa-at aagtgaa-at aagtgaa-at aagtgaa-at aagtgaa-at aagtgaa-at aagtgaa-at aagtgaa-at aagtgaa-at		520 t t c a a a t t a a t t a t a t a t		540 - tgtttt - tgttt - tgttt - tgttct - tgttct
B. stricta	BSTERESTRA_1 BSTERESTRA_2 BSTERESTRA_9 BSTERESTRA_3 BSTERESTRA_4 BSTERESTRA_4 BSTERESTRA_6 BSTERESTRA_6 BSTERESTRA_10 BSTERESTRA_10 BSTERESTRA_11 BSTERESTRA_12 BSTERESTRA_13 BSTERESTRA_14 AITERESTRA_14 AITERESTRA_14	470 ata ata at.at.caa actatccaa actatccaa actatccaa actatccaa actatccaa actatccaa actatccaa actatccaa actatccaa actatccaa actatccaa actatccaa actatccaa actatccaa	480	490 caacttgaat taacttgaat caatttaaat 	500 aagtgaaata aagtgaaata aagtgaaata aagtgaaata aagtgaaata aagtgaaata aagtgaaata aagtgaaata aagtgaaata aagtgaaata aagtgaaata aagtgaaata aagtgaaata aagtgaaata aagtgaaata		520 1 1 c c a a 1 1 c a a a 1 1 t a 1 1 t a 1 1 t a 1 1 t a 1 t t		540 - tgtttt - tgtttt - tgttct - tgttct
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B. stricta A. lyrata B. rapa	BSTERESTRA_1 BSTERESTRA_2 BSTERESTRA_9 BSTERESTRA_3 BSTERESTRA_4 BSTERESTRA_4 BSTERESTRA_6 BSTERESTRA_6 BSTERESTRA_10 BSTERESTRA_10 BSTERESTRA_10 BSTERESTRA_10 BSTERESTRA_12 BSTERESTRA_13 BSTERESTRA_14 AITERESTRA_2 AITERESTRA_2 AITERESTRA_3 AITERESTRA_3 AITERESTRA_3 AITERESTRA_4 BSTERESTRA_6 BTERESTRA_1 BSTERESTRA_2 ESTERESTRA_2 ESTERESTRA_2 ESTERESTRA_2 ESTERESTRA_2 ESTERESTRA_2 ESTERESTRA_2 ESTERESTRA_2	470 at	480 9 9 9 9 9 9 9 9 9 9 9 9 9	490 c a a c t t g a a t t a a c t t g a a t c a a t t t a a a t c a a g t c a a g t c a a g t t g a a c g a g g t a a c c A A G TTGAAC/ GAAGTTGAAC/ g a g g t a a c c a a g t g a c c a g a g a c c a g a g a c c a a g t g a c c a a g t g a c c a a g t g a c c a a g a c c a a g a g a c c a a g a c c a a g a a a c c a a g a c c a a g a a c c a a g a c c a a a a a c c a a a a c c a a a a a a c c a a a a a a a a a a a a a a a a a a a	500 aagtgaaata aagtaaaaa aagtaaaaa aagtaaaaa		520 1 1 c a a a 1 t c a a 1 t t	530 agaaagag - agaaagag - agaagag - agaagaagaagaagaagaagaagaagaagaagaagaaga	540 - tgtttt - ggtttt - tgttct - cgttct - cactct - cactct - cactct - cactct - cactct - cactct
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B. stricta A. lyrata B. rapa E. salsu- gineum	BSTERESTRA_1 BSTERESTRA_2 BSTERESTRA_3 BSTERESTRA_3 BSTERESTRA_4 BSTERESTRA_4 BSTERESTRA_6 BSTERESTRA_6 BSTERESTRA_7 BSTERESTRA_11 BSTERESTRA_12 BSTERESTRA_12 AITERESTRA_13 BSTERESTRA_14 AITERESTRA_2 AITERESTRA_2 AITERESTRA_2 AITERESTRA_4 AITERESTRA_4 BSTERESTRA_6 BITERESTRA_2 ESTERESTRA_2 ESTERESTRA_2 ESTERESTRA_2 ESTERESTRA_2 ESTERESTRA_2 ESTERESTRA_2 ESTERESTRA_2 ESTERESTRA_3 ESTERESTRA_6 ESTERESTRA_7 ESTERESTRA_7 ESTERESTRA_7 ESTERESTRA_7 ESTERESTRA_7 ESTERESTRA_7 ESTERESTRA_6 ESTERESTRA_7	470 atat at.at.caa actatcaa accatccaa actatccaa acacaca acaa acaa acaa actatccaa acaa actatccaa	480 9	490 c a a c t t g a t t t a a c t t g a t t c a a t t t a a t c a a t t t a a t c a a t t a a t c a a t t a a t c a a t t a a a t c a a t a a a t c a a t g a a t c a a a t g a a c c a a a t g a a c c a a g t t g a c c a a t g a c c a a g t t g a c c a a g t t g a c c a a t g a c c a a g t t g a c c a a c t g a c c a a g t t g a c c a a c t g a c c a a g t t g a c c a a c t g a c c c a a g t t g a c c a a c t g a c c c a a g t t g a c c a a c t g a c c c a a g t t g a c c a a c t g a c c c a a g t t g a c c a a c t g a c c c a a c t c c c c c c c c c c c c c c c	500 aagtgaaata aagtaaaata aagtaaaata aagtaaaata aagtaaaata aagtaaata aagtaaata aagtaaata		520 ttt aaa ttt a ttt	530 a g a a a g g c a g a a g g g a g a g g a	540 - tgtttt - ggtttt - tgtct - cactct - cactctt - cactctt - cactct - cactctt - cactcttt - cactctt - cactctt - cactcttt - cactcttt - cactctt - cactcttt - cac
B. stricta A. lyrata B. rapa E. salsu- gineum	BSTERESTRA_1 BSTERESTRA_2 BSTERESTRA_3 BSTERESTRA_3 BSTERESTRA_4 BSTERESTRA_6 BSTERESTRA_6 BSTERESTRA_6 BSTERESTRA_10 BSTERESTRA_10 BSTERESTRA_10 BSTERESTRA_12 BSTERESTRA_12 BSTERESTRA_14 AITERESTRA_14 AITERESTRA_2 AITERESTRA_2 AITERESTRA_3 AITERESTRA_3 AITERESTRA_4 BSTERESTRA_2 ESTERESTRA_2 ESTERESTRA_2 ESTERESTRA_2 ESTERESTRA_2 ESTERESTRA_2 ESTERESTRA_3 ESTERESTRA_1 ESTERESTRA_1 ESTERESTRA_6 ESTERESTRA_1 ESTERESTRA_1 ESTERESTRA_1 ESTERESTRA_1 ESTERESTRA_1 ESTERESTRA_1 ESTERESTRA_1 ESTERESTRA_1 ESTERESTRA_1 ESTERESTRA_1 ESTERESTRA_1 ESTERESTRA_1 ESTERESTRA_1 ESTERESTRA_1 ESTERESTRA_1 ESTERESTRA_1 ESTERESTRA_1 ESTERESTRA_2 ESTERESTRA_1 ESTERESTRA_1 ESTERESTRA_1 ESTERESTRA_1 ESTERESTRA_2 ESTERESTRA_1 ESTERESTRA_2 ESTERESTRA_1 ESTERESTRA_2 ESTERESTRA_	470 atat atat at.at.caa actatccaa accatccaa	480 9	490 caacttgaat taacttgaat caatttaaat 	500 aagtgaa a aagtgaa a aagtgaa at aagtgaa at aat agtgaa at aat agtgaa at at aat agtgaa at at aat at aat at aat at aat at at at				540 - tgtttt - ggtttt - tgttct - cactct - cactct

Figure S11. Transcriptional response of *ONSEN*, *COPIA37* and *TERESTRA* to DNA methylation inhibitor treatments in *A. lyrata*. Relative transcript accumulation after 48 h control, 10 μ M 3-deazaneplanocin A (DZNep) and 40 μ M zebularine treatment. Transcript amounts were normalized to *UBC28*. Error bars indicate variation between two biological replicates and * shows statistically significant differences at $\alpha = 0.05$ in Student's T-test.





Figure S12. Density of RNA-sequencing reads mapping over *APUM9 – ROMANIAT5-2* region.

Figure S13. Putative heat responsive elements (HREs) in 5'/3' long terminal repeats of *ROMANIAT5* elements. HRE types: orange – 3P, yellow – gap, green – step.

		320	330	340	350	360	370
	BsRomaniaT5_5	cgtattca	atattgac	TCACCATTCT	TCTCGAGTTC	tgagtgtaag	gag-aaaaa
P otriata	BsRomaniaT5_4	tgtattca	acactgat		TCTCGAGTTC	tgtgtgtaag	gag-aaaaa
D. SINCIA	BsRomaniaT5_8	tgtattca	acactgatt	ttctgatttt	tctcgagctct	tgtgtgaaag	gagaaaaaa
	BsRomaniaT5_9	tgtattca	acactaatt	tcctgatttt	tttcgagctc1	tgtgtgtaaa	aag-aaaaa
C rubolla	CrRomaniaT5_1	tgtattgg	atgtcaac		CTTCGAGTTC	tgagtataag	gaa-aaaaa
C. Tubella	CrRomaniaT5_4	tatactgg	atatcaac		TCTCGAGTTC	cgagtgtagg	gag-aaaaa
	AtROmaniaT5_1	tgtattgc	a c TTCTACT	ТССТТСТТС	tctcgagctct	tgagtgtagg	gag-aagaa
∆ thaliana	AtRomaniaT5_3	tgtattgc	a c TTCTACT	тссттеттс	tctcgagttct	tgagtgtagg	gag-aagaa
A. thanana	AtRomaniaT5_4	tgtattgc	a c <mark>TTCTAC</mark> T	TCCTTGTTC	tctcgagctc1	tgagtgtagg	gag-aagaa
	AtRomaniaT5_2	tgtattgc	acctctac	тссттоттст	TCTCGAGTTC	tgagtgtaag	gag-aagaa
	BrRomaniaT5_1	aatactcg	atgtccact	tctttattt	tctcgagctco	cttatgtaco	gag-aaaaa
	BrRomaniaT5_2	catactca	atgtccact	tctttattt	tctcgagctct	tttatgtaco	gag-aaaaa
P ropo	BrRomaniaT5_3	tatactcg	atgtccact	tctttattt	tctcgagctco	tttatgtaco	gag-aaaa-
Б. Тара	BrRomaniaT5_6	catactcg	atgtccact	tctttattt	tctcgagctct	cgtatgtatg	gag-aaaaa
	BrRomaniaT5_7	catactca	atgtccact	tctttattt	tctcgagctco	cggacgtato	gag-aaaaa
	BrRomaniaT5_8	catactcg	atgtccac		TCTCGAGTTC	cgtatgtaco	gag-aaaaa
	EsRomaniaT5_7	catactgg	atatcgact	tcttgatttt	tctcgagctct	tgggtgtaag	gag-aaaaa
	EsRomaniaT5_9	catactgg	atatcgact	tcttgattct	tctcgagctct	tgagtataag	gag-aaaaa
E. salsu-	EsRomaniaT5_36	catattgg	a ta <mark>TTCAC</mark> T	TCCTGATTC	tctcgagttct	tgagtgtaag	gag-aaaaa
gineum	EsRomaniaT5_20	catattgg	a t a TTCACT	TCTCAATTAT	TCtcgatttct	tgagtgtaag	gaa-aaaaa
ginean	EsRomaniaT5_12	catattgg	atatccac		TCTAGAGTTC	tgagtgtaag	gag-aaaaa
	EsRomaniaT5 60	catattga	atatccac		TCTCGAGTTC	tgagtataad	gag-aaaaa

At - Arabidop	osis thaliana			
Al - Arabidop	sis lyrata			
Ba - Ballantir	nia antipoda			
Bs - Boecher	a stricta			
Br - Brassica	rapa			
Cr - Capsella	rubella			
Es - Eutrema	salsugineun	ז		
Target	Species	Primer name	Sequence (5' to 3')	Application
COPIA20	At, Al	C20_qF2	TACATGAAGCCACCACCGGGT	RT-qPCR
	At, Al	C20_qR3	TCATCTCCGGGAATGACAAGGTA	RT-qPCR
COPIA37	At	AtC37_F2	AGCTTAACTACAGAAGGGAAGGA	RT-qPCR
	At	AtC37_R2	CTCTCCAATCTCTCATTTTCTCG	RT-qPCR
	Cr	CrC37_F1	GGAGGTAGGTGAGACAAGACA	RT-qPCR
	Cr	C37_LTRR1	AACCGCTACGTCTCGGGG	RT-qPCR
	Al	AlyC37qF3	AACGCAGCCGAAGCTAATC	RT-qPCR
	AI	AlyC37qR3	CTCCATCACCGGCTAACAAC	RT-qPCR
	Br	EsC37-u_F1	ACAGGTGGGyCTTTAATGGGC	RT-qPCR
	Br, Es	C37_u_LTRR1	AACCGSTACGTCTCGGGG	RT-qPCR
	Es	EsC37_F1	ACAGGTGGGTCTTTAATGGGC	RT-qPCR
COPIA78	At, Bs	AtCOPIA78qF2	CGGTGCTCACAAAGAGCAACTATG	RT-qPCR
	At, Bs	AtCOPIA78qR3	ATCCTTGATAGATTAGACAGAGAGCT	RT-qPCR
	Al	AICOPIA78qF3	ACAATGCTCACAAAGAGCAACTATG	RT-qPCR
	Al	COPIA78qR3	ATCCTTGATAGATTAGACAGAGAGCT	RT-qPCR
	Ba	Ba_ONS_F1	ACATGTACCGGATGAGAAGCG	RT-qPCR
	Ba	Ba_ONS_R1	TGTGTCCGGGTTGTAGAGCT	RT-qPCR
	Br	Br_ONS_F1	TTGCGTGCATGATGTCAGGT	RT-qPCR
	Br	Br_ONS_R1	ACGCCAATGGAATGTCGAGT	RT-qPCR
	Es	EsONS_F5	GTCTTGGCTTTGGCATCTTC	RT-qPCR
	Es	EsONS_R5	GCGCTCTTGTTTCTGACTCC	RT-qPCR
GAPC-2	At, Al, Ba, Bs, Br, Cr, Es, Aa	GAPC-2_F	ATCGGTCGTTTGGTTGCTAGAGT	RT-qPCR
	At, Al, Ba, Bs, Br, Cr, Es, Aa	GAPC-2_R	ACAAAGTCAGCTCCAGCCTCA	RT-qPCR
GFP-4	At	GFP4-F	GGCACGACTTCTTCAAGAGC	RT-qPCR
	At	GFP4-R	AAAGGGCAGATTGTGTGGAC	RT-qPCR
TERESTRA	Bs, Br, Es	TERESTRA_F1	TCATGTATGGAGTCATACTTGGT	RT-qPCR
	Bs, Br, Es	IERESTRA_u_R		RI-qPCR
	At, Al	TERESTRAF2	GTATTACGGTCTTGGGCTAGTG	RT-qPCR
	At, Al	TERESTRA_R2	ACCAAGTATGACTCCATACATGAC	RT-qPCR
HSP101	At	HSP101aF	TGAGCTAGCTGTGAATGCAGGACATGCTC	RT-aPCR

 Table S4.
 Primers used in this study.

	At	HSP101qR	ATCACTCTTTCAGCAGATTGAGCTGCGTT	RT-qPCR
ROMANIAT5	At, Al, Br, Bs, Cr, Es	RT5_gener_F2	CGTGGAGGGATATGCTTCGTT	RT-qPCR
	At, Al, Br, Bs, Cr, Es	RT5_gener_R2	TGCAATCTCGTGGCGTTCT	RT-qPCR
	At	ROMANIAT5-2qF	TTGTCACTTGAACGAATGTATTGCACC	RT-qPCR
	At	ROMANIAT5-2qR	GCCAACAAGAATATATGAAGATAATGC	RT-qPCR
	At	ROM_sense	TTCCAATGCTTTGAACATGA	cDNA synthesis
	At	ROM_antiS	TGAATACATCACGAGAAAAGA	cDNA synthesis
PUM9	At	PUM9qF	CATGGTTCCCATTCAGATCTTTGACA	RT-qPCR
	At	PUM9qR	TTTAGTCAACAAGTCCACGAGCTCA	RT-qPCR
	At	PUM9_sense	TCACGTGGCTACTAAACTTCT	cDNA synthesis
	At	PUM9_antiS	AGCTTAACTTCCGAGGAG	cDNA synthesis
UBC28	At,Al, Ba, Bs, Br, Cr, Es, Aa	UBC28qF	TCCAGAAGGATCCTCCAACTTCCTGCAGT	RT-qPCR
	At, Al, Ba, Bs, Br, Cr, Es, Aa	UBC28qR	ATGGTTACGAGAAAGACACCGCCTGAATA	RT-qPCR
18S	At	18S-1062-F	TTATAGGACTCCGCTGGCAC	RT-qPCR
	At	18S-1345-R	CAGGCTGAGGTCTCGTTCAT	RT-qPCR