Supplementary Figure Legends

Figure S1. Sequence alignment of the TGTT1 elements

Sequence identities over 70% were shaded in blue. The TSD site, 5'LTR, PBS, PPT and 3'LTR regions are indicated using red lines and arrows.

Figure S2. Wet laboratory validation of the TGTT and AACA elements.

Each element was randomly selected and analyzed from each family. A schematic view of the LTR-RT, with the location of the region that was amplified (dashed pink boxes), a picture of the PCR amplification of the LTRs using DNA material of the four Rosaceae species (see Table S1), and the alignments of the sequenced PCR products together with the sequences that were mined from the genome sequence are provided. The positions of TSDs, beginnings and ends of LTRs, PBS and PPT are also indicated.

Figure S3. Multiple alignments of PBS sites from TGTT, AACA and normal TGCA elements of the *Ale* lineage.

A 20-bp region of each PBS site was extracted from all of the *TGTT* and *AACA* elements, as were the consensus sequences of the other four *Copia Ale* families from pear [38]. Sequence identities over 70% are shaded in blue.

Figure S4. INT phylogenetic relationships among TGTT, AACA and normal TGCA elements.

The INT domains (the integrase core domain, pfam00665) of 67 elements from the six *Copia-like TGTT* and *AACA* families and the consensus sequences of each normal *Copia* TGCA family from pear [38] were used to build the phylogenetic tree. The *TGTT* and *AACA* elements are indicated by various colored branches, and the normal TGCA families are shown in gray. The nucleotide sequence distances are indicated by the scales.

Figure S5. Evidence of transcriptional activity in five *TGTT* and *AACA* elements.

For each element, the whole-nucleotide sequences were used as queries to construct the HISAT alignments using the RNA-seq data from the NCBI species Sequence Read Archive database. Normal short pair reads are shown in the gray bar. Too long paired reads are shown in the purplish red bar. One-sided sequences are indicated by green or blue boxes.

Figure S1.

TGTT1	400	410	TSD	5' LTR star	t 1 440	450	460	470	480	490	500
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Pbrtgtt1_118/1-5539	caat	tttttgaagt	ggaaacto	jtaaaacgtga	ngttattatcta	aaaaggggatataa	agattgtgta	aatattag	gagteetta	ittaggaagga	tatgtgt
Pbrtqtt1_IT3/1-4500	qaa	tttqtcqaqt	attetet	la la a a a c y t y a 1 y a a a a c y t y a	ng taaa tat t	aaaaqqqaatqtaq	aqattqtqta	actattag	gagtcatta	ittaggaagga	tatatqt
Pbrtgtt1_IT1/1-5498	caat	tttttgaagt	ggaaact	j ta <mark>aaacg t</mark> ga	agttattatcta	aaaaggggatataa	agattgtgta	aatattag	gagtccttta	ttaggaagga	tatgtgt
Pbrtgtt1_IT2/1-5400		- a c t t a g t g t	agataat	tg t a a a c g t g a	ngtc <mark>a</mark> ttga	a a a ta a g ta tg ta a	atatattgtc	a a ta t ta g	gagtccttta	ttag <mark>t</mark> aagga	t t a <mark>a t</mark> t g
Mdtgtt1_IT1/1-5520	tagtt	tttcacttag	tactttt	tgtaaacgtga	ngtotttaa	aaataagtatgtaa aaataagtatgtaa	atatattgta	aatattag	gaatccttt gaatccttt	tcaggaatga	ttattg ttaattg
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Mdtgtt1_1T4/1-5520	gatg	attaacgttg	ttcaacc	tataaacgtga	agttatt t	aaataagtatgtaa	atatattgta	aatactag	gagtccttta	ttaggaagga	tttattg
Mdtgtt1_175/1-5520		a g	catttac	tg t <mark>a a a c g t g</mark> a	ngtcttcaa	a a a ta a g ta tg ta a	atatattgta	a a ta t ta g	gaatccttt	ttaggaagga	ttattg
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Figure S1.

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Pbraaca1_IT2/1-5282 Pbraaca1_IT4/1-5273 Pbraaca1_IT4/1-5273 Pbraaca1_IT1/1-5273 Pbraaca1_IT1/1-5270 Pbraaca1_IT1/1-5282 Pbraaca1_IT2/1-5282 Pbraaca1_IT2/1-5282 Pbraaca1_IT5/1-5288 Pbraaca1_IT1/1-5216 Pmaaca1_IT1/1-5216 Pmaaca1_IT1/1-5216 Pbraaca1_IT1/1-5282 Pbraaca1_IT2/1-5282 Pbraaca1_IT2/1-5282 Pbraaca1_IT2/1-5282 Pbraaca1_IT2/1-5282 Pbraaca1_IT4/1-5278 Pbraaca1_IT		999191. 999191. 999191 999191 999191 999191 999191 999191 999191 991111 9111111		agat agat agat agat agat gtag ct t gtag ct t gaa t ct t gaa a t ct gaa a t ct	5140 - agaa - aga - a - aga -	5150 ag c taaa tg ag c taaa tg c taa taa taa tg c taa taa taa taa taa taa taa taa taa ta				- 11 ag tha tha g a tha g tha tha g a tha g tha tha g a tha g tha tha g g tha g tha tha g tha g tha g tha g tha g tha g tha g tha g tha g g tha g tha g tha g tha g tha g c g tha g tha g tha g tha g tha g c g tha g t	<pre>titiggiat titiggiat titiggiat</pre>	a a g g t a a t g - a g a a a t g - a g a
Pbraaca1_IT2/1-5282 Pbraaca1_IT4/1-5273 Pbraaca1_IT4/1-5273 Pbraaca1_IT5/1-5288 Pbraaca1_IT1/1-9212 Pmaaca1_IT2/1-5232 Pbraaca1_IT2/1-5282 Pbraaca1_IT2/1-5282 Pbraaca1_IT4/1-5276 Pbraaca1_IT1/1-5216 Pbraaca1_IT1/1-5216 Pbraaca1_IT1/1-5216 Pbraaca1_IT1/1-5216 Pbraaca1_IT1/1-5216 Pbraaca1_IT1/1-5216 Pbraaca1_IT1/1-5216 Pbraaca1_IT1/1-5216 Pbraaca1_IT2/1-5282 Pbraaca1_IT2/1-5282 Pbraaca1_IT2/1-5282 Pbraaca1_IT2/1-5282 Pbraaca1_IT2/1-5284 Pbraaca1_IT2/1-5286 Pbraaca1_IT2/1-5286 Pbraaca1_IT2/1-5286 Pbraaca1_IT2/1-5286 Pbraaca1_IT2/1-5286 Pbraaca1_IT2/1-5286 Pbraaca1_IT1/1-5216	tt ag ct tg ag t tt ag ct tg ag t tg g ct tg ag t catg taatta tc atg taatta tt atg taatg tc atg taatta tt atg taatg tc atg taatta tt atg taatg tc atg taatta tc atg taatta t atg taatta tc atg taatta tc atg taatta tc atg taatta t atg taatta tc atg taatta ta atg taatta tc atg taatta ta a catg ag a ata catag a a ata catag a	gggtgt; gggtgt; gggtgt; gggtgt; gggtgt; gggtgt; ggtgtgt; ggtgtgt; ggtgtt gtttat gtttat gtttat gtttat gtttat gtttat gtttat		agat	5140 - agaa - a - agaa - a - agaa - a - a - a - a - a - a - a - a - a -	5150 tag c taaa tg ag c taaa tg cag c taa taa tg cag c				a ita gi ta ita g a ita gi ta ita g g ita gi ta ita g g itg gi ta ita g g itg gi ta ita g g itg g ita ita g g itg g ita ita g g itg g ita ita g g itg g itg ga it - g a itg g a itg a it - a a itg ia ita 5300 C i i i i g ca a g a c i i i g ca a g a	<pre>titiggiat titiggiat titiggiat</pre>	a a a g t a a a g t a a t g a a t g



PbrTGTT1_IT7 (Plus)	TSD PBS PPT TSD wet lab resequence LTR1 LTR	FR2 Marker
Pbr_TGTT1_IT7_LTR1 Resequence	GCTGCCCATTGTGAGGCTTAACCATTCCCCCCACCCACTTAGGGTAGATAATTGTAAACGT GCTGCCCATTGTGAGGCTTAACCATTCCCCCCACCCACTTAGGGTAGATAATTGTAAACGT TSD LTR1 start	99
Pbr_TGTT1_IT7_LTR1 Resequence	GAGTTATTAAAAATAAGTATGTAAATATATTGTCAATATTAGGAGTCCTTTATTAGGAAG GAGTTATTAAAAAATAAGTATGTAAATATATTGTCAATATTAGGAGTCCTTTATTAGGAAG	3
Pbr_TGTT1_IT7_LTR1 Resequence	GATTAATCGTTGTGTCCTTTATTGATTATTGTTTCCATATAGAACAAGGAATGTATTTGT GATTAATCGTTGTGTCCTTTATTGATTATTGTTTCCATATAGAACAAGGAATGTATTTGT LTR1 end PBS	11
Pbr_TGTT1_IT7_LTR1 Resequence	ATATATTTCAAGGAAGTAATACAATAAAAATTATCCCGTAAAATTCTATTTGGCATCAGA ATATATTTCAAGGAAGTAATACAATAAAAATTATCCCGTAAAATTCTATTTGGCATCAGA	where
PBR_TGTT1_IT7_LTR2 RESEQUENCE	GTGATATCTATGCACCAACTTGAGGGGGGAGTGTAAACGTGAGTCATGAAAAATAAGTATG GTGATATCTATGCACCAACTTGAGGGGGGGGGG	-
PBR_TGTT1_IT7_LTR2 RESEQUENCE	TAAATATATTGTAAATATTAGGAGTCCTTTATTAGGAAGGA	
PBR_TGTT1_IT7_LTR2 RESEQUENCE	TTGATTATTGTTTCCATATAGAACAAGGATTGTATTTGTATATATTTCAAGGAAGTAATA TTGATTATTGTTTCCATATAGAACAAGGATTGTATTTGTATATATTTCAAGGAAGTAATA LTR2 end TSD	
PBR_TGTT1_IT7_LTR2 RESEQUENCE		
ATAATT GTAAAC GTGAGTTATT TSD LTR1 start	130 140 150 160 170 180 190 TAAAAATAA G TAT G TAAATATAT T G T CAA TAT T A G G A G G C C T T TAT T A G G A A G G A T T A A T C G T T G T C T A A A A A A A A A A A A A A A A A A A	200 TTATTGATT.
210 ATT G TTT C CATA TA G AA CAA G	00 A A T G T A T A T A T A T A T A T A C A A G G A A G T A A T A C A A T A A A A A T T A T C C C G T A A A A T T C C C C G T A A A A T T C C C C G T A A A A T T C C C C G T A A A A T T C C C C G T A A A A T T C C C C G T A A A A T T C C C C G T A A A A T T C C C C G T A A A A T T C C C C G T A A A A T T C C C C G T A A A A T T C C C C G T A A A A T T C C C C G T A A A A T T C C C C G T A A A A T T C C C C G T A A A A T T C C C C G T A A A A T T C C C C G T A A A A T T C C C C G T A A A A T C C C C G T A A A A T C C C C G T A A A A T C C C C G T A A A A T C A G G A G C A G C A C C C C G T A A A A T C A G C C C G T A A C C C C C G T A A A A T C C C C G T A C C C C C C C C C C C C C C C C C C	MMMM <u>300</u> TCAGAGCCAAG
mhmmmm		PBS MMMMMM
AACTTGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	180 190 200 210 220 230 240 250 TG AG TCAT G AAAAATAA G TAT G TAAATAT T G TAAATAT T A G G AG T C C T T TAT T A G G AA G G AT T AA T T G T T G	260 TGTCCTTTATT
GATTATTGTTTCCATATAGA	٨٨٨٨ ٨٨٨ ٨٨٨ ٨٨٨ ٨٨٨ ٨٨٨ ٨٨٨ ٨٨٨ ٨٨٨ ٨	лмлллмл ³⁵⁰ г т <u>атаат</u> .
MANAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA		d tsd MMMM

MdTGTT1_IT2 (Minus)	TSD PBS	gag pol	PPT TSD	LTR1 LTR2 Marker
Md_tgtt1_IT2_LTR2 Resequence	wet lab resequence AGAACCCATAGAATCAGCACTCAT AGAACCCATAGAATCAGCACTCCT	26 IGGAATAATCATGGA IGGAATAATCATGGA	wet lab resequence	6999
Md_tgtt1_IT2_LTR2 Resequence	ATTTTACGGGATAATTTTCATTGT ATTTTACGGGATAATTTTCATTGT	ГАТТАСТТССТТБАА/ ГАТТАСТТССТТБАА/	ATATATACAAATACAATTCTTG ATATATACAAATACAATTCTTG	
Md_tgtt1_IT2_LTR2 Resequence	ТТТТАТАТGGAAANAATAATCAAT ТТТТАТАТGGAAACAATAATCAAT	TAAAGGACACAANAAT TAAAGGACACAA <mark>C</mark> AAT	TTAAACCTTCCTAATAAAGGAC TTAAACCTTCCTAATAAAGGAC LTR2 start PPT	~
Md_tgtt1_IT2_LTR2 Resequence	τοατααταττταςαατατατττας τοατααταττταςαατατατττας	САТАСТТАТТТТТААТ	IGACTCACGTTTACACTCACCC IGACTCACGTTTACACTCACCC	1
Md_tgtt1_IT2_LTR2 Resequence	TCAAGTTGGTACATAGATATCACA TCAAGTTGGTACATAGATATCACA	ACATGCCCAACTTGAG ACATGCCCAACTTGAG	CAAGTGAGTCACCGAACTTTCG CAAGTGAGTCACCGAACTTTCG	-
Md_tgtt1_IT2_LTR1 Resequence	CAGAAAAAAATCAGTCGACTGAGC CAGAAAAAAATCAGTCGACTGAGC PBS LTR1 end	САСААСАĞАААААСТ САСААСАĞАААААСТ	AGGGTTATGGCAGCCTTGGCTC AGGGTTATGGCAGCCTTGGCTC	-
Md_tgtt1_IT2_LTR1 Resequence	TGATGCCAAATAGAATTTTACGGC TGATGCCAAATAGAATTTTACGGC	GATAATTTTCATTGT/ GATAATTTTCATTGT/	АТТАСТТССТТGАААТАТАТАС АТТАСТТССТТGАААТАТАТАС	
Md_tgtt1_IT2_LTR1 Resequence	AAATACAATCCTTGTTCTATATGA AAATACAATCC <mark>C</mark> TGTTCTATATGA	ААААСААТААТСААТ ААААСААТААТСААТ	AAAGGACACAACAATTAAACCT AAAGGACACAACAATTAAACCT	
Md_tgtt1_IT2_LTR1 Resequence	TCCTAATAAAGGACTCCTAATATI TCCTAATAAAGGACTCCTAATATI LTR1 start TSD	ГТАСААТАТАТТТАС, ГТАСААТАТАТТТАС,	АТАСТТАТТТТ. ААТGACTCAC АТАСТТАТТТТ <mark>А</mark> АТGACTCAC	
Md_tgtt1_IT2_LTR1 Resequence 110 120	GTTTACAGTAATTTGATTGTTTCT GTTTACAGTAATTTGATTGTTTCT 130 140	ITCTTCTGTAATATA ITCTTCTGTAATATA 150 160	TTTCTGTTAGTTTATTGTTCTT TTTCTGTTAGTTTATTGTTCTT 170 180	190 200
TSD LTR2 end				
210 220	230 240	250 260	270 280	290 300
AGGACACAACAATTAAACC	h.	TACAATATATTTACAT	LTR2	start PPT
	MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM	TTTT CATT G TAT TAC T	MMMMMMMMMM ⁸⁰ с с т т 6 ала т ²⁰⁰ т а т а с ала т ²⁰⁰ с ала т	
P MMMAAAMMAAM 330 340	BS LTR1 end	MAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA		WANN AMAYAMAMA
ACAATAAT CAATAAAG GACA	CAACAAT TAAACCTT CC TAATAAA GGA	CTCCTAATATTTACAA	IATATTTACATACTTATTTTTAATG	LTR1 start TSD
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MdTGTT1_IT4 (Plus)	LTR gag pol LTR PPT TSD TSD PBS PPT TSD wet lab resequence wet lab resequence	
Md_tgtt1_IT4_LTR1 Resequence		
Md_tgtt1_IT4_LTR1 Resequence	TTGTAAATACTAGGAGTCCTTTATTAGGAAGGATTTATTGTTGTGTCCTTTATTGATTAG TTGTAAATACTAGGAGTCCTTTATTAGGAAGGATTTATTGTTGTGTCCTTTATTGATTAG	
Md_tgtt1_IT4_LTR1 Resequence		
Md_tgtt1_IT4_LTR1 Resequence		
Md_tgtt1_IT4_LTR2 Resequence	GTGTGATATATATGCACCAACTTGAGGGGGGGGGGGGGG	
Md_tgtt1_IT4_LTR2 Resequence	GTAAATATATTGTAAATACTAGGAGTCCTTTATTAGGAAGGA	
Md_tgtt1_IT4_LTR2 Resequence	ATTGATTAGTGTTTCCTTATAGAACAAGGATTGTATATGTATATATTTCAAGAAAGTAAT ATTGATTAGTGTTTCCTTATAGAACAAGGATTGTATATGTATATATTTCAAGAAAGTAAT	
Md_tgtt1_IT4_LTR2 Resequence	ACAATGGAAAATTACCCCGTAAAATTCTATTCAACCTCTCTATTTTAAAAAACTTCGGATT ACAATGGAAAATTACCCCGTAAAATTCTATTCAACCTCTCTATTTTAAAAAACTTCGGATT \$20 \$30 \$40 \$50 \$60 \$70 \$80 \$90 900	
TSD LTR1 start		TTT
МАЛАА с с т тата даа саа g дат т	MAAAMAAMAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	M
Annanahanna		
240 250 T T G A G G G G G G G G G G G G G G G G	260         270         280         300         310         320         330         340           G A G IT G I T AAA T A A G T AT G T AA AT A T T G T A A A T A C T A G G A G G C C T T T A T T A G G A A G G A T T A T T G T T G T C C T T T A T T G A T A G         G A G T C C T T A A T A A G T A T A T A T A T T G T A A T A C T A G G A G G C C T T T A T T A G G A A G G A T T A T T G T T G T T G T T A T T G A T A G         G A G T T A A T A A G T A T A T A T A T	) TG:
	MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM	N
mmmmm		

PpTGTT1_IT2 (Plus)	LTR gag pol LTR FTSD PBS PPT TSD wet lab resequence wet lab resequence LTR1 LTR2 Marker
Pp_tgtt1_IT2_LTR1 Resequence	TAAATATATTATCCTATTTGGATGAAAGTATGAATTTTCTGTAAACGTGAGTTATTTAAA TAAATATATTATCCTATTTGGATGAAAGTATGAATTTTCTGTAAACGTGAGTTATTTAAA TSD LTR1 start
Pp_tgtt1_IT2_LTR1 Resequence	TAAGTATGTAAATATATTGTGAATATTAGGAGTCCTTTATTAGGAAGGA
Pp_tgtt1_IT2_LTR1 Resequence	GTCCTTTATTGATTAGTGTTTCCTTGTAGAGTAAGGATTATATGTGTATATATTTCAAGG GTCCTTTATTGATTAGTGTTTCCTTGTAGAGTAAGGATTATATGTGTATATATTTCAAGG LTR1 end PBS
Pp_tgtt1_IT2_LTR1 Resequence	AAGTAATACAATGAGAAATTACCCCGTAAAATTCTATTTGGCATCAGAACTTAGGTTGCC AAGTAATACAATGAGAAATTACCCCGTAAAATTCTATTTGGCATCAGAACTTAGGTTGCC
Pp_tgtt1_IT2_LTR2 Resequence	AAAGTTTGGTAACTCACTTGACAAGTTGGGCATGTGTGTG
Pp_tgtt1_IT2_LTR2 Resequence	GGGAGTGTAAACGTGAGTTATTTAAATAAGTATGTAAATATATTGTGAATATTAGGAGTC GGGAGTGTAAACGTGAGTTATTTAAATAAGTATGTAAATATATTGTGAATATTAGGAGTC PPT LTR2 start
Pp_tgtt1_IT2_LTR2 Resequence	CTTTATTAGGAAGGATTTATTGTTGTGTCCTTTATTGATTAGTGTTTCCTTGTAGAGTAA CTTTATTAGGAAGGATTTATTGTTGTGTCCTTTATTGATTAGTGTTTCCTTGTAGAGTAA
Pp_tgtt1_IT2_LTR2 Resequence LTF	GGATTATATGTGTATATATTTCAAGGAAGTAATACAATGAGAAATTACCCCGTAAAATTC GGATTATATGTGTATATATTTCAAGGAAGTAATACAATGAGAAATTACCCCGTAAAATTC 22 end TSD
Pp_tgtt1_IT2_LTR2 Resequence	TATTTTTTCTATATATTAAACAGCACAAATAACTCTTTTACATGAGTTCTGGGCTCATGA TATTTTTTCTATATATAAACAGCACAAATAACTCTTTTACATGAGTTCTGGGCTCATGA
AATTITCT GTAAAC GT G AGT	80     90     100     110     120     130     140     150     160       TATTTAAA TAA GTAT GTAAATATATT GT GAATATTA G GAAGGATTTATT GT TG TG TG TC TTTATT GT TG TG TG TC TTTATT GATTA GT GT TT
	AT GT GT AT AT AT T T CAA GG AA GT AAT AC AA T G A GAA AT T AC CC C C G T AAAAT T C LAT T T G GC AT C A G AA C T T A G G T T           LT GT GT AT AT AT T T C CAA GG AA GT AAT AC CAA T G A GAA AT T AC CC C C G T AAAAT T C LAT T T G GC AT C A G AA C T T A G G T T           LT GT GT AT AT AT T T C CAA GG AA GT AAT AC CAA T G A G AA AT T AC CC C C G T AAAAT T C LAT T T G GC AT C A G AA C T T A G G T T           LT GT GT AT AT AT T T C CAA GG AA GT AAT AC CAA T G A G AA AT T AC CC C C G T AAAAT T C LAT T T G GC AT C A G G AA C T T A G G T T
	$W_{10}^{M} W_{10}^{M} W_{10}^{M$
MMMMM	



PmTGTT1_IT1 (Plus)	LTR gag pol LTR TSD PBS PPT TSD	
	wet lab resequence wet lab resequence	LTR1 LTR2 Marker
Pm_TGTT1_IT1_LTR1 Resequence	AATTTGCTTTCTTTGATTTTCAATCGTATATACAATTACGGAGAGATATTGTTTTTGTAA AATTTGCTTTCTTTGATTTTCAATCGTATATACAATTACGGAGAGATATTGTTTTTGTCT TSD LTR1 start	è e e
Pm_TGTT1_IT1_LTR1 Resequence	ACGTGAGTTATTTAAATAAGTATGTAAATATATTGTGAATACTAGGAGTCCTTTATTAGG ACGTGAGTTATTTAAATAAGTATGTAAATATATTGTGAATACTAGGAGTCCTTTATTAGG	
Pm_TGTT1_IT1_LTR1 Resequence	AAGGATTTATTGTTGTGTCCTTATTGAGTAGTGTTTCCTTGTAGAACAAGGATCATATAT AAGGATTTATTGTTGTGTCCTTATTGAGTAGTGTTTCCTTGTAGAACAAGGATCATATAT	1C (
Pm_TGTT1_IT1_LTR1 Resequence	GTATATATTTCAAGGAAGTAATACAATGAAACTTACCCCGTAATATTCTATTTGGCATCA GTATATATTTCAAGGAAGTAATACAATGAAACTTACCCCGTAATATTCTATTTGGCATCA LTR1 end PBS	
Pm_TGTT1_IT1_LTR1 Resequence	GAACTTAGGTTGCCGTAACCCTAGAATATTTTTTCCGCTGCTGTTGACGGCCGACTCTTT GAGCTTAGGTTGCCGTAACCCTAGAATATTTTTTCCGCTGCTGTTGACGGCCGACTCTTT	
Pm_tgtt1_IT1_LTR2 Resequence	TTGAGGGGGAGTGTAAACGTGAGTTATTTAAATAAGTTTGTAAATATATTGTGACTACTA TTGAGGGGGGGGGG	
Pm_tgtt1_IT1_LTR2 Resequence	GGAGTCCTTTATTAGGAAGGATTTATTGTTGTGTCCTTATTGAGTAGTGTTTCCTTGTAG GGAGTCCTTTATTAGGAAGGATTTATTGTTGTGTCCTTATTGAGTAGTGTTTCCTTGTAG	
Pm_tgtt1_IT1_LTR2 Resequence	AACAAGGATCATATATGTATATATTTCAAGGAAGTAATACAATGAAAATTACCCCGTAAT AACAC <mark>GGATCATATATGTATATATTTCAAGGAAGTAATACAATGAAAATTACCCCGTAAT</mark>	
Pm_tgtt1_IT1_LTR2 Resequence	ATTCTATTGTTTTTATATCAGATGTTTAGCCCATAACTAATGCTT. ATTCTATTGTTTGTATATCAAATGTATGTCCCATCCATAACTTTAA	
ATATTGTTTTTGTCTACGTGAC	370 380 390 400 410 420 430 ЭТТАТТТАААТАА G ТАТ G ТАААТАТАТ I G T G ААТАСТА G G A G T C C T T TATTA G G A A G G AT T TA T G T G T	440 450 C C T T A T T G A G T A G T G T T T
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C T T G T A G A A C A A G G A T C A T A	TAT GTATATAT T T CAAG GAAGTAATACAATG AAACT TACCCCC G TAATATT CTATT T G GCATCAGA	G C T TAG G T T G
MMMMMM 210 220	230 240 250 260 270 280 290	000 310
	GAGTTATTTAAATAAGTTTGTAAATATATTGTGACTACTAGGAGTCCTTTATTAGGAAGGA	TCCTTATTGAGT
320	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	0 400
	CACGGATCATATATGTATATATTTCAAGGAAGTAATACAATGAAAATTACCCCGTAATATTC	2 end TSD
		MINIMAN



LTR gag pol LTR PPT TSD wet lab resequence wet lab resequence
GCACTACTTTCCGTGTGGGCGACTCTCTTGGTATGTAATCTTAATTATGTTAGTCGTGAG GCACTACTTTCCGTGTGGGCGACTCTCTTGGTATGTAATCTTAATTATGTTAGTCGTGAG TSD LTR1 start
TCAATATTAGGGAAAAAAGGGAATGTAAATACTAGGAGTCTTTTATTAGGTAGG
TATAAGCTTTATTATTTGTTTCCTTGTTGAACAATGATTGTACATGTATATATTTCAAAA TATAAGCTTTATTATTTGTTTCCTTGTTGAACAATGATTGTACATGTATATATTTCAAAA LTR1 end PBS
GGAGTAATACCAGAAATTATCCCGTAAAAGTTCTATTTGGTATCAAGAGCCTTGTGTTGT GGAGTAATACCAGAAATTATCCCGTAAAAGTTCTATTTGGTATCAAGAGCCTTGTGTTGT
CTTGAGGGGGAGTGTTAGTCGTGAGTCAATATTAGGGAAAAAAGGGAATGTAAATACTAG CTTGAGGGGGGAGTGTTAGTCGTGAGTCAATATTAGGGAAAAAAGGGAATGTAAATACTAG PPT LTR2 start
GAGTCCTTTATTAGGTAGGTTTGTTTATAAGCTTTATTATTTGTTTCCTTGTTGAACAAT GAGTCCTTTATTAGGTAGGTTTGTTTATAAGCTTTATTATTTGTTTCCTTGTTGAACAAT
GATTGTACATGTATTTATTTCGAAAGGAGTAATACCAGAAATTATCCCGTAAAAGTTCTA GATTGTACATGTATTTATTTCGAAAGGAGTAATACCAGAAATTATCCCGTAAAAGTTCTA LTR2 end TSD
TTAATTAACCCTTGTATTTAATTAGCTGCATTTCATCCATGGACGATTACTTCAATTTTG TTAATTAACCCTTGTATTTAATTAGCTGCATTTCATCCATGGACGATTACTTCAATTTTG
ACAT GTATATATT T CAAAAG GAGTAATAC CA GAAAT TAT CCCC G TAAAAG TTC LAT T G G TATCAAGAG C CTTG T G T T G T LTR1 end PBS PMANAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
т с бт б а б ² с лататта б ² балалала б б ² а а б б ла т б т ла т ла б б а б т с с т т а т т а б б а б с т т т б т т а т т т с с с т т а т т а б с т т т б т т а т т т с с с т т а т т а б с т т т б т т а т т т с с с т т а т т а б с т т т б т т а т т т с с с т т а т т а б с т т т б т т а т т т с с с т т а т т а б с т т т б т т а т т с с т т б т т т а т т с с с т т а т т а б с т т т б т т а т т с с с т т а т т а б с т т т а с с т т б т т а т т а с с т т а т т а с с т т а т т а с с т т а т т а с с т т а т т а с с т т а т т а с с т т б т т а т т т с с с т т а т т а с с т т с с т т а т т а с с т т а т т а с с т т а т т а с с т т а т т а с с т т а т т а с с т т а т т а с с т т п а т т а с с т т а т т а с с т т а т т а с с т т а т т а с с т т а т т а с с т т а т т а с с т т а т т а с с т т а т т а с с т т а т т а с с т т а т т а с с т т а т т а с с т т а т т а с с т т а т т а с с т т а т т а с с т т а т т а с с т т а т т а с с т т а т т а с с т т а т
TGATGGGGGGGGGG



PbrTGTT4_IT2 (Plus)	LTR     gag     pol     LTR       TSD     PBS     PPT     TSD       wet lab resequence     wet lab resequence     wet lab resequence
Pbr_tgtt4_IT2_LTR1 Resequence	GGGGTGCCCACATCATTTCCAGAGCTACTGTATCCACCTTGTTAAAGGAAAGTATTGGAA GGGGTGCCCACATCATTTCCAGAGCTACTGTATCCACCTTGTTAAAGGAAAGTATTGGAA TSD LTR1 start
Pbr_tgtt4_IT2_LTR1 Resequence	GACAGCACAGCAAGCATTTGGACAGAAGGAATATTACAGCAGACTAGCACATGGTGTCAG GACAGCACAGC
Pbr_tgtt4_IT2_LTR1 Resequence	CTCATGTGCTCTGATGTGTTGCAGCATGGGCAACAAGCACGCCACCTTTATAGCTGTA <mark>GC</mark> CTCATGTGCTCTGATGTGTTGCAGCATGGGCAACAAGCACGCCACCTTTATAGCTGTAGT
Pbr_tgtt4_IT2_LTR1 Resequence	ТТАТТЄСАТЄССТСТСТСТААСАТСТАТАТААААССАТТЄСАЄСАЄАААТЄААТСАТАА ТТАТТЄСАТЄССТСТСТСТААСАТСТАТАТААААССАТТЄСАЄСАЄАААТСААТС
Pbr_tgtt4_IT2_LTR1 Resequence	CCAAGAAATATTAAACTCACAATTCATTATGGTATCAAAGCACCGATCCCGGTGACTCTG CCAAGAAATATTAAACTCACAATTCATTATGGTATCAAAGCACCGATCCCGGTGACTCTG LTR1 end PBS
Pbr_tgtt4_IT2_LTR2 Resequrnce	GGTGTGATTGACATTCACACTCCAACTTGAGGGGGAGTGTTAAAGGAAAGTATTGGAAGA GGTGTGATTGACATTCACACTCCAAC <u>TTGAGGGGGAGTGTT</u> AAAGGAAAGTATTGGAAGA PPT LTR2 start
Pbr_tgtt4_IT2_LTR2 Resequrnce	CAGCACAACAAGCATTTGGACAGAAGGAATATTACAGCAGACTAGCACATGGTGTCAGCT CAGCACAACAAGCATTTGGACAGAAGGAATATTACAGCAGACTAGCACATGGTGTCAGCT
Pbr_tgtt4_IT2_LTR2 Resequrnce	CATGTGCTCTGATGTGTGCAGCATGGGCAGCAAGCACGCCACCTTTATAGCTGTAGCTT CATGTGCTCTGATGTGTTGCAGCATGGGCAGCAAGCACGCCACCTTTATAGCTGTAGCTT
Pbr_tgtt4_IT2_LTR2 Resequrnce	ATTGCATGCGTGTGTGTGTAAGATGTATATAAAACCATTGCAGCAGAGAATGAAT
Pbr_tgtt4_IT2_LTR2 Resequrnce	AAGAAATATTAAACTCACAATTCATTACACCTGGTATTGTGAAGCCTTGAACAAACGTTA AAGAAATATTAAACTCACAATTCATTACACCTGGTATTGTGAAGCCTTGAACAAACGTTA
250 260 CCACCTTGTTAAAGGAAAGTA TSD LTR1 start	AT T G G AAG ACA G CAC A G CAA G CATT T G G ACA G AA G G AAT AT T A CAG C A G ACT A G C A CAT G G T G T C A G C T C A T G T G C T C T G A T G T G T G T G T G T G T G T G T
аассаад 460 ататтааас МММММММММ	470 TCACAATT <u>CATTATGGTATCAAA</u> GCACCGATCCCG LTR1 end PBS MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM
T G AG G G G G G G G G T G T T AAA G G PPT LTR2 start	$W = \frac{260}{10} = \frac{270}{10} = \frac{280}{10} = \frac{280}{10} = \frac{290}{10} =$
TGCTCTGATGTGTTGCA	GCAT GG G CAG CAA G CAC G C CACCT TT AT A G C T G T A G C T T A T T G C A T G C G T G T G T A A G A T G T A T A A A A A

Figure S2.	PbrAACA1_IT3 (Plus)	LTR gag pol LTR TSD PBS PPT TSD wet lab resequence wet lab resequence	
	Pbr_aaca1_IT3_LTR1 Resequence	CTTGTACAGAGCTGCTTGTAAGAAAGTTAATATTAAAGATGAAGATGCTATATCATAACT CTTGTACAGAGCTGCTTGTAAGAAAGT <u>TAATATTAAAG</u> ATGAAGATGCTATATCATAACT TSD LTR1 start	
	Pbr_aaca1_IT3_LTR1 Resequence	ACAGTTGTTAGTTATTAGTTTGGTATAAGGTGTCATTCAT	
	Pbr_aaca1_IT3_LTR1 Resequence	GGTAGCTTAGAATAGCTAAATGTAAATAGTCTAAAGACTATATATA	LTR1 LTR2 Marke
	Pbr_aaca1_IT3_LTR1 Resequence	ТАТТТТӨБААТААТӨАӨААТАСАСАӨАААТСТТААТАСТТААБАААТСТТТСТТСССС ТАТТТТӨБААТААТӨАӨААТАСАСАӨАААТСТТААТАСТТААБАААТСТТТСТТСССС	-
	Pbr_aaca1_IT3_LTR1 Resequence	TCTTCTCTCTTCTTTCTCTCTCTCTCTTTTGCAAGAACACAGAACTTCTACATGG TCTTCTCTCTTCTTCTCTCTCTCTCTCTTTTGCAAGAACACAGAACTTCTACATGG LTR1 end PBS	
	Pbr_aaca1_IT3_LTR1 Resequence	TATCCTTCGCCGCTTGCCTCACGGCCATTTCGATCCATTCTTCGCCTTTGTTTCTCTGAT TATCCTTCGCCGCTTGCCTCACGGCCATTTCGATCCATTCTTCCGCTTTGTTTCTCTGAT PBS	
	Pbr_aaca1_IT3_LTR2 Resequence	AATTCTTAATTCTTCCAAGTTTAGCTTGAGGGGGGTGTAAAGATGAAGATGCTATATCATA AATTCTTAATTCTTCCAAGTTTAGCT <u>TGAGGGGGGTGTAAAG</u> ATGAAGATGCTATATCATA PPT LTR2 start	
	Pbr_aaca1_IT3_LTR2 Resequence	ACTACAGTTGTTAGTTATTAGTTTGGTATAAGGTGTCATTCAT	
	Pbr_aaca1_IT3_LTR2 Resequence	TGTGGTAGCTTAGAATAGCTAAATGTAAATAGTCTAAAGACTATATATA	
	Pbr_aaca1_IT3_LTR2 Resequence	TTATTATTTTGGAATAATGAGAATACACAGAAATCTTAATACTTAAGAAATCTTTCTT	
	Pbr_aaca1_IT3_LTR2 Resequence	ТСӨСТСТТСТСТСТТСТТСТСТСТСТСТТТТТТССААБААСАСАБААСТТСТАС ТСӨСТСТТСТСТСТТСТТСТСТСТСТСТСТТТТТТССААБААСАСАБААСТТСТАС	
	LTR2		
	Pbr_aaca1_IT3_LTR2 Resequence	AAATATAGTTTGCTTTGTTTCGTAATGGTTGTGGGGAAGAAAGTTAATATATACACCTTC AAATATAGTTTGCTTTGTTTCGTAATGGTTGTGGGGAAGAAAGTTAATATATACACCTTC	
	100 110	120 130 140 150 160 170 180	190 200

TSD LTR1 start AAAAA. mannanananananananananananan 240 G A 1 250 T G G A T T A T T T T G G A mmm AACTTCTACATGGTATCCTTCGCCGCTGCCTC. 310 TTTCTCGCTCTTCTCTCTCTC 340 350 C T T T C T T T G CAA G A A 420 430 440 TAATTAGTTTATCTTATGTGGT MAN AGCTTAGA MMMMM стстстсттт Immemory management of the second sec

PbrAACA2_IT4 (Plus)	LTR     gag     pol     LTR       TSD     PBS     PPT     TSD       wet lab resequence     wet lab resequence
PbrAACA2_IT4_LTR1 Resequence	ACTAAAGGTAGTTAGATTACTAAGGGAAATGCATAAAGAGTCTAATAGTAGTAGTAGTAGTAGTATAGTAGTAGTAGTAGTA
PbrAACA2_IT4_LTR1 Resequence	AACTGGAGTCAGTTAGACAAGGGTAGTGTGTAATTAATTGTAAATGTTAGGGTTATTTTT AACTGGAGTCAGTTAGACAAGGGTAGTGTGTAATTAATTGTAAATGTTAGGGTTATTTTT LTR1 LTR2 Marker
PbrAACA2_IT4_LTR1 Resequence	ACCCTTGTATTAATGTCTATATATATACTGTTGTAAATGCATTATTGTAAGTAA
PbrAACA2_IT4_LTR1 Resequence	
PbrAACA2_IT4_LTR1 Resequence	PBS AGTCGCCACCGCCTTCCGGCCTTGGTGACTTTTCGATCCTCACGCCACCGTCTTCCGCCT AGTCGCCACCGCCTTCCGGCCTTGGTGACTTTTCGATCCTCACGCCACCGTCTTCCGCCT
PbrAACA2_IT4_LTR2 Resequence	
PbrAACA2_IT4_LTR2 Resequence	TGGAGTCAGTTAGACAAGGGTAGTGTGTAATTAATTGTAAATGTTAGGGTTATTTTTACC TGGAGTCAGTTAGACAAGGGTAGTGTGTAATTAATTGTAAATGTTAGGGTTATTTTTACC
PbrAACA2_IT4_LTR2 Resequence	CTTGTATTAATGTCTATATATATACTGTTGTAAATGCATTATTGTAAGTAA
PbrAACA2_IT4_LTR2 Resequence	GAAGATATTTTTCTACTTCTGAGTTCCTTACAAGTTAAGGTTTCTACAATGCATGGCT GAAGATATTTTTCTACTTCTGAGTTCCTTACAAGTTAAGGTTTCTACAATGCATGGCT
AAT GCATAAA GA GT CTAA TSD LTR1 start	1 ²⁰ 9 TA 9 TA 9 CT ⁶ TATAACT 9 9 ²⁰ 9 TCA 9 TTA 9 ²⁰ CAA 9 T A 9 ²⁰ 9 T 9 T 9 ²⁰ 1 9
TAA GGTTTCTACATGG	
CTATTAAT GT CTATATATAT	270 280 290 390 390 390 390 390 CTAATAATGTAATGTAATGTAATGTAATGTAATGTAATG
	للمناهم المعتقد والمنتقية فقفاتهم اللامية والمقتقة والمعادية والمناقدة والمناقدة والمناقد والمناقد والمناقد

D Imminimum Imminimum

Pbr_AACA3_IT4 (Plus)	LTR gag pol LTR PPT TSD PBS wet lab resequence wet lab resequence	
Pbr_AACA3_IT4_LTR2 Resequence	TACTCCAAGTTTAGTTTGAGGGGGGGGAGTAATAACCATATGAT GTTCAAACTACACTTGGA TACTCCAAGTTTAGTTT	Marker LTR2
Pbr_AACA3_IT4_LTR2 Resequence	TGAGTTAGTTAGAGGTTGTTAGTGAGGGTATTTGGGTCTTTTGCAATAGGCCTAATGACT TGAGTTAGTTAGAGGTTGTTAGTGAGGGTATTTGGGTCTTTTGCAATAGGCCTAATGACT	-
Pbr_AACA3_IT4_LTR2 Resequence	ATAAAAAGGAAGTTGTAGAGATCATTTTCTGTAGAGTAGTGTTCGACTATTGTGATAAAT ATAAAAAGGAAGTTGTAGAGATCATTTTCTGTAGAGTAGTGTTCGACTATTGTGATAAAT	-
Pbr_AACA3_IT4_LTR2 Resequence	ACAGAGAGCATTTCCTTCATCTTCTTTCTTCCTTGTTCATCTTTCTGCCATTGTTTCTTTC	
Pbr_AACA3_IT4_LTR2 Resequence	CAAT <mark>C</mark> TTTCATAGATTCATAGGTTAACATGGTATTTCAATGTAGTTAACATTCTTTTCTA CAAT <mark>T</mark> TTTCATAGATTCATAGGTTAACATGGTATTTCAATGTAGTTAACATTCTTTTCTA	
	170 174 200 210 210 210 210 210 210 200 210 21	230 240 GCCTAATGACTAT.
алалад с 250 алалад с адагт с та с адаг с алала Ма ААА. А Даа	CATTITET GTAGAGTAGTGTEGACTATTGTGATAAATACAGAGAGCATTTCCTTCATCTTCTTCC	
MWWWWWWWWWWWWW TGCCATTGTTTCTTCTTCA	VVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVV	MAAAAMAAAAAA
MMMMMMM		

PbrAACA4_IT6 (Plus)	LTR     gag     pol     LTR       TSD     PBS     PPT     TSD       wet lab resequence     wet lab resequence	LTR1	LTR2	Marke
Pbr_aaca4_IT6_1 Resequence	ТААĞТТТССАААĞТА <mark>С</mark> ТТАААĞТĞТТТ <mark>С</mark> ТТĞТАСĞAAĞCATTTCAAĞTĞTTTTTTTAA ТААĞТТТССАААĞТ <mark>АА</mark> ТТАААĞТĞTTTTTTĞTACĞAAĞCATTTCAAĞTĞTTTTTTTTTAA —			
Pbr_aaca4_IT6_1 Resequence	TATTTAATAACTGATATAACAGAAATATAGTTAGAGGGGTATTATTGTAATTGGAATATA TATTTAATAACTGATATAACAGAAATATAGTTAGAGGGGGTATTATTGTAATTGGAATATA TSD LTR1 start			
Pbr_aaca4_IT6_1 Resequence	TGGCTATATAAGGGATTGTATAGCTAGTATTTCATTAAGTTCATTTTGTATACATTTTAT TGGCTATATAAGGGATTGTATAGCTAGTATTTCATTAAGTTCATTTTGTATACATTTTAT			
Pbr_aaca4_IT6_1 Resequence	CCATTCAATCAATACAATCTTTCTAGTTTTCTCTCTCTATCATCTTTTTCCCTTGTACC CCATTCAATCAATACAATCTTTCTAGTTTTCTCTCTCTATCATCTTTCTCTTTTCCCTTGTACC LTR1 end PBS			11
Pbr_aaca4_IT6_1 Resequence	AACTTTATATTTTGCAATGTAGTTAACATGGTATCAGAGCCACCAGGCTCACGGCATGGA AACTTTATATTTTGCAATGTAGTTAACATGGTATCAGAGCCACCAGGCTCACGGCATGGA			
Pbr_aaca4_IT6_2 Resequence	GGCCAGCTCAAACTTCACTTGGATACTCCAAGTTTAGTTTGAGGGGGGGG			
Pbr_aaca4_IT6_2 Resequence	TATAACAGAAATATAGTTAGAGGGGTATTATTGTAATTGGAATATATGGCTATATAAGGG TATAACAGAAATATAGTTAGAGGGGTATTATTGTAATTGGAATATATGGCTATATAAGGG			
Pbr_aaca4_IT6_2 Resequence	ATTGTATAGCTAGTATTTCATTAAGTTCATTTTGTATACATTTTATCCATTCAATCAA			
Pbr_aaca4_IT6_2 Resequence	CAATCTTTCTAGTTTTCTCTCTATCATCTTTCTTTTCCCTTGTACCAACTTTATATTTTG CAATCTTTCTAGTTTTCTCTCTATCATCTTTCTTTTCCCTTGTACCAACTTTATATTTTG LTR2 end TSD			
Pbr_aaca4_IT6_2 Resequence	СААТGTAGTTAACAATATTCACTTGCATTTTTATTAAAAATTGACTTTAAAAGTATTTT CAATGTAGTTAACAATATTCACTTGCATTTTTATTAAAAATTGACTTTAAAAGTATTTTT			
	230 240 250 260 270 280 1 A T A A C A G A A T A T A G T A G A G G G G T A T T A T A	290 ATTGTATA	300 GCTAGTAT	

TSD LTR1 start 360 A G T 350 C.A. 370 T A 380 T C T 390 T G T. тссст 440 CAGGCT 410 A end PBS ٨A AGGGGGGGGGGAATAACAGA PPT LTR2 start 320 330 340 C G G C T A T A T A A G G G A T T G T A T A G 250 G T T 310 T ( TGT Mr 430 TTCCC AAAA TTGTACCAACTTTATATTTTGCAATGTAGTTAACAATATTC. Ŵ www.www.www.www.www.www.



Figure S3.

## **PBS** Alignment

Pbr7_consensus_Ale/1-20	TGGTATCACTCGCCATTGTT -
Pbr_aaca1_consensus_Ale/1-21	TGGTATCCTTCGCCGCTTGCC
Pm_aaca1_consensus_Ale/1-21	<mark>TGGTATCA</mark> TTCG <mark>C</mark> CTTTT <mark>G</mark> CC
Pbr5_consensus_Ale/1-20	TGGTATCAATCGACGGATAT -
Pbr1_consensus_Ale/1-20	TGGTATCAGAGCAGGTTCCA -
Pbr_tgtt4_consensus_Ale/1-20	TGGTATCAAAGCACCGATCC
Pbr_aaca4_1T7/1-20	TAGTATTAGAACCACCAGGC
Md_aaca4_1T4/1-20	TGGTATCAGAGCAAAGGCTC-
Pbr_aaca4_1T11/1-20	TAGTATCAGAGCCACCAGGC -
Pbr_aaca4_1T1/1-20	TGGTATCAGAGCCACCAGGC-
Pbr_aaca4_1T2/1-20	TGGTATCAGAGCCACCAGGC-
Pbr_aaca4_176/1-20	TGGTATCAGAGCCACCAGGC-
Pbr_aaca4_179/1-20	TGGTATCAGAGCCACCAGGC-
Pbr_aaca4_1T13/1-20	TGGTATCAGAGCCACCAGGC-
Md_aaca4_1T1/1-20	TGGTATCAGAGCCACCAGGC-
Md_aaca4_1T2/1-20	TGGTATCAGAGCCACCAGGC-
Md_aaca4_1T3/1-20	TGGTATCAGAGCCACCAGGC-
Pbr_aaca3_1T3/1-20	TGGTATCAAAGCCACCAGAC-
Pbr_aaca4_1T12/1-20	TGGTATCAGAGTCACCAGGC-
Pbr_aaca4_1716/1-20	TGGTATCAGAGCCATCAAGC-
Pbr_aaca3_1T4/1-20	TGGTATTAGAGCCACCAGGC-
Md_aaca4_175/1-21	TGGTATTAGAGCCACCAAGGC
Pbr_aaca4_1T14/1-21	TGGTATCAAAGCCACCAAGGC
Pbr_aaca4_1T15/1-21	TGGTATCAAAGCCACCAAGGC
Pbr_aaca4_1T3/1-21	TGGTATCAGAGCCACCAAGGC
Pbr_aaca4_1T4/1-21	TGGTATCAGAGCCACCAAGGC
Pbr_aaca4_1T5/1-21	TGGTATCAGAGCCACCAAGGC
Pbr_aaca4_1T8/1-21	TGGTATCAGAGCCACCAAGGC
Pbr_aaca4_1T10/1-21	TGGTATCAGAGCCACCAAGGC
Md_aaca4_176/1-21	TGGTATCAGAGCCACCAAGGC
Pbr_aaca3_171/1-20	TGGTATCAGAGCCACCAAGC-
Pbr_aaca3_1T2/1-20	TGGTATCAGAGCCACCAAGC-
Pm_tgtt1_consensus_Ale/1-20	TGGCATCAAAACTTAGGTTG -
Pp_tgtt1_consensus_Ale/1-20	TGGCATCAGAGCTTAGGTTG -
Pbr_tgtt1_consensus_Ale/1-20	IGGCATCAGAGCCTAGGTTA -
Md_tgtt1_consensus_Ale/1-20	IGGCATCAGAGCCAAGGTTG -
Pbr2_consensus_Ale/1-20	IGGCATCAGAGCACCGATCC-
Pbr_aaca2_consensus_Ale/1-20	IGGIAICAAICGCCACCGCC
Pbr_tgtt3_consensus_Ale/1-21	IGGIAICAAAACCCTACTACC
Pbr_tgtt2_consensus_Ale/1-20	
Md_tgtt2_consensus_Ale/1-20	IGGTATCAAGAGCCTTGTAT -

10

Consensus

TGGTATCAGAGCCACCAGGCC

Figure S4.



### PbrAACA1_IT3



NCBI SRA database: SRX147917



PbrAACA1_IT5



NCBI SRA database: SRX147917



### PbrAACA3_IT4



# NCBI SRA database: SRX147917



### PbrAACA4_IT11



## NCBI SRA database: SRX147917



### PbrAACA4_IT14



## NCBI SRA database: SRX147917



### PbrAACA4_IT15



## NCBI SRA database: SRX147917

