

Table 1 Suppl. Molecular characterization of the rearranged bands identified in *A. suecica*. The number in sequence designation corresponds to its size in base pair; At - *A. thaliana*, Aa - *A. arenosa*, As - *A. suecica*. Search performed using *BLAST* on *NCBI* (National Center for Biotechnology Information, <http://www.blast.ncbi.nlm.nih.gov/>), *TAIR* (*Arabidopsis* Information Resource, <http://www.arabidopsis.org/Blast>), and *PlantSat* (repetitive plant sequences, <http://w3lamc.umbr.cas.cz/PlantSat/blast.php>) databases.

Origin		Presence vs absence			Alignment with <i>A. thaliana</i> genome		
Sequence name (acc. No.)	Primers	At	Aa	As	acc. No.	<i>BLAST</i> values	Notes (information obtained from <i>NCBI</i> , <i>TAIR</i> , and <i>PlantSat</i> databases)
End-AAG_as415 (KJ371929)	<i>Endovir1-1</i> (AAG)6C	-	-	+	gb CP002686.1 base 18299694 to 18300096 (Chromosome 3)	78 % of similarity E value of 7e-89 96 % of query coverage	internal segment of the coding region of Rab-GAP domain of gyp1p superfamily protein
End-AAG_as552 (KJ371930)	<i>Endovir1-1</i> (AAG)6C	-	-	+	gb CP002688.1 base 340279 to 340095 (Chromosome 5)	77 % of similarity E value of 4e-37 36 % of query coverage	(1-355) absence of any significant alignment; (356-552) aligned with the coding region of RING-H2 finger protein ATL74 (AT5G01880)
Tat_at944 (KJ371934)	<i>Tat1</i>	+	-	-	gb CP002684.1 base 7672039 to 7672967 (Chromosome 1)	99 % of similarity E value of 0.0 98 % of query coverage	internal segment of the coding region of SKU5 similar 7 protein
Tat_aa740 (KJ371931)	<i>Tat1</i>	-	+	-	gb CP002686.1 base 8554125 to 8554840 (Chromosome 3)	77 % of similarity E value of 8e-161 97 % of query coverage	(1-637 bp) - coding region of one uncharacterized protein (id="AEE76808.1"), (638-740 bp) - adjacent intergenic region
Endovir_aa929 (KJ371933)	<i>Endovir1-1</i>	-	+	-	gb CP002686.1 base 3597497 to 3598421 (Chromosome 3)	80 % of similarity E value of 0.0 98 % of query coverage	(1-455 bp) - coding region of glycerol-3-phosphate acyltransferase 5 gene, (456-929 bp) adjacent intergenic region
End-AAG_aa387 (KJ371928)	<i>Endovir1-1</i> (AAG)6C	-	+	-	gb CP002687.1 base 10196786 to 10197157 (Chromosome 4)	88 % of similarity E value of 7e-127 97 % of query coverage	(1-18 bp) end of coding sequence of D-Tyr-tRNA(Tyr) deacylase family protein, (19-285 bp) - the adjacent intergenic regions, (286-387) -subsequent coding sequence for <i>A. thaliana</i> ATP-dependent RNA helicase DDX35
Romania_aa951 (KJ371932)	<i>RomaniaT5</i>	-	+	-	CP002684.1 CP002685.1 CP002686.1 CP002687.1 CP002688.1 (Chromosomes 1-5)	81-84 % of similarity E value of 0.0 94-96 % of query coverage	retrotransposons fragments, mainly partial LTR of gypsy-like retrotransposon family (<i>Athila</i>)
Romania_aa1357 (KJ371935)	<i>RomaniaT5</i>	-	+	-	CP002684.1 CP002685.1 CP002686.1 CP002687.1 CP002688.1 (Chromosomes 1-5)	89-92 % of similarity E value of 8e-93 99 % of query coverage	(1-446 bp) - 180 bp centromeric repeat of <i>A. arenosa</i> , (447-1357 bp) - <i>Athila</i> family retrotransposons

Table 2 Suppl. Internal segments expected sizes and position of internal primers in the sequences.

Sequence	Expected fragment size (bp)				
	[1]	position	[2]	position	[1-2]
End-AAG_as552	247	forward - 78 (+18) reverse - 305(+20)	268	forward - 218 (+20) reverse - 467(+19)	408
Romania_aa951	294	forward - 265 (+20) reverse - 539 (+20)	279	forward - 498 (+22) reverse - 758 (+19)	512
Romania_aa1357	217	forward - 576 (+20) reverse - 773 (+20)	387	forward - 720 (+20) reverse - 1087 (+20)	531