SUPPLEMENTARY INFORMATION



b

С

% increase in reads falling into pericentromeric heterochromatin in *atxr5 atxr6* mutants relative to WT



atxr5 atxr6 log2(16C/2C)

Supplementary Figure 1. Characterization of increased DNA copy number in nuclei of different ploidy levels in *atxr5 atxr6* nuclei compared to wild-type.

(a) The log2 ratios of genomic DNA Illumina reads from atxr5 atxr6 compared to wild-

type 2C nuclei are plotted across the chromosomes in 100kb-sliding windows.

(b) Quantification of the increase in DNA copy number in *atxr5 atxr6* mutants. Percent of total Illumina reads falling into defined pericentromeric regions in nuclei with different ploidy levels in wild type and *atxr5 atxr6* mutants were computed. The percent change in these values in *atxr5 atxr6* mutants compared to wild type is shown.
(c) A similar set of regions show increased DNA content in 8C and 16C *atxr5 atxr6* mutants were binned in 3 kb windows and log2 ratios of the scores of 16C to 2C bins and 8C to 2C bins along the chromosome were calculated and compared. The P-value was calculated by shuffling the bins and re-computing Pearson correlation coefficients 100,000 times.



Supplementary Figure 2. Heterochromatin is over-replicating in *atxr5 atxr6* mutants
(a) Distribution of the sizes of re-replicating regions in the arms of *atxr5 atxr6* mutants.
(b) The percentage of high copy number regions in the arms of *atxr5 atxr6* mutants that overlap with H3K9me2 regions is shown.

(c) Chromosomal views of log2 ratios of H3 ChIP-seq reads to INPUT genomic DNA reads in *atxr5 atxr6* mutants relative to wild type over chromosomes 1,2,4 and 5 are plotted in 100kb sliding windows (see main text for chromosome 3).



Pericentromeric heterochromatin

Euchromatin (re-replicating sites)

Euchromatin

Supplementary Figure 3. Confirmation of re-replicating sites by quantitative PCR

Six re-replicating sites in pericentromeric heterochromatin (*Ta3*, *TSI*, *CACTA*) and in the arms of chromosomes 1 and 2 (*AT1G44510*, *AT2G04160*, *AT2G16670*) were analyzed by qPCR on genomic DNA extracted from 16N nuclei of Col (white bars) and *atxr5 atxr6* (black bars). *At1g51800*, a non-re-replicating site in the arm of chromosome 1, was used as control. The averages and standard deviations from three independent experiments are shown. Primers for *Ta3*, *TSI*, *CACTA* are previously described² and all other primers are listed in Supplementary Table 2.



b

a

INPUT DNA





Low molecular weight DNA

High molecular weight DNA



Supplementary Figure 4. Size separation of DNA and analysis of re-replicating sites

by quantitative PCR

(a) Schematic representation of the size separation of Col and atxr5 atxr6 DNA.

(b) Three non re-replicating sites (*AT1G31440*, *AT3G24320* and *AT2G40000*) and four re-replicating sites (*CACTA*, *AT1G31355*, *AT1G34080* and *AT2G29210*) were analyzed by qPCR on total, high molecular weight and low molecular weight genomic DNA extracted from Col (white bars) and *atxr5 atxr6* (black bars). *AT1G31440*, a non-re-replicating site in the arm of chromosome 1, was used as control. The averages and standard deviations from two independent experiments are shown. All primers are listed in Supplementary Table 2.



b



Supplementary Figure 5. Genome-wide profiling of H3K27me1 reveals that H3K27me1 is a silencing mark that correlates with sites of re-replication in *atxr5 atxr6* mutants, and anticorrelates with H3K4 methylation.

(a) H3K27me1 ChIP-seq normalized to H3 ChIP-seq reads plotted over either the 5' end (left) or 3' end (right) of TAIR8 protein-coding genes. Two kilobases upstream or downstream of genes, and 1 kilobase into the genes are shown. Black=all genes, red=genes with the top 10% expression, pink=top10~30% expression, yellow=top30~50% expression, green=50~70% expression, cyan=70~90% expression, blue= lowest 10% expression. (**b**) Genome browser view of examples of re-replicating regions that are enriched in H3K27me1.

(c) H3K27me1 anticorrelates with H3K4 methylation. Each protein-coding gene in the genome was split into regions containing either H3K4me0, -me1, -me2 or -me3, and the density of H3K27me1 and H3 ChIP-seq reads in each of these regions was computed. The % of genes where the ChIP-seq read densities were 2-fold greater in the H3K4 unmethylated regions relative to H3K4 methylated regions were calculated.



Supplementary Figure 6. Validation of effect of the point mutations inserted to ATXR6 constructs.

(a) Binding of ATXR6 to AtPCNA1 is compromised by mutations in the PIP motif.
Interaction between AtPCNA1 and WT ATXR6 or an ATXR6 mutant (Q92A, I95A, F98A, F99A) in the PIP motif (ATXR6(pip)) was assessed using the yeast-two-hybrid system (Invitrogen, Carlsbad, CA). As controls for self-activation, AtPCNA1, ATXR6, and ATXR6(pip) were co-expressed with empty vectors.

(**b**) Replacement of leucine 49 with tryptophan in the PHD domain of ATXR6 prevents binding to H3. *In vitro* histone peptide binding assay using purified GST-tagged PHD domains ATXR6 (WT and mutant) and biotinylated H3 peptides with different methylated lysines. Interaction between the peptides and the GST-PHD domains was visualized by Western blot using a GST antibody.

(c) A point mutation (Y243N) in the SET domain of ATXR6 impairs the methyltransferase activity. *In vitro* histone methyltransferase assay using an H3K27me1 antibody to detect the monomethylation of H3.

	DAPI	H3K27me1
Col		
atxr5-atxr6	a de a	
<i>atxr5-atxr6</i> + ATXR6		
<i>atxr5-atxr6</i> + ATXR6(set)	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
<i>atxr5-atxr6</i> + ATXR6(phd)		
<i>atxr5-atxr6</i> + ATXR6(pip)	and a	

Supplementary Figure 7. The PHD- and SET domains, and the PIP motif of *ATXR6* **are required to restore normal H3K27me1 levels.** Immunolocalization of H3K27me1 in nuclei isolated from mature leaves of Col or *atxr5 atxr6* mutants. T1 lines (+ ATXR6) are expressing either wild-type *ATXR6*, or different point mutants in each of the three functional elements (PIP motif, PHD- and SET domains) of the protein. Supplementary Table 1. List of re-replicating regions in the arms of chromosomes.

chromosome	start	stop	size	overlap with H3K9me2	overlap with inverted repeats	overlap with tandem repeats	Transposable element	
chr1	181681	191880	10199	YES	NO	NO		
chr1	236341	240960	4619	YES	NO	YES		
chr1	266041	277800	11759	NO	NO	YES		
chr1	337501	360840	23339	YES	YES	YES	ATGP2	LTR/Gypsy
chr1	389641	39/380	1/39	NO	NO	NU		
chr1	981661	421660	14679	YES	YES	NO		
chr1	1471621	1486620	14999	YES	NO	YES	ATGP1	LTR/Gvpsv
chr1	1638961	1643040	4079	NO	YES	YES		, _, p=,
chr1	1797061	1807920	10859	NÖ	NO	YES		
chr1	2181841	2191200	9359	YES	NO	YES	BRODYAGA1A	DNA/MuDR
chr1	2224861	2232900	8039	NO	YES	NO		
chr1	2290561	2303100	12539	NO	YES	NO		
chr1	2453401	245/480	40/9	NU	YES	NO		BC/Holitron
chr1	2456741	2564040	5039	NO	YES	YES	AIREFS	KC/Helition
chr1	2783821	2800560	16739	YES	NO	YES	VANDAL14	DNA/MuDR
chr1	2959561	2970300	10739	NO	NO	YES		
chr1	3058261	3067380	9119	YES	NO	YES		
chr1	3406501	3417600	11099	YES	NO	YES	RP1_AT	DNA
chr1	3991201	4007880	16679	NO	NO	YES		
chr1	4406101	4411380	5279	YES	NO	YES	META1	LTR/Copia
chr1	4677781	4682160	4379	NO	NO	YES		
chr1	5091361	5108/60	17399	YES NO	NO	YES		DNA/MUDR BC/Holitrop
chr1	5304961	5143200	7250	NO	NO	NO	HELITRONZ	RC/ Helltroll
chr1	5443861	5456400	12539	YES	NO	YES	VANDAL1	DNA/MuDR
chr1	5688241	5711520	23279	YES	YES	YES	ATCOPIA89	LTR/Copia
chr1	5965861	5975880	10019	YES	NO	YES	ATHPOGON1	DNA/Pogo
chr1	6193981	6201780	7799	YES	YES	YES	HELITRONY1D	RC/Helitron
chr1	6260161	6265680	5519	YES	NO	YES		
chr1	6268561	6285240	16679	YES	YES	YES	TAG2	DNA/HAT
chr1	6520261	6525480	5219	YES	YES	NO		
CNF1	6/1/661	6727980	10319	YES VEC	NU	TES		LI R/Copia
chr1	6943961	6946420	13010	NO	TES NO	VES	ATREP3	RC/Helitron
chr1	7061701	7080600	18899	YES	NO	YES	ATLANTYS2	ITR/Gynsy
chr1	7353481	7365120	11639	YES	NO	YES	VANDAL14	DNA/MuDR
chr1	7862941	7872120	9179	NO	YES	NO		
chr1	7984741	7990620	5879	YES	YES	YES	HELITRONY3	RC/Helitron
chr1	8451961	8467920	15959	YES	YES	YES	VANDAL6	DNA/MuDR
chr1	8673241	8685240	11999	YES	NO	YES		
chr1	8761021	8847660	86639	YES	YES	YES	VANDAL6	DNA/MuDR
chr1	8923381	8938560	151/9	YES	NO	NU	AIREP1	RC/Helitron
chr1	9004801	9020640	15839	YES VEC	TES NO	YES		DNA/MUDR
chr1	9569521	9579900	10379	YES	YES	YES	HELITRON1	RC/Helitron
chr1	9661201	9665580	4379	NO	NO	NO	HEEIMONI	ite/fieldfoll
chr1	9676201	9694020	17819	YES	NO	YES	VANDAL2	DNA/MuDR
chr1	9701941	9711360	9419	YES	NO	YES		
chr1	9904501	9913620	9119	YES	NO	YES	ATCOPIA95	LTR/Copia
chr1	11124781	11130960	6179	YES	YES	YES	VANDAL20	DNA/MuDR
chr1	11144821	11152740	7919	YES	NO	NO	ATCOPIA25	LTR/Copia
chr1	11174281	11196540	22259	YES	YES	YES	ATCOPIA28	LTR/Copia
chr1	11224981	11243760	18779	YES	YES	YES		LI R/Copia
chr1	11301301	11324400	23099	NO	NO	NO	TAG1	DNA/HAT
chr1	17838421	17850840	12419	YES	YES	YES	RP1 AT	DNA
chr1	18035641	18048600	12959	YES	NO	YES	ATREP4	RC/Helitron
chr1	18114421	18121500	7079	YES	NO	YES		-
chr1	18156421	18170160	13739	YES	YES	YES	ATENSPM9	DNA/En-Spm
chr1	18406141	18426660	20519	YES	YES	YES	ATREP3	RC/Helitron
chr1	18437341	18443700	6359	YES	YES	NO	BRODYAGA1	DNA/MuDR
cnr1	18806461	18813120	6659	YES	YES	YES	ATREPIÓD	RC/Helitron
chr1	18842341	18859980	1/639	YES	NO	YES	ATENSPM5	DNA/En-Spm
chr1	18062101	18080460 10333300	49/9	VES	YES	YES		LTR/GVDSV
chr1	19338121	19356480	18359	YES	NO	YES		DNA/MuDR
chr1	19676821	19685520	8699	YES	YES	YES	ATENSPM4	DNA/En-Som
chr1	19877821	19890540	12719	YES	NO	NO	ATREP11	RC/Helitron
chr1	20201461	20215080	13619	YES	NO	YES	ATREP10D	RC/Helitron
chr1	20312641	20329800	17159	YES	NO	YES	HELITRON5	RC/Helitron
chr1	20471761	20484360	12599	YES	YES	YES	ATGP2N	LTR/Gypsy
chr1	20971561	20994600	23039	YES	YES	YES	ATDNAI27T9A	DNA/MuDR
chr1	21120841	21132420	11579	YES	NO	YES	HELITRONY2	RC/Helitron
chr1	211/6/61	21191040	14279	YES VEC	TES NO	TES NO	ATCODIA22	UNA/HAI
chr1	21330341 21452401	21334900	4019	YES	YES	YES	TSCI	LINE?
chr1	21686641	21697560	10919	YES	NO	NO	RathE1 cons	RathE1 cons
chr1	21769981	21780960	10979	YES	NO	NO	ATREP6	RC/Helitron
chr1	21799561	21817260	17699	YES	NO	NO	ATCOPIA87	LTR/Copia
chr1	21832741	21854400	21659	YES	NO	NO	ATCOPIA87	LTR/Copia
chr1	21992941	22003260	10319	YES	YES	YES	ARNOLDY1	DNA/MuDR
chr1	22095781	22113240	17459	YES	YES	YES	ATCOPIA5	LTR/Copia
cnr1	22492741	22501560	8819	YES	NU	YES	HELITRONY3	RC/Helitron
cnr1	23173741	23185920	12179	TES VEC	TES	TES VEC	BKUDYAGA2	DNA/MUDR
chr1	23308141 24272241	233/3840	10120	VES	NO	YES	ATCOPIA15	UNA
chr1	24882301	24886380	4070	YES	YES	NO	HELITRONY1D	RC/Helitron
chr1	25447261	25461060	13799	YES	NO	YES	TAG1	DNA/HAT
chr1	25809841	25815660	5819	NO	NO	YES	ATGP1	LTR/Gypsy
chr1	25992661	26002800	10139	YES	YES	YES	ATREP4	RC/Helitron
chr1	26274421	26284980	10559	YES	YES	NO		

chr1	26369521	26373600	4079 YES	NO	YES	ATCOPIA11	LTR/Copia
oh ut	27110501	27126440	17030 VEC	NO	VEC	TACONI	DNA (HAT
CIT	27118301	27130440	17939 113	NO	IL3	TAGSINI	DNATIA
chr1	27427921	27438120	10199 YES	YES	YES	HELITRONY1D	RC/Helitron
chr1	27865501	27872220	6719 NO	YES	NO		
chr1	28173061	28188780	14810 VES	NO	VES		
	20175901	20100700	14013 113	110	TES NES	ATDINAIZ715C	DNA/HUDR
chr1	28370341	28376520	61/9 YES	NO	YES	VANDAL17	DNA/MuDR
chr1	28836421	28845480	9059 NO	YES	YES	LIMPET1	DNA/MuDR
chr1	30132961	30139440	6479 YES	NO	YES		
ala ut	20206001	20212200	7770 NO	110	YEC		
CULT	30306001	30313380	7379 NO	NO	YES		
chr2	901	108780	107879 YES	YES	YES	VANDAL6	DNA/MuDR
chr2	112261	121500	9239 YES	YES	NO	HELITRONY1B	RC/Helitron
	112201	121500	5255 125	TES NES	110	There	
chr2	122641	185340	62699 YES	YES	YES	AIMU1	DNA/MuDR
chr2	187321	204840	17519 YES	NO	NO	ATREP10B	RC/Helitron
chr7	206401	212260	ADED VEC	NO	VEC		-
CITZ	200401	213300	0939 TES	NO	IL5		
chr2	214861	223380	8519 NO	NO	NO	ATREP10D	RC/Helitron
chr2	225181	232980	7799 YES	YES	NO	DT1	DNA/Mariner
chr7	234661	258480	23810 VES	VEC	VES	ATI INFIII	I TNE/L1
	234001	230400	25015 115	TE5	ILS .	ATLINLIN	
chr2	267601	301080	33479 YES	NO	YES	AIREP17	DNA/MuDR
chr2	305461	354780	49319 YES	YES	YES	ATHATN4	DNA/HAT
chr7	257601	264020	7210 VEC	NO	NO	ATDED1 E	BC/Holitrop
CITZ	337001	304920	7319 TL3	NO	NO	AIRLFIJ	RC/Helitron
chr2	366901	390180	23279 YES	NO	YES	RathE1_cons	RathE1_cons
chr2	400801	408240	7439 YES	YES	YES	ATHPOGON3	DNA/Pogo
chr2	414541	426500	210E0 VEC	NO	VEC	ATTIDTA 1	DNA/Te1
CHIZ	414541	436500	21959 165	NO	TES	ATTIKIAI	DNA/ ICI
chr2	473041	494160	21119 YES	YES	YES	SIMPLEGUY1	DNA/Harbinger
chr2	504781	509880	5099 YES	NO	YES		
ah n D	E140C1	E43000	20010 VEC	VEC	VEC	TA11	
CHIZ	514661	542660	28019 165	TES	TES	IAII	LINE/LI
chr2	552481	565200	12719 YES	NO	YES	ATREP10A	RC/Helitron
chr2	583921	588120	4199 YES	NO	NO		
chr2	607201	620700	13/00 VEC	NO	VEC	ATPEDIE	PC/Halitran
CIII Z	00/201	020700	13433 IES	NO	1LD	AIREPID	RC/ Helluron
chr2	629461	639960	10499 YES	NO	YES	ATTIR16T3A	DNA
chr2	652681	657060	4379 YES	NO	YES	ATREP15	RC/Helitron
chr?	660401	668Eou	8000 VEC	NO	VEC		RC/Halitron
5002	000401	000000	0099 IL3		1123		NC/ Hellu UII
chr2	675061	697260	22199 YES	YES	YES	ATREP10D	RC/Helitron
chr2	716641	721260	4619 YES	NO	NO	ATLINE2	LINE/L1
chr2	724001	742440	7550 755	NO	VEC	ATDED11A	DC/Lisitson
uirz	/34881	/42440	1009 TES	NO	TES	AIKEPIIA	KC/ Helitron
chr2	744181	752820	8639 YES	YES	YES	ATTIRTA1	DNA/Tc1
chr2	754501	767040	12539 YES	YES	YES	ATREP3	RC/Helitron
-law2	707601	70/010	7070 VEC	120	YEC	ATREPO	DC/U alltara
CITZ	/8/621	/94/00	7079 TES	NO	TES	AIREPZ	RC/ Helltroll
chr2	815641	833460	17819 YES	YES	YES	ATGP10	LTR/Gypsy
chr2	838081	849780	11699 YES	NO	YES	ATCOPIA36	ITR/Conia
-law2	050001	063600	11630 VEG	110	YES	ATDED17	DNA (M. DD
CITZ	651041	002000	11039 155	NO	TES	AIREP17	DNA/MUDR
chr2	864121	873840	9719 YES	YES	YES	ATIS112A	DNA/Harbinger
chr2	880381	898320	17939 YES	YES	YES	HELITRONY1B	RC/Helitron
chr2	041641	040900	81E0 NO	NO	VEC		
	541041	545000	0133 110	NO	ILS .		
chr2	953281	967440	14159 YES	YES	YES	AIREP15	RC/Helitron
chr2	982261	999000	16739 YES	NO	YES	ATLINE1A	LINE/L1
chr2	1014481	1055940	41459 YES	YES	YES	HELITRONY3	RC/Helitron
-h-2	1014401	1000040	15020 VEC	NO.	YES	ATLINET 24	
cnr2	1066501	1082340	15839 YES	NO	YES	AILINEI_3A	LINE/LI
chr2	7227481	7243020	15539 YES	YES	YES	ATCOPIA70	LTR/Copia
chr7	8023441	8048820	25370 VES	VES	VES	ATDED11	PC/Helitron
	0025441	0040020	25575 125	165	TES NES	AIREFTT	RC/Helitron
chr2	8083561	8088300	4/39 YES	YES	YES	HELITRONY3A	RC/Helitron
chr2	8202241	8208480	6239 YES	YES	YES	ATREP10D	RC/Helitron
chr7	85718/1	8581140	0200 VES	NO	NO	ATCOPIA69	ITP/Conia
	00/1041	0001140	5255 TES	110	NO	ATCOFIA05	LIN Copia
chr2	9047761	9058980	11219 YES	NO	NO		
chr2	9064021	9072360	8339 YES	NO	YES	LIMPET1	DNA/MuDR
chr2	9194101	9210840	16739 YES	YES	YES	ΔΤΟΟΡΙΔ 76	ITR/Conia
	5154101	9210040	10/33 113	165	TE5	ATCOLIATO	Enty Copia
chr2	9268441	9276420	7979 YES	YES	NO	BRODYAGAZ	DNA/MuDR
chr2	9659221	9668580	9359 YES	YES	YES	ARNOLDY2	DNA/MuDR
chr2	9926101	9936960	10859 YES	YES	NO	TSCI	LTNE2
-h-2	10000001	10010300	10055 125	NO.	NO	15CE	
CITZ	10002961	10016260	13319 155	NO	TES	VANDALZI	DNA/MUDR
chr2	10811281	10818780	7499 YES	YES	YES	ATREP9	RC/Helitron
chr2	10992481	11004420	11939 YES	NO	YES	HELITRONY1E	RC/Helitron
chr2	11177541	11140060	20510 YES	VEC	VEC	ΔΤματοίο	DNA /UAT
cnr2	1112/541	11148060	20519 YES	TES	YES	ATHAIN7	DNA/HAI
chr2	11332201	11342400	10199 YES	NO	YES	HARBINGER	DNA/Harbinger
chr2	12304741	12315840	11099 YES	YES	YES	HELITRONY3	RC/Helitron
chr2	10561061	12572460	10400 YES	. 25 NO	VEC	ATDEDDA	DC/Lisiteran
CITZ	12301901	125/2400	10499 165	NO	TES	AIREPZA	RC/ Helltroll
chr2	13098361	13106520	8159 YES	NO	YES	ATDNAI27T9C	DNA/MuDR
chr2	13227061	13235700	8639 YES	NO	YES	TSCL	LINE?
chr2	12450201	12460240	0050 450	NO	VEC		
uirz	13450381	13400340	AADA LEP	NO	TES		
chr2	13664521	13672320	7799 YES	YES	NO	ATHPOGON1	DNA/Pogo
chr2	13867861	13879920	12059 YES	YES	YES	ATMU9	DNA/MuDR
chr2	1//1/761	14410000	E210 VEC	VEC	VEC	ATENCOMI	DNA/En Char
uirz	14414/01	14419980	3219 TES	TED	TES	ATENSPIT	DIVA/EN-SPM
chr2	15079681	15088020	8339 YES	NO	NO		
chr2	15144001	15148320	4319 YES	NO	NO		
ah z	151(0081	15176760	7670 NO	NO	YEC		
CIII Z	12102001	101/0/00	7079 NU	NO	165		
chr2	15598081	15605520	7439 YES	YES	YES	ATMU7	DNA/MuDR
chr2	15695101	15704760	9659 YES	NO	NO	HELITRONY1D	RC/Helitron
chr2	1 5052001	15850400	1100 VEC	VEC	VEC	ATPEDE	PC/Holitron
uirz	12823281	10008480	4499 1E5	TED	TES	AIKEPS	KC/ Helitron
chr2	17209441	17220960	11519 YES	NO	YES	ATREP1	RC/Helitron
chr2	18747601	18751680	4079 NO	NO	NO		
chr2	10103101	19111260	8159 NO	NO	VES		
critiz alta 2	19103101	10/072	10610 106	110	11.5		
chr2	19476661	19487280	10619 YES	NO	NÔ		
chr2	19595101	19605300	10199 YES	NO	YES		
chr2	19650541	19660500	9959 NO	NO	NO		
abu2	12020241	17000300	11450 VEC	NO VEC		DD1 4T	
chr3	35881	47340	11459 YES	YES	YES	RP1_AT	DNA
chr3	255661	265500	9839 YES	NO	NO		
chr3	267721	273000	5279 NO	NO	NO		
chr2	207721	207440	0020 NO	NO	VEC		
uirs	32/601	33/440	9039 NU	NU	TES		
chr3	444121	457980	13859 NO	NO	YES		
chr3	517441	532200	14759 YES	YES	YES		
chr2	11/1771	1172020	11000 YES	VEC	VEC	ATDMATOTOC	
uno 	1101/21	11/2020	11033 IES	11.5	165	ATDINALZ/ TYC	DINA/ MUDK
chr3	1227781	1235040	7259 YES	NO	YES		
chr3	1606861	1615140	8279 YES	NO	NO	ATLANTYS3	LTR/Gvpsv
chr3	10/0521	1860400	10010 VEC	NO	VEC		, 0, po,
uno 	1049301	1000400	10313 IES	NO	165		
chr3	1958701	1972740	14039 YES	YES	YES	RathE2_cons	RathE2_cons
chr3	1982221	1991040	8819 YES	NO	YES	ATCOPIA6	LTR/Copia

chr3	2089081	2099400	10319 YES	NO	YES	ATTIRTA1	DNA/Tc1
chr3	2362861	2368200	5339 YES	NO	YES		
chr2	2710021	2727120	8000 NO	VEC	VEC		
CIIIS	2719021	2/2/120	8099 NO	TES	TE5		
chr3	2764861	2774760	9899 YES	NO	YES	VANDAL13	DNA/MuDR
chr3	2808541	2820660	12119 YES	NO	YES	VANDAL16	DNA/MuDR
chr2	2111061	2117260	6200 VEC	NO	NO		LTR (Cypey)
CIIIS	5111001	5117500	0299 113	NO	NO	ATLANTISS	LIK/Gypsy
chr3	3493741	3503340	9599 YES	NO	YES	TSCL	LINE?
chr3	3805081	3815940	10859 YES	NO	NO	ATGP3	ITR/Gynsy
cin 5	5005001	102110	10055 125	110	110		EntyGypSy
chr3	4921021	4934160	13139 YES	YES	YES	VANDAL21	DNA/MUDR
chr3	5092501	5096880	4379 NO	NO	YES	VANDAL17	DNA/MuDR
-l D	5052501	5050000	15110 XEC	NO	VEG	VANDAL 17	DNA (MuDD
CHL3	52/5081	5290200	15119 YES	NO	YES	VANDAL17	DNA/MUDR
chr3	5588341	5602680	14339 YES	YES	YES	ATREP1	RC/Helitron
chr2	E700001	E704040	4010 NO	NO	NO		,
CIIIS	5760621	5764640	4019 NO	NO	NU		
chr3	5806201	5819340	13139 YES	NO	YES	ATGP1	LTR/Gypsy
chr3	71375/11	71/15700	8150 VES	VES	VEC	ATPED5	PC/Helitron
ciii 5	/15/541	/145/00	0155 125	125	1L5	AIREFS	KC/Helicion
chr3	7274161	7281180	7019 YES	NO	YES	VANDAL8	DNA/MuDR
chr3	7443781	7448280	4499 NO	NO	YES		
ah n7	7652041	7657020	4070 NO	NO	NO		
CHL3	/652941	/65/920	4979 NO	NO	NU		
chr3	7665001	7681800	16799 YES	YES	YES	ATREP10D	RC/Helitron
chr2	7706761	7012260	16400 VEC	VEC	VEC	VANDALS	
ciii 5	7790701	7015200	10499 113	125	1L5	VANDALO	DINATIODIC
chr3	8209021	8216100	7079 YES	NO	YES	ATCOPIA28	LTR/Copia
chr3	8406901	8414040	7139 YES	NO	YES	ATHILA6A	LTR/Gypsy
ah n7	0520661	0544060	E300 VEC	NO	NO	ATCD7	
CHL3	8238001	8544060	5399 YES	NO	NU	AIGP7	LIR/Gypsy
chr3	8842981	8859240	16259 YES	NO	YES	VANDAL2	DNA/MuDR
chr2	0007161	0005060	8600 NO	NO	VEC	ATCODIAGE	ITR/Conia
CIII 5	009/101	0903000	8099 NO	NO	1123	ATCOPIAGO	LI K/COpia
chr3	8924761	8946240	21479 YES	YES	YES	ATHAT10	DNA/HAT
chr3	9723601	9736800	13199 YES	NO	YES	VANDAL14	DNA/MuDR
ah n7	0704501	0700620	6110 VEC	NO	VEC		
CIIIS	9764501	9790620	0119 155	NU	TE5	ATLINEZ	LINE/LI
chr3	10060321	10065480	5159 NO	YES	NO		
chr3	10066021	10083840	16010 VES	NO	VEC	PathE3 cons	PathE3 cons
CIIIS	10000921	10003040	10919 113	NO	TL3	Ratific3_cons	Ratific3_cons
chr3	10115401	10122660	7259 YES	NO	YES		
chr3	10143741	10153680	10439 YES	NO	YES	ATREP5	RC/Helitron
-h - C	1720000	174112000	10.00 100	NCC NCC	VEC	ATOPON	
cnr3	17398861	1/411280	12419 YES	YES	YES	AIGP2N	LI R/Gypsy
chr3	17668261	17678280	10019 YES	NO	NO	ATTIR16T3A	DNA
ch-7	10625107	10646000	11270 VEC	NO	VEC	ATDEDLOD	DC/Hallton
cnr3	18635101	19040380	112/9 YES	NU	TES	ATKEP10D	KC/Helitron
chr3	19581841	19595100	13259 YES	NO	YES		
chr2	20211001	20210220	7210 VEC	VEC	VEC		
CIIIS	20211901	20219220	7319 113	IL3	TL3		
chr3	20471461	20487840	16379 YES	YES	YES	ATLINE1_3A	LINE/L1
chr3	21303421	21308280	4850 NO	VES	NO		
ciii 5	21393421	21390200	4039 110	125	NO		
chr3	22243021	22256700	13679 YES	NO	YES	VANDAL6	DNA/MuDR
chr3	22523041	22532940	9899 YES	NO	NO	ATLANTYS2	LTR/Gypsy
ah n7	22500201	22504200	FOOD VEC	NO	VEC	VANDALG	DNA (MuDD
CIIIS	22566201	22594200	2999 TE2	NO	TES	VANDALO	DNA/MUDR
chr3	22653301	22662000	8699 YES	YES	YES	BRODYAGA2	DNA/MuDR
chr3	23113021	23132280	10250 VES	VES	VEC	ATLANTVS3	ITP/Gypsy
ciii 5	25115021	23132200	19239 113	125	IL5	ATEANTISS	EIIQ Gypsy
chr3	23306221	23316120	9899 NO	NO	YES		
chr4	901	26160	25259 YES	YES	YES	AT9TSD1	DNA/MuDR
elin 1	21021	120200	104750 ¥56	VEC	VEG	NANDAL 22	DNA (MuDD
CNr4	31921	130080	104759 YES	TES	YES	VANDALZZ	DNA/MUDR
chr4	143281	202680	59399 YES	YES	YES	ATREP9	RC/Helitron
chr4	203881	215280	11300 NO	NO	NO	ATPED5	PC/Helitron
CIII-F	205001	215200	11555 NO	NO	NO	ATREFJ	icc/riencion
chr4	221581	368040	146459 YES	YES	YES	BOMZH2	DNA/MuDR
chr4	381841	394860	13019 YES	NO	YES	VANDAL1	DNA/MuDR
elin 1	207001	417000	10070 //20	VEC	VEG	ATENCOMO	DNA (Fr. Craw
CNr4	397681	41/060	19379 YES	TES	YES	ATENSPM9	DNA/En-Spm
chr4	418321	436680	18359 YES	YES	NO	ATHATN9	DNA/HAT
chr4	427041	462000	JEGEO VEC	NO	VEC	VANDAL 17	
CIII 4	437941	403000	23639 165	NO	TES	VANDAL17	DNA/MUDR
chr4	466441	471060	4619 YES	YES	YES	ATREP5	RC/Helitron
chr4	475501	486840	11339 YES	NO	YES	ΔΤΗΔΤΝ1	DNA/HAT
	475501	100040	11555 125	110	NES NES	Amanu	DINAYINA
cnr4	50/601	519840	12239 NO	NO	YES		
chr4	521221	552000	30779 YES	NO	YES	ATREP15	RC/Helitron
ob #4	ECACC1	F71200	(E20 NO	NO	VEC		
CIII 4	304001	5/1200	0223 100	NO	TES		
chr4	573241	586920	13679 YES	NO	YES	TAG2	DNA/HAT
chr4	592501	604320	11819 YES	YES	YES	ΔΤΙ ΙΝΕΙΙΙ	I INE/I 1
Cilii 4	552501	004520	11015 125	125	TES	ATEINEIII	
chr4	624721	677100	52379 YES	YES	YES	HELITRONY1D	RC/Helitron
chr4	679261	695040	15779 YES	YES	YES	ATREP3	RC/Helitron
chr4	726E41	727520	10070 VEC	VEC	VEC	ATCINEDA	CINE
CIII4	720341	/3/320	10979 113	TL3	1123	ATSINEZA	SINC
chr4	743821	761220	17399 YES	YES	YES	BRODYAGA2	DNA/MuDR
chr4	769021	812340	43319 YES	NO	NO	ATREP11	RC/Helitron
	703021	012040	10070 100	NGC NEC	NG NEC	ATTICACTO	DNA
cnr4	829381	845460	160/9 YES	YES	YES	ATTIR16T3A	DNA
chr4	852481	900420	47939 YES	YES	YES	ATLINE1A	LINE/L1
chr4	901921	913740	11819 NO	NO	YES		
	201221	047760	10050 100	NO	123		DC/UZ III
cnr4	927901	947760	19859 YES	NO	YES	HELITRON1	KC/Helitron
chr4	958501	963180	4679 YES	NO	YES		
chr4	064221	005600	21250 VEC	NO	VEC	DathE1 came	DathE1 con-
cnr4	964321	902080	5122A JE2	NU	IES	KdUIE1_CONS	KaUIE1_CONS
chr4	986881	1001400	14519 YES	YES	NO	ATREP4	RC/Helitron
chr4	1002001	1010340	7439 VEC	NO	NO	RathF1 cons	RathE1 conc
C114	1002901	1010340	7433 IL3		NO		NachL1_CONS
chr4	1012081	1050480	38399 YES	YES	YES	HELITRONY3	RC/Helitron
chr4	1056661	1072740	16079 YES	NO	YES	ATIS1124	DNA/Harhinger
	1072001	1100100	26210 VEC	VEC	VEC	ATDEDE	DC/Uniterrations
cnr4	10/3881	1100100	20219 YES	TES	TES	ATKEP5	KC/Helitron
chr4	1101181	1120440	19259 YES	YES	YES	ATREP10D	RC/Helitron
chr4	11770/1	11/5700	22850 VEC	VEC	VEC		RC/Halitron
0114	1122041	1143/00	22039 113	11.5	11.5		NC/THEILTOIT
chr4	1147981	1166940	18959 NO	NO	NO	ATREP7	RC/Helitron
chr4	1187941	1212480	24539 YES	YES	YES	ATREP5	RC/Helitron
ehr 4	1221241	1241100	10010 100	VEC	VEC	BRODVACAD	
chr4	1221241	1241160	19919 YES	YES	YES	BRODYAGA2	DNA/MuDR
chr4	1254301	1280280	25979 YES	NO	YES	TSCL	LINE?
ch - 4	1207701	1207220	12610 VEC	VEC	VEC	ATIC1134	
cnr4	1283701	1297320	13619 YES	YES	YES	AHS112A	DNA/Harbinger
chr4	1298641	1307220	8579 YES	YES	YES	ATREP10B	RC/Helitron
chr4	1200421	1210160	10720 VEC	NO	VEC	ATCODIAC	ITD/Comin
cnr4	1308421	1313190	10/39 YES	NU	TES	ATCOPIA2	LI К/ Соріа
chr4	1323121	1344780	21659 YES	YES	YES	ATDNA2T9C	DNA/MuDR
	1057061	1275020	19650 VEC	VEC	VEC	ATDED2	DC/Hallton
CNT4	135/261	13/2820	1002A 1E2	TES	TES	AIKEP3	KC/Helltron
chr4	1445341	1482780	37439 YES	YES	YES	VANDAL2	DNA/MuDR
chr4	1110011	6201120	4979 VEC	NO	VEC		RC/Helitron
CIII 4	63761/1	D \ A ' ' ' '''				AUNEF14	NC/ HEILI UII
	6376141	0301120	4575 125	NO	TE5		
chr4	6376141 6526201	6542760	16559 YES	YES	YES	ATGP1	LTR/Gypsy
chr4 chr4	6376141 6526201 6913321	6542760 6923040	16559 YES	YES	YES	ATGP1	LTR/Gypsy
chr4 chr4	6376141 6526201 6913321	6542760 6923040	16559 YES 9719 YES	YES	YES	ATGP1 ATCOPIA22	LTR/Gypsy LTR/Copia
chr4 chr4 chr4	6376141 6526201 6913321 6944521	6542760 6923040 6960600	16559 YES 9719 YES 16079 YES	YES NO NO	YES NO YES	ATGP1 ATCOPIA22 ATREP15	LTR/Gypsy LTR/Copia RC/Helitron
chr4 chr4 chr4 chr4	6376141 6526201 6913321 6944521 7135201	6542760 6923040 6960600 7144500	16559 YES 9719 YES 16079 YES 9299 YES	YES NO NO YES	YES NO YES YES	ATGP1 ATCOPIA22 ATREP15 VANDAL21	LTR/Gypsy LTR/Copia RC/Helitron DNA/MuDR
chr4 chr4 chr4 chr4	6376141 6526201 6913321 6944521 7135201	6542760 6923040 6960600 7144500	16559 YES 9719 YES 16079 YES 9299 YES	YES NO NO YES	YES NO YES YES	ATGP1 ATCOPIA22 ATREP15 VANDAL21	LTR/Gypsy LTR/Copia RC/Helitron DNA/MuDR
chr4 chr4 chr4 chr4 chr4 chr4	6376141 6526201 6913321 6944521 7135201 7243741	6542760 6923040 6960600 7144500 7251180	16559 YES 9719 YES 16079 YES 9299 YES 7439 YES	YES NO NO YES NO	YES NO YES YES YES	ATGP1 ATCOPIA22 ATREP15 VANDAL21 HELITRONY1E	LTR/Gypsy LTR/Copia RC/Helitron DNA/MuDR RC/Helitron
chr4 chr4 chr4 chr4 chr4 chr4 chr4	6376141 6526201 6913321 6944521 7135201 7243741 7297621	6542760 6923040 6960600 7144500 7251180 7303500	16559 YES 9719 YES 16079 YES 9299 YES 7439 YES 5879 YES	YES NO NO YES NO NO	YES NO YES YES YES NO	ATGP1 ATCOPIA22 ATREP15 VANDAL21 HELITRONY1E ATLINE1_1	LTR/Gypsy LTR/Copia RC/Helitron DNA/MuDR RC/Helitron LINE/L1

chr4	7353181	7358580	5399 YES	YES	NO	ATDNAI27T9A	DNA/MuDR
chi 1	7417261	7420560	12200 VEC	VEC	VEC	ATDED2	DC/Uelitree
cnr4	/41/261	7429560	12299 YES	YES	TES	ATREP3	RC/Helitron
chr4	7506661	7516860	10199 NO	YES	YES	HELITRONY1C	RC/Helitron
chr4	7755001	7762920	7919 YES	NO	YES	ATHILA6A	LTR/Gypsy
chr4	9120721	9147640	7010 VES	NO	VEC	ATREDA	DC/Holitron
0114	0139721	8147040	7919 113	NO	IL3	ATKLF4	KC/Helition
chr4	8668081	8674200	6119 YES	NO	YES	ATLINE1A	LINE/L1
chr4	8702761	8709420	6659 YES	NO	NO		
chr4	8897221	8909520	12299 YES	NO	YES	ATLINE1 2	LINE/L1
chi 4	0050661	0005520	12255 TES	NGC NEC	YES	VANDALC	
cnr4	8958661	8965620	6959 YES	YES	TES	VANDAL6	DNA/MUDR
chr4	9174421	9199080	24659 YES	YES	YES	ATREP3	RC/Helitron
chr4	9249121	9261600	12479 NO	NO	YES		
chi 1	0450001	0463000	4070 VEC	NO	VEC		DC/Halitzan
CIII 4	9456621	9463600	4979 TES	NO	TES	HELITKONTID	RC/ Helltroll
chr4	9465301	9475140	9839 YES	NO	YES		
chr4	9482101	9495840	13739 YES	YES	YES	ATCOPIA4	LTR/Copia
chr4	0505001	0516060	11970 VEC	NO	VEC	ATCD2	LTR/Cypey
0114	9303081	9310900	110/9 113	NO	IL3	AIGF2	LIR/Gypsy
chr4	9793021	9801000	7979 YES	NO	YES	SIMPLEHAT1	DNA/HAT
chr4	9951481	9959880	8399 YES	NO	YES	VANDAL8	DNA/MuDR
chr4	10800961	10811/00	10430 VES	NO	VES	HELITRONV1E	PC/Helitron
	10000501	10011400	10439 1123	110	TE5	ATOPOLTO	
chr4	11109661	11123040	13379 YES	YES	YES	AIGP9LIR	LIR/Gypsy
chr4	11204341	11215440	11099 YES	YES	YES	VANDAL6	DNA/MuDR
chr4	11413861	11422380	8519 YES	NO	VES		
chi 1	11667661	11672100	5515 125 FE10 NO	NO	VEC		
CIII 4	1100/001	110/3100	2213 NO	NO	TES		
chr4	11818741	11827980	9239 YES	NO	NO	ATGP3	LTR/Gypsy
chr4	11844241	11849340	5099 YES	NO	YES	ATLINEIII	I INE/I 1
chi 1	11015161	11033100	3010 NO	VEC	VEC	ATCODIACO	LTD/Conin
CIII 4	11912101	11922160	7019 NO	TES	TES	ATCOPIAZ5	LIR/Copia
chr4	12085681	12093000	7319 YES	NO	NO	BRODYAGA1	DNA/MuDR
chr4	12885841	12892320	6479 NO	NO	YES		
chr4	13027501	13036260	8759 NO	VES	VES		
chi 4	1202/201	12024520	6739 NO	TE5	ILS VEC	VANDALI	DNIA (MUDD
cnr4	13869301	138/4520	5219 NO	NO	TES	VANDALI	DNA/MUDR
chr4	14565361	14571060	5699 NO	NO	YES		
chr4	15155101	15165060	9959 NO	YES	YES		
ala u 4	15205201	15212440	3535 110	120	YEC		
cnr4	15305/61	15313440	7679 NO	NO	TES		
chr4	15561721	15565860	4139 YES	YES	YES	ATLANTYS3	LTR/Gypsy
chr4	16276741	16285080	8339 YES	NO	YES	ATHILA6A	ITR/Gynsy
chi 1	17142201	17140700	6430 NO	NO	VEC	VANDAL 17	
cnr4	1/142301	1/148/80	6479 NO	NO	TES	VANDAL17	DNA/MUDR
chr4	17621041	17628840	7799 NO	NO	NO		
chr4	17989381	17998020	8639 NO	NO	NO		
ala u 4	10060101	10002520	14220 NO	110	VEC	ATDEDE	DC (Us literation
cnr4	18069181	18083520	14339 NO	NO	TES	ATREP5	RC/Helitron
chr4	18265201	18278040	12839 YES	NO	YES	ATHILA	LTR/Gypsy
chr5	54961	78180	23219 YES	NO	YES	ATCOPIA27	ITR/Conia
eh = F	107561	141660	14000 VEC	NO	NO	, (10011)(E)	Enty copia
CIIIS	12/561	141000	14099 165	NO	NO		
chr5	234901	243720	8819 NO	NO	NO		
chr5	320941	329880	8939 NO	NO	NO		
chr5	1373101	1383180	10079 NO	NO	NO		
	13/3101	1303100	10079 110	110	NO		
chr5	1410121	1415460	5339 YES	NO	NO		
chr5	1813321	1821660	8339 YES	YES	YES	HELITRON1	RC/Helitron
chr5	2035981	2042940	6959 YES	NO	YES		
	2055501	2042340	0939 123	110	TE5		
chr5	2083621	2091900	8279 NO	NO	YES		
	2102021		0000 1/50				1 7815 /1 4
chr5	2102621	2112120	9299 YES	NO	NO	ATLINE1_2	LINE/L1
chr5	2102821	2112120 2155020	9299 YES 4079 NO	NO NO	NO	ATLINE1_2	LINE/L1
chr5 chr5	2102821 2150941	2112120 2155020	9299 YES 4079 NO	NO NO	NO NO	ATLINE1_2	LINE/L1
chr5 chr5 chr5	2102821 2150941 2257321	2112120 2155020 2264100	4079 NO 6779 YES	NO NO NO	NO NO YES	ATLINE1_2	LINE/L1
chr5 chr5 chr5 chr5	2102821 2150941 2257321 2268361	2112120 2155020 2264100 2273760	9299 YES 4079 NO 6779 YES 5399 NO	NO NO NO NO	NO NO YES NO	ATLINE1_2	LINE/L1
chr5 chr5 chr5 chr5 chr5	2102821 2150941 2257321 2268361 2372521	2112120 2155020 2264100 2273760 2397360	9299 YES 4079 NO 6779 YES 5399 NO 24839 YES	NO NO NO NO	NO NO YES NO YES	ATLINE1_2	LINE/LI
chr5 chr5 chr5 chr5 chr5 chr5	2102821 2150941 2257321 2268361 2372521	2112120 2155020 2264100 2273760 2397360 2412600	9299 YES 4079 NO 6779 YES 5399 NO 24839 YES	NO NO NO NO NO	NO NO YES NO YES	ATLINE1_2 ATLINE1_1	LINE/L1
chr5 chr5 chr5 chr5 chr5 chr5 chr5	2102821 2150941 2257321 2268361 2372521 2398921	2112120 2155020 2264100 2273760 2397360 2412600	9299 YES 4079 NO 6779 YES 5399 NO 24839 YES 13679 YES	NO NO NO NO NO	NO NO YES NO YES YES	ATLINE1_2 ATLINE1_1	LINE/L1
chr5 chr5 chr5 chr5 chr5 chr5 chr5 chr5	2102021 2150941 2257321 2268361 2372521 2398921 2455201	2112120 2155020 2264100 2273760 2397360 2412600 2468820	9299 YES 4079 NO 6779 YES 5399 NO 24839 YES 13679 YES 13619 YES	NO NO NO NO NO YES	NO NO YES NO YES YES YES	ATLINE1_2	LINE/L1
chr5 chr5 chr5 chr5 chr5 chr5 chr5 chr5	2102821 2150941 2257321 2268361 2372521 2398921 2455201 2592001	2112120 2155020 2264100 2273760 2397360 2412600 2468820 2596500	9299 YES 4079 NO 6779 YES 5399 NO 24839 YES 13679 YES 13619 YES 4499 NO	NO NO NO NO NO YES NO	NO NO YES NO YES YES YES YES	ATLINE1_2	LINE/L1
chr5 chr5 chr5 chr5 chr5 chr5 chr5 chr5	2102621 2150941 2257321 2268361 2372521 2398921 2455201 2592001 2817961	2112120 2155020 2264100 2273760 2397360 2412600 2468820 2596500 2828400	9299 YES 4079 NO 6779 YES 5399 NO 24839 YES 13679 YES 13619 YES 4499 NO 10439 NO	NO NO NO NO NO YES NO VES	NO NO YES NO YES YES YES YES NO	ATLINE1_2	LINE/L1
chrS chrS chrS chrS chrS chrS chrS chrS	2150941 2257321 2268361 2372521 2398921 2455201 2592001 2817961	2112120 2155020 2264100 2273760 2397360 2412600 2468820 2596500 2828400	9299 YES 4079 NO 6779 YES 5399 NO 24839 YES 13679 YES 4499 NO 10439 NO	NO NO NO NO VES NO YES	NO NO YES NO YES YES YES YES NO	ATLINE1_2	LINE/L1
chrS chrS chrS chrS chrS chrS chrS chrS	2102821 2150941 2257321 2268361 2372521 2398921 2455201 2592001 2817961 3031381	2112120 2155020 2264100 2273760 2397360 2412600 2468820 2596500 2828400 3049020	9299 YES 4079 NO 6779 YES 5399 NO 24839 YES 13679 YES 13619 YES 4499 NO 10439 NO 17639 NO	NO NO NO NO VES NO YES YES YES	NO NO YES NO YES YES YES NO YES	ATLINE1_2 ATLINE1_1 HELITRON2	LINE/L1 LINE/L1 RC/Helitron
chrS chrS chrS chrS chrS chrS chrS chrS	2102821 2150941 2257321 2268361 2372521 2398921 2455201 2592001 2817961 3031381 3153541	2112120 2155020 2264100 2273760 2397360 2412600 2468820 2596500 2828400 3049020 3181320	9299 YES 4079 NO 6779 YES 5399 NO 24839 YES 13679 YES 4499 NO 10439 NO 17639 NO 27779 YES	NO NO NO NO YES YES YES NO	NO NO YES NO YES YES YES NO YES YES	ATLINE1_2 ATLINE1_1 HELITRON2	LINE/L1 LINE/L1 RC/Helitron
chrS chrS chrS chrS chrS chrS chrS chrS	2102821 2150941 2257321 2268361 2372521 2398921 2455201 2817961 3031381 3153541 3248281	2112120 2155020 2264100 2273760 2397360 2412600 2448820 2596500 2828400 3049020 3181320 3287400	9299 YES 4079 NO 6779 YES 5399 NO 24839 YES 13619 YES 13619 YES 13619 NO 10439 NO 17639 NO 27779 YES 39119 YES	NO NO NO NO YES NO YES YES YES NO	NO NO YES NO YES YES YES NO YES YES YES	ATLINE1_2 ATLINE1_1 HELITRON2 HELITRONY3	LINE/L1 LINE/L1 RC/Helitron
chrs chrs chrs chrs chrs chrs chrs chrs	2105821 215941 2257321 2268361 2372521 2398921 2455201 2592001 2817961 3031381 3153541 3248281 3248281	2112120 2155020 2264100 2273760 2412600 2468820 2596500 2828400 3049020 3181320 3287400	9299 YES 4079 NO 6779 YES 5399 NO 24839 YES 13619 YES 4499 NO 10439 NO 17639 NO 27779 YES 39119 YES	NO NO NO NO VES NO YES YES NO YES	NO NO YES NO YES YES YES NO YES YES YES YES	ATLINE1_2 ATLINE1_1 HELITRON2 HELITRONY3	LINE/L1 LINE/L1 RC/Helitron RC/Helitron
chr5 chr5 chr5 chr5 chr5 chr5 chr5 chr5	210321 2150341 2257321 2268361 2372521 2398921 2455201 2592001 2817961 3031381 3153541 3248281 3363001	2112120 2155020 2264100 2273760 2412600 2468820 2596500 2828400 3049020 3181320 3287400 3379740	9299 YES 4079 NO 6779 YES 5399 NO 24839 YES 13619 YES 13619 YES 4499 NO 10439 NO 17639 NO 27779 YES 39119 YES 16739 YES	NO NO NO NO YES YES YES YES NO YES NO	NO NO YES NO YES YES YES NO YES YES YES YES YES YES	ATLINE1_2 ATLINE1_1 HELITRON2 HELITRONY3 VANDAL22	LINE/L1 LINE/L1 RC/Helitron RC/Helitron DNA/MuDR
chr5 chr5 chr5 chr5 chr5 chr5 chr5 chr5	21050941 2257321 2268361 2372521 2398921 2455201 2817961 3031381 3153541 3248281 3363001 3701281	2112120 2155020 2264100 2273760 2397360 2412600 2468820 2596500 2828400 3049020 3181320 3287400 3379740 3379740	9299 YES 4079 NO 6779 YES 5399 NO 24839 YES 13679 YES 4499 NO 10439 NO 17639 NO 27779 YES 39119 YES 16739 YES 22199 YES	NO NO NO NO VES VES YES NO YES NO YES NO	NO NO YES NO YES YES YES NO YES YES YES YES NO	ATLINE1_2 ATLINE1_1 HELITRON2 HELITRONY3 VANDAL22 HELITRONY3	LINE/L1 LINE/L1 RC/Helitron DNA/MuDR RC/Helitron
cnr5 chr5 chr5 chr5 chr5 chr5 chr5 chr5 ch	2105321 2150941 2257321 2268361 2372521 2398921 2455201 2592001 2817961 3031381 3153541 3248281 3363001 3701281 4057861	2115120 2155020 2264100 2273760 2412600 2468820 2596500 2828400 3049020 3181320 3287400 3379740 3379740 3379740	9299 YES 4079 NO 6779 YES 5399 NO 24839 YES 13679 YES 13619 YES 4499 NO 10439 NO 17639 NO 27779 YES 39119 YES 16739 YES 2199 YES 4199 NO	NO NO NO NO YES NO YES YES NO YES NO NO NO	NO NO YES NO YES YES YES NO YES YES YES YES YES NO NO	ATLINE1_2 ATLINE1_1 HELITRON2 HELITRONY3 VANDAL22 HELITRONY3	LINE/L1 LINE/L1 RC/Helitron RC/Helitron DNA/MuDR RC/Helitron
Chr5 chr5	210321 2150941 2257321 2268361 2372521 2398921 2455201 2817961 3031381 3153541 3248281 3363001 3701281 4057861	2115120 2155020 2264100 2397360 2412600 2412600 2596500 2828400 3049020 3181320 3287400 3723480 4062060 4159200	9299 YES 4079 NO 6779 YES 5399 NO 24839 YES 13679 YES 13619 YES 4499 NO 10439 NO 17639 NO 27779 YES 39119 YES 16739 YES 22199 YES 4199 NO 4959 NO	NO NO NO NO VES VES YES NO YES NO YES NO NO NO NO	NO NO YES NO YES YES YES NO YES YES YES YES NO NO NO	ATLINE1_2 ATLINE1_1 HELITRON2 HELITRONY3 VANDAL22 HELITRONY3	LINE/L1 LINE/L1 RC/Helitron DNA/MuDR RC/Helitron
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chr5 chr5 chr5 chr5 chr5 chr5 chr5 chr5	21050941 21550941 2257321 2398921 2455201 2592001 2817961 3031381 3153541 3248281 3363001 3701281 4057861 4154941 4311841	2115120 2155020 2264100 2273760 2412600 2468820 2596500 2828400 3049020 3181320 3287400 3379740 3723480 4062060 4159800 4330440 4530900	9299 YES 4079 NO 6779 YES 5399 NO 24839 YES 13679 YES 13619 YES 4499 NO 10439 NO 17639 NO 27779 YES 39119 YES 16739 YES 2199 YES 4199 NO 4859 NO 18599 YES 4319 YES	NO NO NO NO NO YES YES NO YES NO YES NO NO NO NO NO NO NO NO	NO NO YES NO YES YES YES YES YES YES YES NO NO NO NO NO YES NO	ATLINE1_2 ATLINE1_1 HELITRON2 HELITRONY3 VANDAL22 HELITRONY3 ATLINE2 ATLINE1I	LINE/L1 LINE/L1 RC/Helitron DNA/MuDR RC/Helitron LINE/L1 LINE/L1
cnr5 chr5 chr5 chr5 chr5 chr5 chr5 chr5 ch	2105321 2150941 2257321 2398921 2455201 2817961 3031381 3153541 3248281 3363001 3701281 4057861 4154941 4311841 4526581	2115120 2155020 2264100 2273760 2397360 2412600 2468820 2596500 2828400 3049020 3181320 3287400 33723480 4062060 4159800 4330440 4330440	9299 YES 4079 NO 6779 YES 5399 NO 24839 YES 13679 YES 13679 YES 4499 NO 10439 NO 17639 NO 27779 YES 36119 YES 2679 YES 21199 YES 4199 NO 4859 NO 18599 YES 4319 YES 4319 YES	NO NO NO NO VES NO YES YES NO YES NO NO NO NO NO NO NO NO NO	NO NO YES NO YES YES YES NO YES YES YES YES NO NO NO NO NO NO YES NO	ATLINE1_2 ATLINE1_1 HELITRON2 HELITRONY3 VANDAL22 HELITRONY3 ATLINE2 ATLINE11 ATLINE11 ATLINE11	LINE/L1 LINE/L1 RC/Helitron RC/Helitron RC/Helitron LINE/L1 LINE/L1 LINE/L1
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cnr5 chr5 chr5 chr5 chr5 chr5 chr5 chr5 ch	2105321 2150941 2257321 2398921 2455201 2592001 2817961 3031381 3153541 3248281 33663001 3701281 4057861 4154941 4311841 4526581 4786381 4979221	2115120 2155020 2264100 2273760 2397360 2412600 2596500 2596500 2828400 3049020 3181320 3287400 3379740 3379740 3723480 4062060 4159800 4330440 4530900 4804020 4993260	9299 YES 4079 NO 6779 YES 5399 NO 24839 YES 13679 YES 13679 YES 4499 NO 10439 NO 17639 NO 27779 YES 39119 YES 16739 YES 22199 YES 4199 NO 18599 YES 4319 YES 13639 YES 13639 YES 13639 YES	NO NO NO NO VES YES YES NO YES NO NO NO NO NO NO NO NO NO NO NO NO NO	NO NO YES NO YES YES YES NO YES YES YES YES NO NO NO NO YES NO YES NO YES YES	ATLINE1_2 ATLINE1_1 HELITRON2 HELITRONY3 VANDAL22 HELITRONY3 ATLINE2 ATLINE1 ATLINE111 ATLANTYS3	LINE/L1 LINE/L1 RC/Helitron DNA/MuDR RC/Helitron LINE/L1 LINE/L1 LINE/L1 LINE/L1
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Chr5 ch	2100321 2100321 2257321 2398921 2455201 2592001 2817961 3031381 3153541 3248281 3363001 3701281 4057861 4154941 4311841 4526581 4786381 4786381 4786381 4786381 5092501 5093461 5642761 6678421 6678421 6678421 7856881 7937161 8082001 8147521 8177161 8295181 8454961 8501581 8543881 8551581 8543851 8551581 8543851 8551581	2115120 2155020 2264100 2273760 2397360 2412600 2596500 22995500 2828400 3049020 3181320 3287400 3379740 3723480 4062060 4159800 4330440 4530900 4804020 4993260 5018040 5505860 5971200 6335760 6689580 6635760 6689580 6635760 6689580 6635760 6689580 8163676140 7955360 8087580 8163660 8189460 8303520 8466180 8506200 8558400 85585800 85585800 85585800 85585800 85585800 85585800 85585800 85585800 85585800 85585800 85585800 8558580	9299 YES 5399 NO 6779 YES 5399 NO 24839 YES 13679 YES 13619 YES 4499 NO 10439 NO 17639 NO 27779 YES 30119 YES 16739 YES 22199 YES 4199 NO 18599 YES 4319 YES 17639 YES 17639 YES 17639 YES 16739 YES 5039 YES 5039 YES 5039 YES 5339 YES 5339 YES 5339 YES 5339 YES 5339 YES 5339 YES 5579 YES 6299 NO 10259 NO 10259 NO 10259 NO 10259 NO 10259 YES 15539 YES 15539 YES 15539 YES 15539 YES 1529 YES 1529 YES 1529 YES 1529 YES 1529 YES 1529 YES 1529 YES 1529 YES 1519 NO 23159 YES 1519 YES	NO NO NO NO NO YES YES NO YES NO NO NO NO NO NO YES YES NO NO NO NO YES YES NO YES YES NO YES YES NO YES YES NO NO NO NO NO YES YES NO NO NO NO NO NO NO NO NO NO NO NO NO	NO NO YES NO YES YES YES YES YES YES YES YES YES YES	ATLINE1_2 ATLINE1_1 HELITRON2 HELITRONY3 VANDAL22 HELITRONY3 ATLINE2 ATLINE1I ATLANTYS3 ATREP9 ARNOLDY1 VANDAL8 HELITRONY3 BRODYAGA1A ATDNA127T9A ATREP10A ATREP5 ATCOPIA30 ATMU2 ATREP5 ATCOPIA95 HELITRONY3 ATHATN6 ATENSPM2 ATHILA66 ATREP3 ATMU3N1 ATCOPIA27 ATLINE11	LINE/L1 LINE/L1 RC/Helitron DNA/MuDR RC/Helitron DNA/MuDR RC/Helitron DNA/MuDR RC/Helitron DNA/MuDR RC/Helitron LTR/Copia DNA/MuDR RC/Helitron LTR/Copia DNA/MuDR RC/Helitron LTR/Copia RC/Helitron LTR/Copia RC/Helitron DNA/MUDR RC/Helitron DNA/MUDR RC/Helitron DNA/MUDR RC/Helitron DNA/MUDR RC/Helitron DNA/HAT DNA/En-Spri LTR/Copia LTR/Copia LTR/Copia LTR/Copia LTR/Copia LTR/Copia
cnr5 chr5 chr5 chr5 chr5 chr5 chr5 chr5 ch	2105321 2105041 2257321 2398921 2455201 2592001 2817961 3031381 3153541 3248281 33663001 3701281 4057861 4154941 4311841 4526581 4786381 4797221 5002501 5093461 5642761 5966161 6630421 6678421 6678421 6678421 6678421 7778821 77856881 7074841 7778821 7856881 7937161 8082001 8147521 8171161 8295181 8501581 8501581 8501581 8551581	2115120 2155020 2264100 2273760 2412600 2468820 2596500 2828400 3049020 3181320 3287400 3379740 3723480 4062060 41539800 4330440 4530900 4330440 4530900 4330440 4530900 4330440 4530900 5105460 5650860 5971200 6392460 6335760 6689580 6974820 7865120 7865120 7865120 7865120 7865120 7865120 7865120 7865120 7865120 7865120 7865120 7865120 8163060 8189460 8189460 8158400 8558400 8558400 8558400 8558400 8558400 856200 856200 856200 856200 856200 856200 856400 8597700 8648280 8904720 839220 16284600 16727520	9299 YES 5399 NO 6779 YES 5399 NO 24839 YES 13679 YES 13679 YES 13619 YES 14499 NO 10439 NO 17639 NO 27779 YES 36119 YES 16739 YES 22199 YES 4199 NO 48599 YES 17639 YES 17639 YES 1639 YES 5039 YES 5039 YES 5039 YES 5039 YES 5539 YES 8759 YES 8759 YES 8759 YES 5579 YES 11159 NO 10259 NO 10259 NO 10259 NO 10259 YES 15539 YES 155	NO NO NO NO NO YES YES YES NO YES NO NO NO NO YES YES YES YES YES YES YES YES YES YES	NO NO YES NO YES NO NO NO YES YES <td>ATLINE1_2 ATLINE1_1 HELITRON2 HELITRONY3 VANDAL22 HELITRONY3 ATLINE2 ATLINE2 ATLINE1II ATLANTYS3 ATREP9 ARNOLDY1 VANDAL8 HELITRONY3 BRODYAGA1A ATREP10A ATREP10A ATCOPIA30 ATREP5 ATCOPIA30 ATREP5 ATCOPIA30 ATREP5 ATCOPIA30 ATREP5 ATCOPIA30 ATREP5 ATCOPIA30 ATREP5 ATCOPIA30 ATREP5 ATCOPIA30 ATREP5 ATCOPIA30 ATREP5 ATCOPIA30 ATREP5 ATCOPIA30 ATREP5 ATCOPIA30 ATREP5 ATCOPIA25 HELITRONY3 ATHATN6 ATENSPM2 ATHILA6B ATREP3 ATUNI11 ATCOPIA27 ATLINE11 ATLINE1_6</td> <td>LINE/L1 LINE/L1 RC/Helitron RC/Helitron DNA/MuDR RC/Helitron DNA/HuDR DNA/MuDR DNA/MuDR DNA/MuDR RC/Helitron LTR/Copia RC/Helitron DNA/HuDR RC/Helitron DNA/HuDR RC/Helitron DNA/HaT DNA/En-Spm LTR/Copis RC/Helitron DNA/En-Spm LTR/Copis RC/Helitron</td>	ATLINE1_2 ATLINE1_1 HELITRON2 HELITRONY3 VANDAL22 HELITRONY3 ATLINE2 ATLINE2 ATLINE1II ATLANTYS3 ATREP9 ARNOLDY1 VANDAL8 HELITRONY3 BRODYAGA1A ATREP10A ATREP10A ATCOPIA30 ATREP5 ATCOPIA30 ATREP5 ATCOPIA30 ATREP5 ATCOPIA30 ATREP5 ATCOPIA30 ATREP5 ATCOPIA30 ATREP5 ATCOPIA30 ATREP5 ATCOPIA30 ATREP5 ATCOPIA30 ATREP5 ATCOPIA30 ATREP5 ATCOPIA30 ATREP5 ATCOPIA30 ATREP5 ATCOPIA25 HELITRONY3 ATHATN6 ATENSPM2 ATHILA6B ATREP3 ATUNI11 ATCOPIA27 ATLINE11 ATLINE1_6	LINE/L1 LINE/L1 RC/Helitron RC/Helitron DNA/MuDR RC/Helitron DNA/HuDR DNA/MuDR DNA/MuDR DNA/MuDR RC/Helitron LTR/Copia RC/Helitron DNA/HuDR RC/Helitron DNA/HuDR RC/Helitron DNA/HaT DNA/En-Spm LTR/Copis RC/Helitron DNA/En-Spm LTR/Copis RC/Helitron
Chr5 ch	2100301 2100301 2100301 2257321 2398921 2455201 2592001 2817961 3031381 3153541 3248281 3363001 3701281 4057861 4154941 4311841 4526581 4786381 4786381 4786381 4786381 5092501 5093461 5642761 6678421 6678421 6678421 7856881 7937161 8082001 8147521 8171161 8295181 8543881 8551581 8543851 8554581 8555581 8555581 8555581 8555581 8555581 8555581 8555581 8555581 8555581 855555	2115120 2155020 2264100 2273760 2397360 2412600 2596500 22995500 2828400 3049020 3181320 3287400 3379740 3723480 4062060 4159800 4330440 4530900 4804020 4993260 5018040 5505860 5971200 6395200 6395200 6395200 6689580 6689580 6689580 6689580 6689580 6689580 6689580 6689580 6689580 6689580 6689580 8165060 8189460 8303520 8163600 8189460 8303520 8466180 8506200 8558400 8558400 8558400 8558400 8558400 8558400 8558400 8558400 8558400 8558400 8558400 8558400 8597700 848280 8094720 8332220 16284600	9299 YES 5399 NO 6779 YES 5399 NO 24839 YES 13679 YES 13619 YES 4499 NO 10439 NO 17639 NO 27779 YES 30119 YES 16739 YES 22199 YES 4199 NO 18599 YES 16539 YES 16539 YES 16539 YES 5039 YES 5039 YES 5039 YES 5339 YES 5339 YES 5339 YES 5339 YES 5339 YES 5339 YES 5339 YES 5339 YES 5539 YES 5539 YES 5539 YES 11159 NO 5639 YES 5579 YES 5579 YES 1529 NO 10259 NO 10259 NO 10259 NO 10259 YES 1529 YES 15179 YES 1	NO NO NO NO NO NO YES YES NO YES NO NO NO NO NO YES YES NO NO YES YES NO YES YES NO YES YES NO YES YES NO NO NO NO YES YES NO NO NO NO NO NO NO NO NO NO NO NO NO	NO NO YES NO YES YES YES YES YES YES NO NO YES YES YES YES YES YES YES YES YES YES	ATLINE1_2 ATLINE1_1 HELITRON2 HELITRONY3 VANDAL22 HELITRONY3 ATLINE2 ATLINE1I ATLANEY33 ATREP9 ARNOLDY1 VANDAL8 HELITRONY3 BRODYAGA1A ATDNA127T9A ATREP10A ATREP10A ATREP5 ATCOPIA30 ATMU2 ATREP5 ATCOPIA30 ATMU2 ATREP5 ATCOPIA95 HELITRONY3 ATHATN6 ATENSPM2 ATHILA66 ATREP3 ATUINE11 ATLINE1_6	LINE/L1 LINE/L1 RC/Helitron DNA/MuDR RC/Helitron DNA/MuDR DNA/MuDR DNA/MuDR RC/Helitron DNA/MuDR RC/Helitron LTR/Copia DNA/MuDR RC/Helitron LTR/Copia DNA/MuDR RC/Helitron LTR/Copia DNA/MuDR RC/Helitron LTR/Copia RC/Helitron DNA/HAT DNA/En-Spn LTR/Gypsy RC/Helitron DNA/HAT

chr5	17089501	17100000	10499 YES	NO	YES	ATREP10B	RC/Helitron
chr5	17612221	17626800	14579 YES	NO	YES	ENDOVIR1	LTR/Copia
chr5	17905741	17918640	12899 YES	NO	YES	VANDAL6	DNA/MuDR
chr5	17980621	17990940	10319 YES	YES	YES	ATREP5	RC/Helitron
chr5	18133681	18151380	17699 YES	YES	YES	VANDAL14	DNA/MuDR
chr5	18204301	18221040	16739 YES	NO	YES	ATENSPM5	DNA/En-Spm
chr5	18273301	18278580	5279 YES	NO	NO	ATLINE1_1	LINE/L1
chr5	18443641	18455400	11759 YES	YES	YES	ATREP15	RC/Helitron
chr5	18486781	18498240	11459 YES	YES	YES	VANDAL6	DNA/MuDR
chr5	18536041	18541380	5339 YES	YES	YES	HELITRONY1D	RC/Helitron
chr5	18944881	18957840	12959 YES	NO	YES	ATCOPIA58	LTR/Copia
chr5	19371661	19383540	11879 YES	NO	YES	ATREP5	RC/Helitron
chr5	19409701	19419540	9839 NO	NO	YES	ATREP15	RC/Helitron
chr5	19905481	19909740	4259 YES	NO	YES	ATHILA6A	LTR/Gypsy
chr5	20801881	20810100	8219 YES	NO	NO		
chr5	21967321	21974520	7199 NO	NO	YES		
chr5	22213561	22223340	9779 YES	NO	NO		
chr5	22235581	22246320	10739 YES	NO	YES		
chr5	22694881	22702320	7439 NO	YES	NO	ATREP10D	RC/Helitron
chr5	24033421	24049140	15719 YES	NO	YES	VANDAL17	DNA/MuDR
chr5	24332461	24342540	10079 YES	NO	NO	BRODYAGA2	DNA/MuDR
chr5	24710641	24719280	8639 YES	YES	YES	ATREP15	RC/Helitron
chr5	24874681	24881640	6959 NO	NO	YES		
chr5	25597621	25603080	5459 NO	NO	NO		
chr5	26144101	26149800	5699 YES	NO	NO		
chr5	26512201	26520060	7859 NO	NO	YES	ATDNAI27T9A	DNA/MuDR

Supplementary Table 2. Primers used for qPCR experiments to measure DNA quantity.

For qPCR in Supplementary Figure3 the following primers were used:

gene	Primers	Sequence
AT1G44510	2709-CHR1-2-F1	GCCTAGAGGTATAAAGCCGGTTG
	2710-CHR1-2-R1	CCACACCGGTCCTCTGTCTTCAG
AT2G04160	2713-CHR2-1-F1	GTGAGCTGTGTGGCTGGAAGGAC
	2714-CHR2-1-R1	CTTGGATCGCTTGACCCTATAAAG
AT2G16670	2721-CHR2-3-F1	GGCGTCGGAACAACTTCAGTGTC
	2722-CHR2-3-R1	GGGCTCCAATAGTTGATGGGC
At1g51800	2436-1g51800-F2	ACTTTACCTCCTCTGCTCAACGC
	2437-1g51800-R2	CAGTCAATCTTGTTCACGCCG

For qPCR in Supplementary Figure4 the following primers were used:

gene	Primers	Sequence
AI 1G31440	JP/583	CUIGIACCAGCCACCIGAAI
	JP7584	GGGAACTCAGTCTCGCTGTC
AT3G24320	JP7220	CAAGCATGGGAAAATAATGC
	JP7221	TTGTTGCAGATACCATGAAGC
AT2G40000	JP7429	GCCGACCAAACGAGATCTATAG
	JP7430	CTTCTCCAGCAAGTAAACATCG
САСТА	1P8158	TGTGTGGAAGGGTCTTGTGGACTT
chem	JP8159	AACTTACATGTTTGCGGGCACGAG
AT1G31355	107591	GGGAAGTGCAGACAGACCTT
AI1031333	JP7582	AGGAGGCAATTGTGTGAAGC
451 02 4000	IDC 470	
AI 1G34080	JP64/9	CAAGGCGAAGICCIGCIAAC
	JP6480	TCAAGTTCTCGCGGATTTTC
AT2G29210	JP6485	GGTCGCGGTCACCTATTAGA
	JP6486	GAGAACGGTGACGCCTAGC