

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 species-specific families.

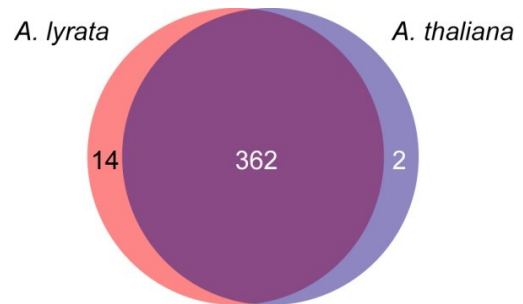


Figure S2. Unrooted phylogenetic tree of heat-responsive and -non-responsive COPIA TEs. The tree is based on the reverse transcriptase amino acid sequences (Additional file 10) of the following heat-responsive (ONSEN, TERESTRA, COPIA37 and ROMANIAT5) and -non-responsive (COPIA19, COPIA23, COPIA35, COPIA45,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

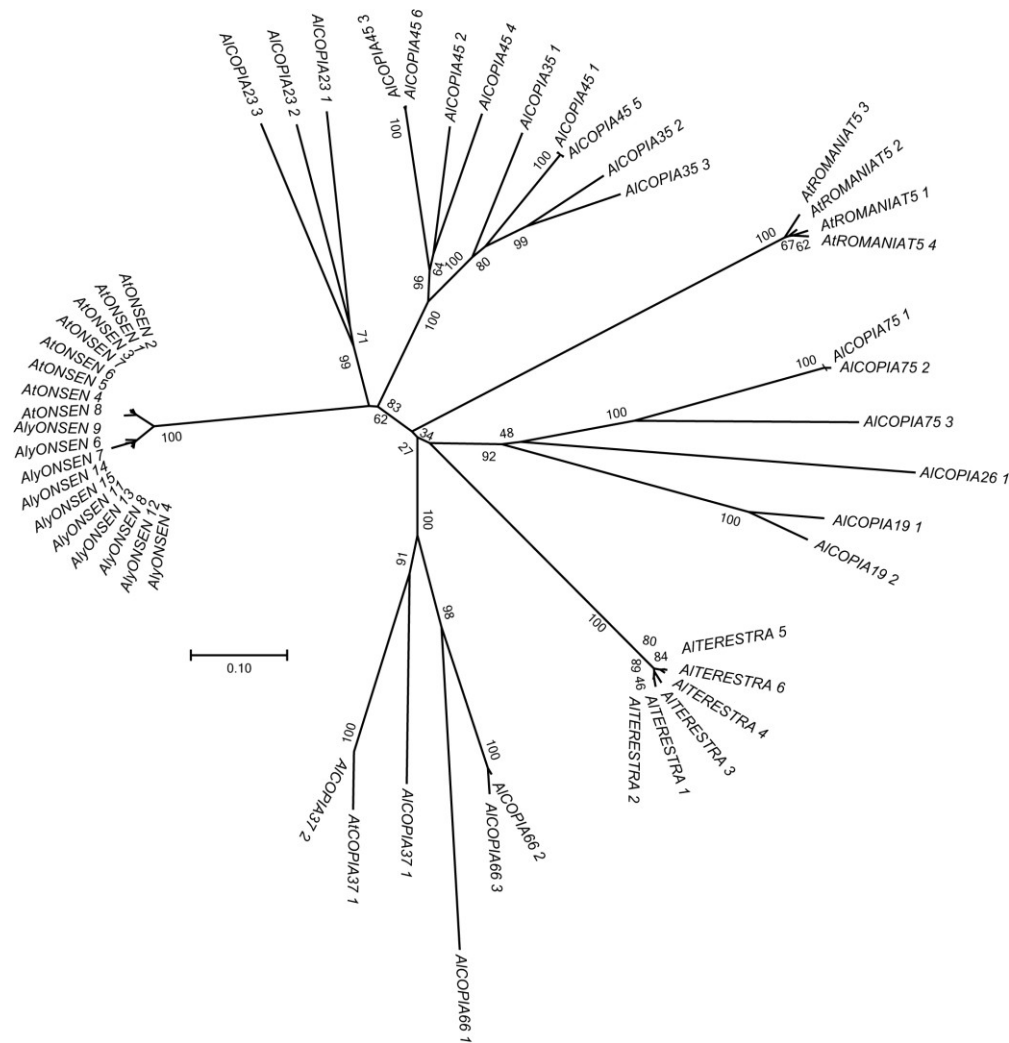


Table S1. List of *ONSEN* elements in *A. thaliana* Col-0 genome. *Heat responsiveness is based on the RNA-sequencing data of this study. **Names of *ONSEN1* to *ONSEN8* are based on Cavrak et al., 2014; HRE - Heat responsive element. RT - reverse transcriptase. ***Additional sequence insertion between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

	Element**	AGI code	Chr	Start	End	Size	Type	HRE
Heat responsive*	<i>AtONSEN1</i>	AT1TE12295	1	3780765	3785720	4956	full-length	4P
	<i>AtONSEN2</i>	AT3TE92525	3	22695566	22700521	4956	full-length	4P
	<i>AtONSEN3</i>	AT5TE15240	5	4208083	4213084	5002	full-length	4P
	<i>AtONSEN4</i>	AT1TE71045	1	21524995	21529850	4855	full-length	3P
	<i>AtONSEN5</i>	AT1TE59755	1	18013162	18018117	5273	full-length	4P
	<i>AtONSEN6</i>	AT3TE89830	3	22059535	22064329	4795	full-length	4P
	<i>AtONSEN7</i>	AT1TE24850	1	7714708	7715145	438	full-length***	4P
				7717356	7722547	5191		
<i>AtONSEN8</i>	AT3TE54550	3	13369174	13374107	4934	full-length	4P	
Heat-non responsive*								
	<i>AtONSEN9</i>	AT1TE57015	1	17201388	17201573	185	truncated solo LTR	none
				17201917	17202175	258		
	<i>AtONSEN10</i>	AT1TE10935	1	3360540	3361316	776	pre-Integrase region	none
	<i>AtONSEN11</i>	AT2TE45420	2	10582288	10582517	229	fragmented solo LTR	none
	<i>AtONSEN12</i>	AT2TE26505	2	6483643	6483961	318	fragmented solo LTR	none
	<i>AtONSEN13</i>	AT2TE12265	2	2780086	2781859	1773	fragment - RT & Rnase_H1	none
	<i>AtONSEN14</i>	AT2TE62740	2	14190558	14191027	469	RT fragment	none
	<i>AtONSEN15</i>	AT3TE59075	3	14401313	14403971	2658	RT & Rnase_H1+3'LTR	none
	<i>AtONSEN16</i>	AT3TE59080	3	14403653	14403946	293	fragment of 5'LTR and gag-polyprotein	none
	<i>AtONSEN17</i>	AT3TE31680	3	7539914	7540288	274	solo LTR	none
	<i>AtONSEN18</i>	AT4TE42010	4	9320200	9320565	265	truncated solo LTR	none

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	Type	HRE	Ito et al. (2013)
Heat responsive*	<i>AIONSEN1</i>	1	11268872	11273881	5010	full-length	gap/step	5
	<i>AIONSEN2</i>	1	24919344	24919772	429	solo LTR	gap	n.a.
	<i>AIONSEN3</i>	2	1120762	1121196	440	solo LTR	none**	n.a.
	<i>AIONSEN4</i>	2	4268383	4273330	4978	full-length	gap/step	3
	<i>AIONSEN5</i>	2	12788861	12789817	956	solo LTR	gap/step	n.a.
	<i>AIONSEN6</i>	3	13033504	13038475	4972	full-length	gap + 4P	2
	<i>AIONSEN7</i>	3	14350695	14355704	5010	full-length	gap + 4P	1
	<i>AIONSEN8</i>	3	23055604	23059108	3504	contig end	gap	n.a.
	<i>AIONSEN9</i>	4	16304811	16309766	4956	full-length	gap + 4P	10
	<i>AIONSEN10</i>	5	4327023	4327410	388	solo LTR	4P	17
	<i>AIONSEN11</i>	5	9883484	9888427	4944	full-length	gap + 4P	7
	<i>AIONSEN12</i>	6	22653438	22658398	4961	full-length	gap	4
	<i>AIONSEN13</i>	7	23781774	23786710	4937	full-length	gap	7
	<i>AIONSEN14</i>	8	15966326	15970217	3892	full-length	gap + 4P	n.a.
	<i>AIONSEN15</i>	247	3711	8654	4944	full-length	gap + 4P	8
	<i>AIONSEN16</i>	1007	2411	3818	1408	contig end	none**	n.a.
	<i>AIONSEN17</i>	638	3577	4818	1242	contig end	gap + 4P	12
	<i>AIONSEN18</i>	7	8283764	8284127	363	fragmented solo LTR	none	n.a.
	<i>AIONSEN19</i>	1007	42	1686	1645	RT	none	n.a.
Heat-non responsive*	<i>AIONSEN20</i>	3	14003080	14004319	1239	truncated 5'LTR & gag-polypeptide	none	n.a.
	<i>AIONSEN21</i>	3	14016614	14019627	3013	RT & RNase H1 & 3'LTR	none	n.a.
	<i>AIONSEN22</i>	1	10332397	10332510	113	3'LTR fragment	none	n.a.
	<i>AIONSEN23</i>	1	13615947	13616317	370	fragmented solo LTR	none	n.a.
	<i>AIONSEN24</i>	1	24919900	24920073	173	solo LTR fragment	none	n.a.
	<i>AIONSEN25</i>	1	25691749	25692168	419	RT fragment	none	n.a.
	<i>AIONSEN26</i>	1	25692678	25692869	191	RNase H1 fragment	none	n.a.
	<i>AIONSEN27</i>	2	11661689	11661997	308	solo LTR fragment	none	n.a.
	<i>AIONSEN28</i>	2	10259067	10259437	370	fragment	none	n.a.
	<i>AIONSEN29</i>	2	10974958	10975001	43	LTR fragment	none	n.a.
	<i>AIONSEN30</i>	2	11911062	11911137	75	LTR fragment	none	n.a.
	<i>AIONSEN31</i>	3	9491471	9491721	250	fragment	none	n.a.
	<i>AIONSEN32</i>	3	14002611	14002810	199	truncated solo LTR	4P***	n.a.

<i>AIONSEN33</i>	3	23040531	23040611	80	solo LTR fragment	none	n.a.
<i>AIONSEN34</i>	4	15133412	15133767	355	solo LTR fragment	none	n.a.
<i>AIONSEN35</i>	4	15138010	15138365	355	solo LTR fragment	none	n.a.
<i>AIONSEN36</i>	5	18806876	18807231	355	solo LTR & fragments	none	n.a.
<i>AIONSEN37</i>	5	9649982	9650265	283	solo LTR fragment	none	n.a.
<i>AIONSEN38</i>	5	9943036	9943399	363	solo LTR fragment	none	n.a.
<i>AIONSEN39</i>	5	11358443	11358638	195	solo LTR fragment	none	n.a.
<i>AIONSEN40</i>	5	12394243	12394562	319	fragment	none	n.a.
<i>AIONSEN41</i>	5	12398029	12398350	321	fragment	none	n.a.
<i>AIONSEN42</i>	5	12560877	12561493	616	gag-polypeptide	none	n.a.
<i>AIONSEN43</i>	5	13036269	13036319	50	solo LTR fragment	none	n.a.
<i>AIONSEN44</i>	5	18802278	18802633	355	fragmented solo LTR	none	n.a.
<i>AIONSEN45</i>	7	3003523	3003877	354	fragmented solo LTR	none	n.a.
<i>AIONSEN46</i>	7	8288370	8288733	363	fragmented solo LTR	none	n.a.
<i>AIONSEN47</i>	7	14850284	14850721	437	solo LTR	none	16
<i>AIONSEN48</i>	7	10045372	10046134	762	fragmented solo LTR	none	n.a.
<i>AIONSEN49</i>	7	13857185	13857510	325	Integrase core domain fragment	none	n.a.
<i>AIONSEN50</i>	7	20135759	20135891	132	RT fragment	none	n.a.
<i>AIONSEN51</i>	7	23674987	23675327	340	truncated solo LTR	none	n.a.
<i>AIONSEN52</i>	8	6163632	6163987	355	fragmented solo LTR	none	n.a.
<i>AIONSEN53</i>	8	6159031	6159386	355	fragmented solo LTR	none	n.a.
<i>AIONSEN54</i>	8	15685300	15685663	363	fragment	none	n.a.
<i>AIONSEN55</i>	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.

	<i>BrONSEN3</i>	<i>BsONSEN1</i>	<i>BsONSEN2</i>	<i>EsONSEN</i>	<i>AtONSEN8</i>	<i>AtONSEN7</i>	<i>AtONSEN5</i>	<i>AtONSEN3</i>	<i>AtONSEN6</i>	<i>AtONSEN4</i>	<i>AtONSEN1</i>	<i>AtONSEN2</i>	<i>AIONSEN7</i>	<i>AIONSEN9</i>	<i>AIONSEN6</i>	<i>AIONSEN14</i>	<i>AIONSEN4</i>	<i>AIONSEN11</i>	<i>AIONSEN15</i>	<i>AIONSEN12</i>	<i>AIONSEN8</i>	<i>AIONSEN13</i>
<i>BrONSEN3</i>	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
<i>BsONSEN1</i>	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
<i>BsONSEN2</i>	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
<i>EsONSEN</i>	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
<i>AtONSEN8</i>	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
<i>AtONSEN7</i>	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
<i>AtONSEN5</i>	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
<i>AtONSEN3</i>	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
<i>AtONSEN6</i>	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
<i>AtONSEN4</i>	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
<i>AtONSEN1</i>	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
<i>AtONSEN2</i>	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
<i>AIONSEN7</i>	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
<i>AIONSEN9</i>	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
<i>AIONSEN6</i>	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
<i>AIONSEN14</i>	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
<i>AIONSEN4</i>	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
<i>AIONSEN11</i>	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
<i>AIONSEN15</i>	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
<i>AIONSEN12</i>	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
<i>AIONSEN8</i>	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
<i>AIONSEN13</i>	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.

	BrONSEN2	BsONSEN1	BsONSEN2	EsONSEN	AiONSEN2	BaONSEN1	BaONSEN2	BaONSEN3	AtONSEN4	AtONSEN8	AtONSEN7	AtONSEN6	AtONSEN5	AtONSEN2	AtONSEN1	AtONSEN3	AiONSEN10	AiONSEN14	AiONSEN6	AiONSEN7	AiONSEN9	AiONSEN11	AiONSEN15	AiONSEN8	AiONSEN13	AiONSEN3	AiONSEN16	AiONSEN17	AiONSEN4	AiONSEN5	AiONSEN1	AiONSEN12	BrONSEN3	BrONSEN1	BrONSEN4	BrONSEN5	BrONSEN6	
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	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	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	92.6	91.3	92.7	92.5	92.9	92.7	92.5	92.9	92.5	92.3	89.2	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	92.9	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	73.6	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	73.5	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	85.6	75.3	77.3	
AiONSEN15	63.5	68.4	75.7	73.7	78.5	78.6	76.6	81.8	90.1	92.5	92.4	92.7	92.5	92.9	92.9	92.9	92.3	97.0	96.6	98.0	97.5	99.3	100.0	97.9	97.7	91.8	92.9	92.9	93.4	93.4	93.4	93.2	73.7	74.1	85.0	75.0	76.8	
AiONSEN8	64.1	68.3	75.1	73.5	78.4	77.1	75.7	81.3	89.6	92.1	92.2	92.5	92.1	92.5	92.5	92.5	91.3	96.3	97.7	97.2	97.5	98.6	97.9	100.0	99.3	91.6	92.7	92.7	94.2	94.2	92.8	92.6	73.4	73.8	85.6	75.0	76.0	
AiONSEN13	64.7	68.6	75.1	74.1	78.7	77.8	76.3	81.3	89.3	91.8	92.0	92.3	91.8	92.3	92.3	92.3	93.1	96.1	97.5	97.0	97.2	98.4	97.7	99.3	100.0	91.8	93.0	93.0	94.2	94.2	93.0	92.8	73.4	73.8	86.3	74.4	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	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	81.9	88.3	90.0	89.4	89.7	89.4	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		
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	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.																	

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.

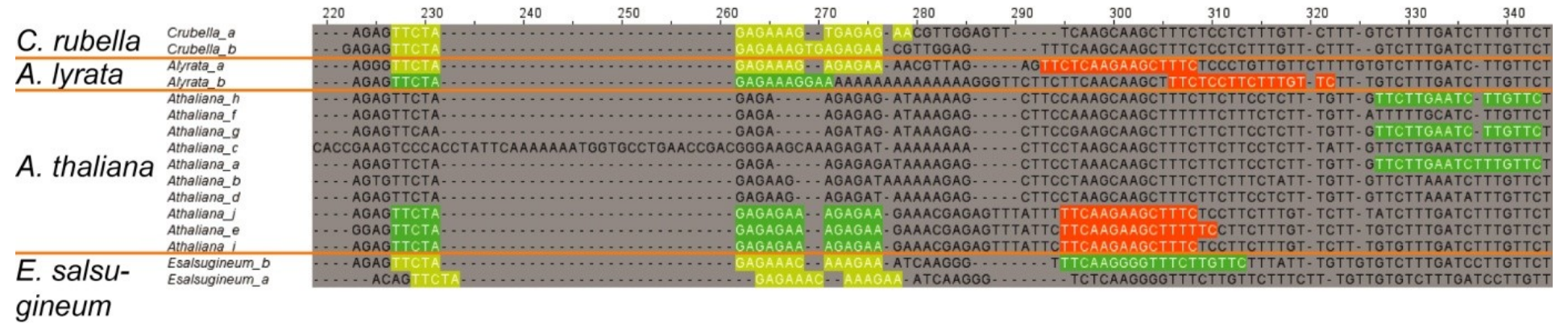


Figure S7. Consensus DNA sequence of *A. lyrata* *TERESTRAS*. Specific regions were indicated in different colors according to Fig. 3c: 5' LTR (grey), PBS (underlined), **GAG polyprotein** (green), **integrase** (violet), **reverse transcriptase** (yellow), **RNase H1** (blue), **PPT** (red), 3' LTR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

TGAAGTTAAACTTGATTTTGGTTTAAAGCTTAATTATGGGTTTATAATTCAATATTCTATATTGGATAAAACCCAAAGTTAAGCC
 TAAGTTCTAGATTTCTCTAGAGCATCATAGAAAAATCATCACCTCCTTAAATGTTCTAGAGAATTTATTAGATAGATATTTAG
 AWAATTATGTAGAATAATCTAGAAGTTTGAAGATAAAATCTAGATATTTTAGTAGAGTTATAGAGATGATGGTAGAATAATCT
 AGAGACTTTGTAAGCTAACCTTGGAGGCTATAAATACCTCCTCACCCCMTCATTTGTAATWTGTGAGGAAGTTGAACAAG
 TGAATAAAAAGAAAGTTCAAATAAAAGAACACTCTTTAAAAGTTCTAAGTCTCTCCAAAAGTCTTCAAGTAGTCTCTAATT
 GTTCTTCCAAATTTCTATCATACTTAGAGGGTTTCTTATCTTGATTATATCGAGTTTCTCGGGTATTACGGTCTTGGGCTAGT
 GCTAAGCACTATCGAGTTCGGTTTCTTACATGGTATCACTCGAGGACCCATTCTAATCTTGCTCTTCAAGATCGGGATT
 ATAGGAAGACTCGGATCTACTAAGTATGGAATCTATGGGTCGTGTTGGATTGGGAATGGAGATCTAAACCAATCTA
 ACTACCGGTATGGAAGTCATGATGGAGTCACTTGGTTAGTGAGGACTTATGGGATGTCGTGGCGGGAAGTAATACTT
 CACCACCTACCGGAGATGCTGCAACCGCGGAAGCGACAAGGAGTGGACACGTAATAATGCCAAGGCGGARTTTRCTTTA
 AAGAGGTCAATATCTCAGGAGTATTGAGCATGTCTCAAGGTGCACATCCGCTAGTTCATTTGGCAAGCGTTAGATCGAC
 TGTTCAACAAGAAARAAAYGAAGCTCGTCTACAATTGTTAGAAAAAGAGTTGGCRAATGCGAAGCAGGGGAGTCTTCAAT
 CGGAGTTTTCATCAAGGTAAGAACCTTTGCTCTGAGTMAATGATCTTAATCCGGAGGAATCAATCTCGGATGCTCGGT
 GAAGCGGTTTATTATCGAGGTCTACGACCCGAGTATACACCGTTTGTGACTTCGGTTCAAGGATGGGCTACACAACCTTC
 CTTGGARGAGTTTGAATAATTTGCTYGCCTCGCAAGAATCACTAGCRGTACAAATGGCCGGGAGTCAAAAATTCATGATGACTCG
 GGRAGCGCYTTTGTAGCTAGGAGGCAACAMAACCTTYAAGCCAAATCYAATGAYGGTGGTCCAAGAAATATGATGGACAT
 GAAGGATCTTTCAAGGGAGATAAGAAAAAATCAAGTGCATCCGGTGTGGAAAACCTWGGCATTTTAAAAARGATTGGCCGA
 GTCAGCTGAAGGAAACAACATGGCRGAATCAAAGGTCAATGAAGACGAAGAAATGGGGAAAATGTTTTACGRTGGAG
 GCTGCATCTTCAAGTACATCTACACCTAAGAARGTGGAAAATTAATTGGATCGTAGATTCTGGTTGTAGCCATCATATYACYG
 GAGACGAGAAATATTTCTAGTCTTCAACGCCATGAAGGAAAAGCAATCATTACCGCGGATAATTCAATCCATCACGT
 TGAGAAGGAAGGAACGGTGGTCTATCAAAAGGAGATGATGGAAGCCCAATCACTCTYRAGAACGTTTACCATGTTCTGGAGT
 AAAAAAAGTCTTCTCCTCGTGGTAAATGCGGTGGACTCAGGTAATATGTYTTATTTGGCCCAAGAGATGTTAAATCTTAA
 AGAATATTCAAGAGTTAAAGGCGGAYGTGGTTCACACTGGAGCACGRGTTAAAGATCTRTACGTTTTATCGGCGTCAAACCTC
 TTATGTGGAGAAGTAGTACCAACGATAATGCTTTTATATGGCATGCTAGGCTTGGTCAAYATAAATGACTAARCTCAAG
 GTTATGGTRAATAAGAYTTGGTCAACGGGCTCCCAAGTTGAAGATCCAAGATGAAGGCACACTTTGTGAAGGATGTCAT
 ATGGAAGTCTCATAGACTTCCATTTGACTATTCCACTTCAAGGTGCAGTGTCCGTTGGARAGGGTCCAYAGTGACTTGT
 GGGTCCGACAAGAACCCTCATATTYCGGGTATCRCTACATGTTGTTGTTGTTGTTGAYGACTTCTCWCGGTACACTTGGT
 ATACTTGTGAAGGAAAAATCTGAAGTATTCTCCAAGTTCTAGAATTCAAGGTTACCGTGGAAAGGGGAGTTAGGTGAGAAG
 ATCAAGACTTAAGCGGATAATGGAGGGGAGTTCATGTAAGGAGTTTCTCTTTTTGTAGATAATGGTATCAAGA
 GAGAAATTTACATGTCCGCATACACCTCAACAAAATGGAGTAGCAGAGGAAAGATCAGACATCTAAGTGAAGACGTGAGAA
 GTTGGCTCCATGGHAAAGATTTGCCTAAGGAGTTATGGGCGGAGGGMATGAGATGTGCAGCCTATGTCATCAACCGGATG
 CCACTTAGTCCAAACAATATGAAGTCTCCTTATGAGATGGTTCATGGGAAGAAGCCAACGGTGAACATCTCAGAATATTTG
 GATCAGTCTGCTACGTYCATGTGTTTATTACAAAAGTAAGTTGGAGGCAAGGCAAGAAATGCATATTTGTGCGGCTA
 TGATGAACAAAGGAAGGTTGGAGGTGATGGATCCTGACACAGATATGTTGTGTCTCGTGTGTTGTTGTTGTTGTTGTTGAA
 GTTCTTCTACTACGGGCCACCTCAAGTCTTGGTTGAAAAAGATGGTGCRAAGTCTTCCAAGATCGATGAATCAACTCTCC
 AAGTACCATGTGAGARTGGAAGTCTTGGAAATAAATCAAGGTCAAGGGGGAGCACTAACCAAGAAGAGGAACAAG
 ATCATGGTTCGATGGTCAATCAACGGCCGAAAAGAAACATTGCAAGCTGCAAGATATAGAGATGAAGAATCATCACTAC
 TTATTGATCTTCTTCGAGTCCGTTAGATGATGATGAGCATCTTCTTATGATGAAGCTAAAGGATCCAAGAATGGGAA
 GCTGCAATGAAGGAGGAGATGAGTGTCTMAAGAAAATGAAACTTGGGATCTGGTTCCAAAACCCAAAGGATGTTGAGCCC
 GTTCTTGTCAAATGGGTGTATCGAATTAAGCGAAAAGCAGATGGGAGCATTGATAGRTTAAAGCAAGGTTGGTTGCTCGG
 GGATCTCTCAAARTATGGAGAAGATTATGATGAGACATTYAGTCCWGTGGCGAAGATGACTACGGTACGCTCACTYTTAT
 CTTAGCAGCAWGYTTTGGTGAAGTTATGGCAACTTGTGTAAGATGCTGAAAGATGCCTTTCTATATGGTGAAGTAAAGAT
 CTTGATGGAGCAACACCTGTTTTGCAATCAGCAGAGCATCYTGATCATGTGTGCAAGCTGAAAAAGGCCTGTACGGATT
 AAAACAAGCTCCACGAGCTTGGTATGGAAGGTTGCTCARTTCTTCAATTTTGGCGCTATGAGGCATCAAATCTGACCCG
 AGTCTATTCTTCAAAGAAGAAAGGAGGAGTYCACGTAGTAGTTCTTCTTACGTGGATGATATGATAATTACYGGGAATGATG
 ATGCAGAAATGCTCGCTTACAAGAAGAYATGTCGATAAGGTTGAGATGAAGAAGTTGGGTGAGCTGAATAACTTCTTGG
 CCTAGAGGTTGAAAGAGKAAAKGATGGAATTTCTGTTGGCAACAAGTTATGCAAGAAGGATTGTTGAGAAGTTCCGGGT
 GCACGAAGGAAAGAYGCGCACTACTCCGATGGATGTGAACATCAAGCTCAAACGTGATGAAGGTTTATTGTTACCTGATCC
 TCGACCTTATCGYGTCTTGTGGGAAGTCTTCTATACTTAACCATACAAGACCTGATATTGCCCTCGCRGTAGGTCTKGTA
 AGTCCGTTTATGCAAGCACCAAGGAAACACACTTAGAAGCGGCAAGAAGATCTTGAAGTATGTCGAAGACAACCTTGGAC
 ATGGGCTTGGTGTACAAGTACAATGCAAAAGATTTCTCTCATGGTTTTACAGATGCTGACTTTGGTGGAGATCTAGATGACC
 GAAAATCAACTTCGGGCTATGTGTTCTTATGTGGAGACACAAGCATTTCGTGGTGTAGCAAGAAACAACCAACGGTATCGCT
 ATCTACCACTGAAGCGGAGTATAAAGCTTCCACACTCGCTGCTCAAGAGTGTATATGGCTTCGAAGACTCTTGAAGATTTG
 TTCGAGCCATAAATAACCGGTGGCTATCTACGGAGATAATCAAAGTGTATCAAGTTAGCTAACAATCCGGTGTTCATG
 CAAGGACAAARCATATTGAGTTAGAACATCACTTATAAGGGGAGAAGTTCTTCTTGTGGAACAATGAAGCCTTGGAAAGT
 TCGAAGTGAGGACAACGTTGCAGACATCTTCAACCAAGTCATTACCAAAAGGCCAATTCGAGTTACTTCGCTYGAAGCTCGG
 GATGGTTGACAAAATCAAGTTTAAAGGGGAGTATTGAAGTTAACTTGATTTGGTTAAGCTTAATTATGGGTTTATAATTC
 AATATTCTATATTGGATAAAACCCAAAGTTAAGCCTAAGTTCTAGATTTCTAGAGCATCATAGAAAAATCATCACCTCCTTA
 AATGTTCTAGAGAAATTTAGATAGATATTAGAWAATTAGTAATAATCTAGAATACTAGAAGTTTGAAGATAAATCTAGATAT
 TTAGTAGAGTTATAGAGATGATGGTAGAATAATCTAGAGACTTTGTAAGCTAACCTTGGAGGCTATAAATACCTCCTCACCC
 CCMTCAATTTGTAATWTGTGAGGAAGTTGAACAAGTGAATAAAAAGAAAGTTCAAATAAAAGAACACTCTTAAAAGTTCTCT
 AAGTCTCTCCAAAAGTCTTCAAGTAGTCTAATTTGTTCTTCCAAATTTCTATCATACTTAGAGGRTTTCWTATCTTGATTA
 TATCGAGTTTCTCGGATATTACGGTCTTGGGCTAGTGCTAAGCACTATCGADYTCGGDTTCTTAAACCAATCA

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

Line	Arabidopsis Biological Resource Centre ID	Line	Arabidopsis Biological Resource Centre ID
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).

TGAATAACTGAACGGGTAACAGAATTATGGTTAAGCTTAATTATGGGTTTATAATTCAATATCCTATATTGA
 ACAAACCCAAAGTTAAGCCAAAGTTCTAGATTTCTCTAGAGCATCATAGAAAAATCATCACCTCCTTAAGTGT
 TCTAGAAAATTTTATTAATAGATATTTAGATAATTATGTAGAATAATCTAGAAGTTTGTAAAGATAAAATCTAGAT
 ATTTTAGTAGAGTTATAGAGATGATTTTAGAATAATCTAGAGACTTTGTAAGCTAACTTTGGAGGCTATAAATA
 CCTCCTCACCCCTCATTGTAATCAAGTTGAACAAGTGAATAAAAAAGAAAGTTCAAATAAAAGAACCCTCTAT
 ATAAATTCTCTAAGTCTCTCTAAAAGTCTTTCAAGTAATCTCTAGTTGTTCTTCCAAATTTTCTATCATACTTAGA
 GGATTTCTTATCTTGGTTATATCGAGTTTCTCGGGTATTACGGTCTTGGGCTAGTGCTAAGCACTATCGAGTC
 GGTTTCTTACATGATATCAGAGCCATTCTAATCTTGTGCTCATCAAGATCAAGGTTATAGAGAACTCGGGTTT
 ACTCTAAGTATGGAATCTATGGGTCGTGTTGTTGGATTGGGAATGGAGATC TTAAACCAATCTAACTACCGG
TATGGAAGTCATGTATGGAGTCATACTTGGTTAGTGAGGACTTATGGGATGTCGTGCGCGGAAGTAGTACTT
CACCACCTACCGGAGATGCTGCTACTGCGGAAGCGACAAAGGAGTGGACACGTAATAATGCCAAGGCGGAG
TTTGCTTTAAAGAGGTCAATATCCTCGGGAGTATTGAGCATGTCTCAAGGTGTACATCCGCTAGTTCAATTT
GGCAAGCTTTAGATCTACTGTTCAACAAGAAGAACGAAGCTCGTCTATAATTGTTAGAAAACGAGTTGGCGAA
TGCGAAGCTGGGGGAGTCTCAATCTCGGAGTTTTTCATCAAAGTCAAGAACCTTTGCTCTGAGATCAATAGT
CTTAATCCGGAGGAATCAATCTCGGATGCTCGGTTGAAGCGGTTTATTATTGAGGCTTAGACCCGAGTATA
CACCGTTTGTGACTTCGGTTCAAGGATGGGCTACACAACCTTCCTTGGAAGAGTTTGAAAATTTGCTTGCTTC
 GCAAGAATCACTAGCGGTACAAATGGCGGGAGTCAAAATTCATGATGACTCGGGGAGCGCTTTTGTAGCTAG
 GAGGCAACACAACCTCAAAGCCAAATCCAATGATGGTGGTCCAAGAAAAATGATGGACATGAAGGATCTTC
 TAAGGGAGATAAGAAAAAATCAAGTGCTATCGGTGTGAAAACCTTGGGCATTTTAAAAAAGATTGCCGAGTC
 AAGCTGAAGGAAACAAAGATGGCAAAATCAAAGGTCATAATGAAGACGAAGATGGGGAAAATGTTTTATG
 GTGGAGGCTGCATCTTCAAGTACATCTACACCTAAGAAGGTGGAAAATAATTGGATCGTAGATTCTGGTTGTA
 GCCATCATATCACCGGAGACGAGGAATTTTTCTAGTCTTCAACGCCATGAAGGAAAAGAAGCAATCATTAC
 CGCGAATAATTCAATCCATCACGTTGAGAAGGAAAGAACGGTGGTCATCAAAGGAGATGATGGAAGCCCAAT
 CACTCTCGAGAACGTTTACCATGTTCTGAGTAAAAAAGAATCTTCTCTCCGTGGTAAATGCGGTGGAGTCA
 GGTAATATGTTTTATTTGGCCCAAGAGATGTAAATTCTTAAAGAATATTCAAGAGTTAAAGGCGGACATGGT
 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.

```

GGTTTTCTTATCTTGGTTATATCGAGTTTCTCGGATATTACGGTCTTGGGCTAGTGCTAAGCACTATCGAGTC
GGTTTTCTTACATGGTATCAGAGCCATTCTAATCTTGTGCTCTTCAAGATCGGGTTATAGAGAACTCGGGTT
TACTCTAAGTATGGAATCTATGGGTCGTGTTGTTGGATTGGGAATGGAGATCTAAACCAATCTAACTACCGG
TTATGAAAGTCATGTATAGAGTCACTTGGTTAGTGAGGACTTATGGGATGTCGTCGGCGGAAGTAATACTT
CACCACCTACCGGAGATGCTGCAACCGCGGAAGCGACAAAGGAGTGGACACGTAAAAATGCCAAGGCGGA
GTTTGCTTTAAAGAGGTCAATATCTTCGGGAGTATTTGAGCATGCTCAAGGTGCACATCCGCTAGTTCTATT
TGGCAAGCGTTAGATCGACTGTTCAACAAGAAGAACGAAGCTCGTCTACAATTGTTAGAAAACCGAGTTGGCG
AATGCGAAGCAGGGGGAGTCTTCAATCTCAGAGTTTTTCATCAAGGTAAAAAACCTTTGCTCTGAGATCAATA
GTCTTAATCCGGAGGAATCAATCTCGGATGCTCGGTTGAAGCAGTTTATTATTCGAGGTCTACGACCCGAGT
ATACACCGTTTGTGACTTCGGTTCAAGGATGGGCTACACAACCTTCCCTGGAGGAGTTTGAAAATTTGCTTGC
TTCGCAAGAATCACTAGCGGTACAAATGGCGGGAGTCAAATTCATGATGACTCGGGGAGCGTTTTGTAGC
TAGGAGGCAACACAACCTTCAAAGCCAAATCTAATGATGGTGGTCCAAGAAATAATGATGGACATGAAGGATCT
CTAAGGGAGATAAGAAAAAATCAAGTGTATCGGTGAAAACCTGGGCATTTAAAAAGGATTTGCCGAG
TCAAGCTGAAGGAACAAACATGGCGGAATCAAAGGTCAAATGAAGACGAAGAATGAGGAAAATGTTTTTA
CGGTGGAGGCTGCATCTTCAAGTACATCTACACCTAAGAAAGTGGAAAATAATTGGATCGTAGATTCTGGTTG
TAGCCATCATATCACTGGAGACGAGAAATTTTTCTAGTCTTCAACGCCATGAAGGAAAAGAAGCAATCATT
ACCGCAGATAATTCAATCCATCACATTGAGAAGGAAGGAACGGTGGTCAATCAAGGAGATGATGGAAGCCCA
ATCACTCTCGAAAACGTTTACCATGTTCCCTGGAGTAAAAAGAATCTTCTCTCCGTGGTGAATGTGGTGGACT
CAGGTAACATGTTTTATTTGGCCCAAGGGATGTTAAATCTTAAAGAATATCCAAGAGTTAAAGGCGGACGC
GCTTCACACTGGAGCACGGGTTAAAGATTTATACGTTTTATCGGCGTCAAACCTTATGTGAAAAGATGAGT
ACCAACGATAATGTCTTTATATGGCATGCTAGGCTTAGTCACATAAATAAGACTAAACTCAAGGTTATGGTGAA
TAAAGATTTGGTGAACGGGCTCCCAAAGTTGAAGATCCAAGATGGAGGCACAATTTGTGAAGGATGTCAATA
TGAAAATCTCATAGGCTTCCATTTGACTATTCCATTTCAAGGTGCAGTTTTCCGTTGGAGAGGGTCCACAGT
GACTTGATGGGTCCGACAAGAACCCTCATATTCGGGTATCTCTACATGTTGTTGTTGCTGACGACTTCT
CTCGGTACACTTGGGTATACCTTGTGAAGGAAAAATCTGAAGTATTCTCCAAGTTTCTAGAATCAAGGTTACC
GTGGAAGGGGAGTTAGGTCAGAAGATCAAGACTTTAAGGACGGATAATGGAGGGGAGTTTCATGTCTAAGGA
GTTTCTCTCTTTTTGTCGAGATAATGGTATCAAGAGAGAATTTACATGTCCGCATACACCTCAACAAAATGGAG
TAGCAGAGAGGAAGATCAGACATCTAAGTGAGAGCTGAGAGCTGATAAGTTGGCTCCATGGAAAAGATTTGCCAAGG
CGTTATGGGCGGAAGGCATGAGATGTGCAGCTTATGTACATCAACCGGATGCCACTTAGTCCAAACAATATGA
AGTCTCCTTATGAGATGGTTCATGGGAAGAAGCCAACGGTGAACATCTCAGGATATTTGGATCAGTCTGCTT
CGTCCATGTGTTTGATTACAAAAGAACCAAGTTGGAGGCAAAGGCGAAAAAATGCATATTTGTCGGCTACGAT
GAACAAAGGAAGGGTTGGAGGTGTATGGATTCCGAGACACACAAGTATGTTGTGCTCGTGATGTTGTCTTT
GATGAAGTTTCTTCACTACGGGTCACCTCAAGTCTTGGTTGAGAAAGATGGTGCTAATTCCTTAAGAACG
ATGAATCAACTCTCAAGTACCATGTGAGATGGGAAGTCCGAAAATAAATCAAGGTGAAAAGGGGAGCA
CTAACCAAGAAGAAGAAGAGGAACAAGATCATGGTTCGATCAATCAACGGTCAAGGAAAGAAACATTGTCA
AGCCTGCAAGATATAGAGATGAAGTATTCATCACTACTTATTCTGCTTCTTACAGCTCCTCTAGATGATGAT
GAGCCATCTTCTTATGATGAAGCTAAAGGAGTTCAAGAATGGGAAGTTGCAATGAAGGAGGAGATGAGTGCT
CTCAAGAAAATGAAAACCTGGCATCTGGTTCCAAAACCCAAGGATGTTGAGCCCGTTTTCTTGCAAAATGGGTGT
ATCGAATTAAGCAAAAAGCGGATGAGAGCATTGATAGGTTTAAAGCAAGGTTGGTTGCTCGGGGATTCTCTC
AAAAATATGGAGAAGATTATGATGAGACATTTAGTCTGTGGCGAAGATGACAACCTTGATGTGAAGAAATGCTT
TTCTATATGGTGAGCTTGATAAAAGTATCTTCATGGAGCAACCCTGGTTTCGAATCGCGAGAGCATCCTGA
TCATGTGTGCAAGCTGAAAAGGCCTTGTACGGATTAACAACAGCTCCACAAGCTTGGTATGAAAAGGTTGCG
TCAATTCCTTCAATTTTGTGGCTATGAGGCATCAAATTCGACCCGAGTCTATTCTTCAAGAAGAAGGAGGA
GTCCACGTAGTAGTTCTTCTTTACGTGGATGATGATAATTACCGGGAATGATGATGCAGAAATTGCTCGCT
TACAAGAAGACATGTCGATAAGGTTGAGATGAAGAAGTTGGGTGAGCTGAATAACTTCTTGGCCTAGAGG
TTGAAAGAAGAAAGGATGGAATATTCGTTGGTCAACAAGGTTATGCAAGAAGGATTGTTGAGAAATTCAGGGT
GCACGAAGGAAAGACGCGCACTACTCCGATGGATGTGACCATCAAGCTCAAACGTGATGAAGGTTCAATGTT
ACCTGATCCTCGACCTTATCGCGCTCTTGTGGGAAGTCTTCTATACTTAACCATTACAAGACCTGATATTGCC
TTCGCAAGTGTGTTGTAAGTCGGTTTATGCAAGCACAAGGAAACCACTTAGAAGCGGCAAGAAGATC
TTGAAGTATGTCAAGACAACCTTTGACATGGGCTTGGTGTACAAGTACAATGCAAAGATTTCTCTTATTGGTTT
TACGGATGCTGACTTTGGTGGAGATCTAGATGACCGAAAATCAACTTCGGCAATGTGTTCTTATGTGGAGA
CACAAGCATTTGCTGGTGTAGCAAGAACAACCAACGGTATCGCTATCTACCACTGAAGCGGAGTATAAAGC
TTCCACACTCGCTGCTCAAGAGTGTAATGGCTTCGAAGACTCTTGAAGATTTGTTTCGAGCCTATAAATAAA
CCGGTGGCTATCTACGGAGATAATCAAAGTGCTATCAAGTTAGCTAACAATCCGGTGTTCATGCAAGGACAA
AGCATATTGAGTTAGAACATCACTTCATAAGGGGAGAAGGTTCTTGATGGAACAATTGAAGCCTTAGAAGTTCCG
AAGTAGGACACACGTTGCGGACATCTTCAACCAAGTACTTCAAAAAGGCCAATTCGAGTTACTTCGCTCGAA
GCTCGGGATGGTTGACAAAATCAAGTTTAAAGGGGAGTATTGAAGTTAAACTTGATTTTGGTTAAGCTTAAT
TATGGGTTTATAATTCAATATTCTATATTGGACAAAACCCAAAAGTTAAGCCTAAGTTCTAGATTTCTCTAGAGC
ATCATAGAAAAATCATCACCTCCTTAAATGTTGAACAAGTGAATAAAAAGAAAGTTCAAATAAAAATTAAGAAC
ACTCTTAAAAGTTCTCTAAGTCTCTCCAAAAGTCTTCAAGTAATCTCTAATTGTTCTTCCAAAATTTCTATCAT
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.

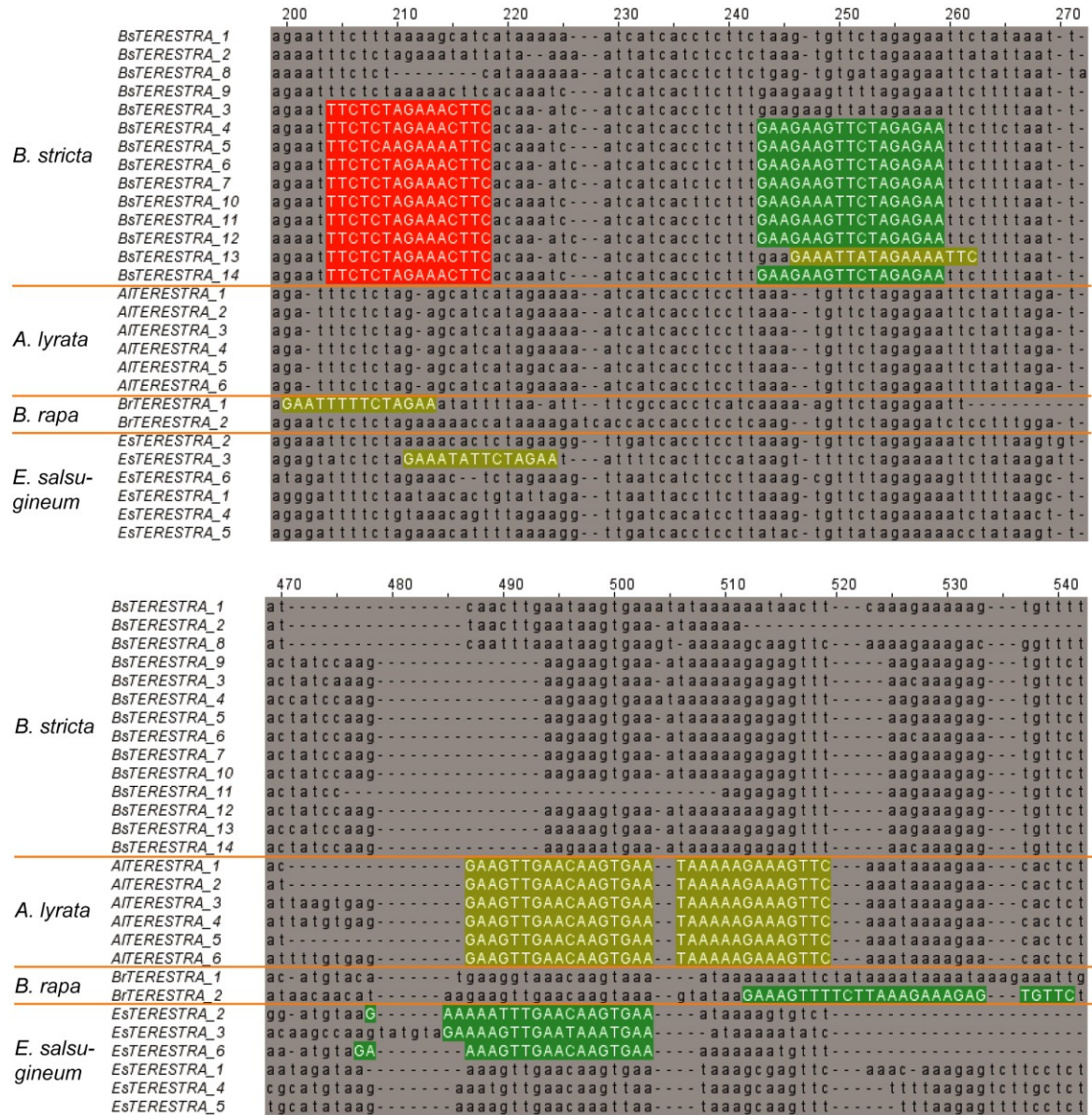


Figure S11. Transcriptional response of *ONSEN*, *COPIA37* and *TERESTRA* to DNA methylation inhibitor treatments in *A. lyrata*. Relative transcript accumulation after 48 h control, 10 μ M 3-deazaneplanocin A (DZNep) and 40 μ M zebularine treatment. Transcript amounts were normalized to *UBC28*. Error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

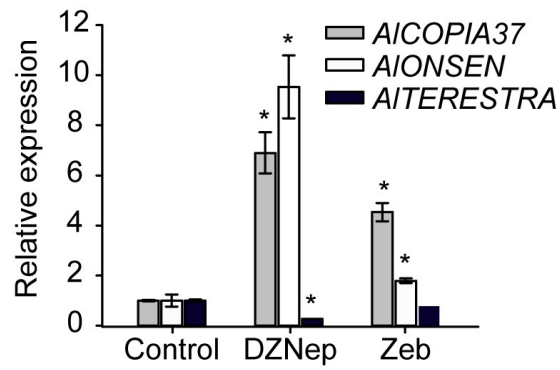


Figure S12. Density of RNA-sequencing reads mapping over *APUM9* – *ROMANIAT5-2* region.

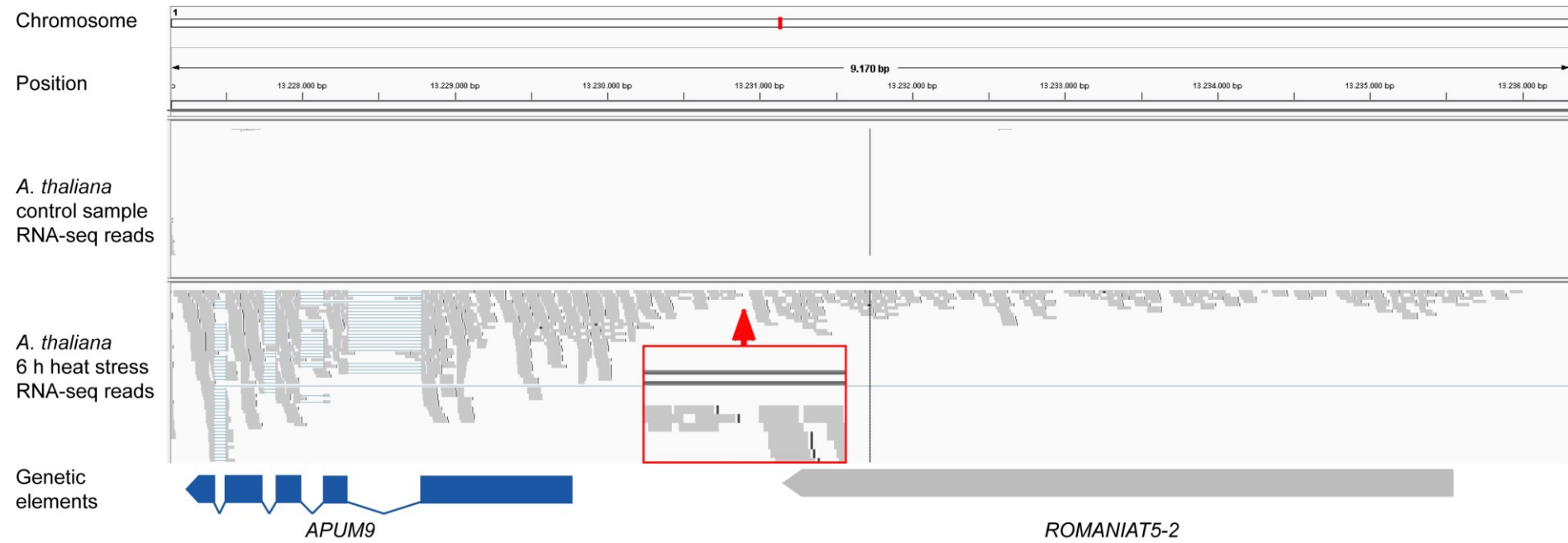


Figure S13. Putative heat responsive elements (HREs) in 5'/3' long terminal repeats of *ROMANIAT5* elements. HRE types: orange – 3P, yellow – gap, green – step.

		320	330	340	350	360	370
	<i>BsRomaniaT5_5</i>	cgtattcaataatgac	TTCACCATTCTTCTCGAGTTC	ttgagtgtaagag-aaaaa			
<i>B. stricta</i>	<i>BsRomaniaT5_4</i>	tgtattcaacactgat	TTCCTGATTTTTCTCGAGTTC	ttgtgtgtaagag-aaaaa			
	<i>BsRomaniaT5_8</i>	tgtattcaacactgat	tttctgatttttctcgagcctt	ttgtgtaaaagagaaaaa			
	<i>BsRomaniaT5_9</i>	tgtattcaacactaat	tttctgatttttctcgagcctt	ttgtgtaaaag-aaaaa			
<i>C. rubella</i>	<i>CrRomaniaT5_1</i>	tgtattggatgtcaac	TTCCTTCTTTTTCTCGAGTTC	ttgagataaagaa-aaaaa			
	<i>CrRomaniaT5_4</i>	tatactggatatacaac	TTCCTTGTTTTCTCGAGTTC	tcgagtgtaggag-aaaaa			
<i>A. thaliana</i>	<i>AtRomaniaT5_1</i>	tgtattgcac	TTCTACTTCCTTGTTTC	ttctcgagcctt	ttgagtgtaggag-aagaa		
	<i>AtRomaniaT5_3</i>	tgtattgcac	TTCTACTTCCTTGTTTC	ttctcgagttct	ttgagtgtaggag-aagaa		
	<i>AtRomaniaT5_4</i>	tgtattgcac	TTCTACTTCCTTGTTTC	ttctcgagcctt	ttgagtgtaggag-aagaa		
	<i>AtRomaniaT5_2</i>	tgtattgcaccctctac	TTCCTTGTTCTTCTCGAGTTC	ttgagtgtaagag-aagaa			
<i>B. rapa</i>	<i>BrRomaniaT5_1</i>	aaatactcgaatgccac	ttctttatftttctcgagcctcc	ttatgtacgag-aaaaa			
	<i>BrRomaniaT5_2</i>	catactcaatgiccac	ttctttatftttctcgagcctt	ttatgtacgag-aaaaa			
	<i>BrRomaniaT5_3</i>	tatactcgaatgccac	ttctttatftttctcgagcctc	ttatgtacgag-aaaa-			
	<i>BrRomaniaT5_6</i>	catactcgaatgccac	ttctttatftttctcgagcctc	tcgtagtag-aaaaa			
	<i>BrRomaniaT5_7</i>	catactcaatgiccac	ttctttatftttctcgagcctcc	ggagtag-aaaaa			
	<i>BrRomaniaT5_8</i>	catactcgaatgccac	TTCTTTATTTTTCTCGAGTTC	ccgtagtag-aaaaa			
<i>E. salsugineum</i>	<i>EsRomaniaT5_7</i>	catactggatatacgac	ttcttgatttttctcgagcctt	ttgggtgtaagag-aaaaa			
	<i>EsRomaniaT5_9</i>	catactggatatacgac	ttcttgatttttctcgagcctt	ttgagataaagag-aaaaa			
	<i>EsRomaniaT5_36</i>	catactggata	TTCACTTCCTGATTC	ttctcgagttct	ttgagtgtaagag-aaaaa		
	<i>EsRomaniaT5_20</i>	catactggata	TTCACTTCTCAATTATTC	tcgatttct	ttgagtgtaagaa-aaaaa		
	<i>EsRomaniaT5_12</i>	catactggatataccac	TTCTTGATTTTTCTAGAGTTC	ttgagtgtaagag-aaaaa			
	<i>EsRomaniaT5_60</i>	catactgataataccac	TTCCTGATTTTTCTCGAGTTC	ttgagataaagag-aaaaa			

Table S4. Primers used in this study.

<i>At - Arabidopsis thaliana</i>				
<i>Al - Arabidopsis lyrata</i>				
<i>Ba - Ballantinia antipoda</i>				
<i>Bs - Boechera stricta</i>				
<i>Br - Brassica rapa</i>				
<i>Cr - Capsella rubella</i>				
<i>Es - Eutrema salsugineum</i>				
Target	Species	Primer name	Sequence (5' to 3')	Application
<i>COPIA20</i>	<i>At, Al</i>	C20_qF2	TACATGAAGCCACCACCGGGT	RT-qPCR
	<i>At, Al</i>	C20_qR3	TCATCTCCGGGAATGACAAGGTA	RT-qPCR
<i>COPIA37</i>	<i>At</i>	AtC37_F2	AGCTTAACTACAGAAGGGAAGGA	RT-qPCR
	<i>At</i>	AtC37_R2	CTCTCCAATCTCTCATTTTCTCG	RT-qPCR
	<i>Cr</i>	CrC37_F1	GGAGGTAGGTGAGACAAGACA	RT-qPCR
	<i>Cr</i>	C37_LTRR1	AACCGCTACGTCTCGGGG	RT-qPCR
	<i>Al</i>	AlyC37qF3	AACGCAGCCGAAGCTAATC	RT-qPCR
	<i>Al</i>	AlyC37qR3	CTCCATCACCGGCTAACAAC	RT-qPCR
	<i>Br</i>	EsC37-u_F1	ACAGGTGGGyCTTTAATGGGC	RT-qPCR
	<i>Br, Es</i>	C37_u_LTRR1	AACCGSTACGTCTCGGGG	RT-qPCR
	<i>Es</i>	EsC37_F1	ACAGGTGGGTCTTTAATGGGC	RT-qPCR
<i>COPIA78</i>	<i>At, Bs</i>	AtCOPIA78qF2	CGGTGCTCACAAAGAGCAACTATG	RT-qPCR
	<i>At, Bs</i>	AtCOPIA78qR3	ATCCTTGATAGATTAGACAGAGAGCT	RT-qPCR
	<i>Al</i>	AlCOPIA78qF3	ACAATGCTCACAAAGAGCAACTATG	RT-qPCR
	<i>Al</i>	COPIA78qR3	ATCCTTGATAGATTAGACAGAGAGCT	RT-qPCR
	<i>Ba</i>	Ba_ONS_F1	ACATGTACCGGATGAGAAGCG	RT-qPCR
	<i>Ba</i>	Ba_ONS_R1	TGTGTCCGGTTGTAGAGCT	RT-qPCR
	<i>Br</i>	Br_ONS_F1	TTGCGTGCATGATGTCAGGT	RT-qPCR
	<i>Br</i>	Br_ONS_R1	ACGCCAATGGAATGTCGAGT	RT-qPCR
	<i>Es</i>	EsONS_F5	GTCTTGGCTTTGGCATCTTC	RT-qPCR
	<i>Es</i>	EsONS_R5	GCGCTCTTGTCTGACTCC	RT-qPCR
<i>GAPC-2</i>	<i>At, Al, Ba, Bs, Br, Cr, Es, Aa</i>	GAPC-2_F	ATCGGTCGTTTGGTTGCTAGAGT	RT-qPCR
	<i>At, Al, Ba, Bs, Br, Cr, Es, Aa</i>	GAPC-2_R	ACAAAGTCAGCTCCAGCCTCA	RT-qPCR
<i>GFP-4</i>	<i>At</i>	GFP4-F	GGCAGACTTCTTCAAGAGC	RT-qPCR
	<i>At</i>	GFP4-R	AAAGGCCAGATTGTGTGGAC	RT-qPCR
<i>TERESTRA</i>	<i>Bs, Br, Es</i>	TERESTRA_F1	TCATGTATGGAGTCATACTTGGT	RT-qPCR
	<i>Bs, Br, Es</i>	TERESTRA_u_R1	CACCTTGAGACATGCTCAAATA	RT-qPCR
	<i>At, Al</i>	TERESTRAF2	GTATTACGGTCTTGGGCTAGTG	RT-qPCR
	<i>At, Al</i>	TERESTRA_R2	ACCAAGTATGACTCCATACATGAC	RT-qPCR
<i>HSP101</i>	<i>At</i>	HSP101qF	TGAGCTAGCTGTGAATGCAGGACATGCTC	RT-qPCR

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