

A)

TCsat14

SatDNA	From	To	Rebase	From	To	Dir	Sim	Pos/Mm:Ts	Score
TCsat14	168	227	HAT-14_Mad	1525	1587	c	0.7903	1.2857	242

168 ATTTCCACAAAAA--AGTGTG-GTTCAGTTCTAAATATTTTACAAT--AATTTAACTTTTTTAG 227
 |||||:||||:--||||-||:|--|||||||:||||--|||:||||: |||
 1587 ATTTCCACGAAAGCCAGTGTGTGTTAG--CTAAATATTTACAATGGAAATCAACCTTCGTAG 1525

TCsat15

SatDNA	From	To	Rebase	From	To	Dir	Sim	Pos/Mm:Ts	Score
TCsat15	495	522	Academ-3_LMi	72	99	c	0.9643	1.0000	244

495 TCGGAAAGAGCACATCAAATCTATAAG 522
 |||:||||||||||||||||||
 99 TCGAAAAGAGCACATCAAATCTATAAG 72

SatDNA	From	To	Rebase	From	To	Dir	Sim	Pos/Mm:Ts	Score
TCsat15	663	693	Transib-N1_CQ	908	938	c	0.8710	1.3333	213

663 CCTATGCAAAATGATCCGGGGAATCGATTGG 693
|:||||:|||| :|||||||
938 CTTATGTAAAAAATCCGGGGAATCGATTGG 908

SatDNA	From	To	Rebase	From	To	Dir	Sim	Pos/Mm:Ts	Score
TCsat15	1037	1102	Sola1-2 LMi	1445	1506	d	0.7846	2.0000	203

1037 AAAAAATTTACTGGAGTGAGTTTAAAAAAAAATTTTTTTTACCT-CTTGAAAGTTAAGTGATTATT 1102
| | | | | | | | | | : | - | | --- | | | | | | | | | | : | : | - | : | | | | | | - | | | | | : | |
1445 AAAAAATTTACTGAA-TG---TTAATAATACATTTTTTTTTTACTTTCTCTGAACTTT-GTGTATTGTT 1506

TCsat16

SatDNA	From	To	Rebase	From	To	Dir	Sim	Pos/Mm:Ts	Score
TCsat16	148	184	DNAX-1_TCa	1481	1517	c	0.9189	1.0000	308

148 TGTACAGGGTGCCGATTTTGGATATCCGAATAGGAG 184
 |||||:|||||:|||||:|
 1517 TGTACAGGGTGCTGCATTTTGGATGTCCGAATAGGGG 1481

SatDNA	From	To	Rebase	From	To	Dir	Sim	Pos/Mm:Ts	Score
TCsat16	208	285	Dada-tV_PeFlu	7776	7849	d	0.7200	1.5833	234

208 ATGCAATAAAAAATTGTACTACTGCTAAATCGAATCCAAC TTGTTCAATTAACAGTAAATATATGTATC- 276
| | : | | | | | - - - - | | | | | : | : | | : | : | | | | | | | | | | : | | | : | : | | | | | | | -
7776 ATACAATAA-----TG TACTATTATTAAGTTGAATTCAACTTTTTACCAGTAGCAGCATGTAAAAGTATTA 7840

277 TTGTCACAA 285
| | | | | : | |
7841 TTGTCATAA 7849

TCsat19

SatDNA	From	To	Rebase	From	To	Dir	Sim	Pos/Mm:Ts	Score
TCsat19	13	77	MuDR-7_Cas	8094	8155	c	0.7778	1.7143	246

13 GTTATT-TATCGAAATTTGTATACTGATCTTGATTTTTTTATTTTCAGTAGGCTCTATTCTAAGA 77
 ||||| - ||| ||:|||||----|| |:|||||||:|| |||: |:|||||:|| |||:|
 8155 GTTATTGTATCTAAGATTTGT----TGCTTTTGATTTCTTTTTTTTTTGCAGGTCCATGCTAGGA 8094

TCsat21

SatDNA	From	To	Rebase	From	To	Dir	Sim	Pos/Mm:Ts	Score
TCsat21	16	82	HipGal-6.520	280	353	c	0.7971	1.5000	220

```

16  AGTCGCAATAAAATTTGT-----TAATTTGAAAATAAAAT--TTAATTCGC---GCTTCAAATTAATAAAA 75
    ||  |||||:|:|:|-----|||  |||||-----:||||:-|---:||||---|||
353  AGGCGCAATGAATCTGTCAGATTAATTAGAAAATAAAATACCTAATT-ACTAAGTTTCAA--TAATAAAA 287

76  ATGTACT 82
    |:|
286  CTATACT 280

```

TCsat23

SatDNA	From	To	Rebase	From	To	Dir	Sim	Pos/Mm:Ts	Score
TCsat23	1	164	Rehavkus-1_TC	7923	8086	c	0.9939	1.0000	1441

```

1 TTTAATATTATTAATAAAATGTTGACATATTTCAAAC TAAGGGTTGGATGTCTTCCCAAAC TTTTAGAGG 70
  |||
8086 TTTAATATTATTAATAAAATGTTGACATATTTCAAAC TAAGGGTTGGATGTCTTCCCAAAC TTTTAGAAG 8017

71 GTTGAAATTTTCAGGAAAGGTAGAGTATTTAATGGGCTTT CATGTGGAATGGGTTAAATGCGTCGACAAA 140
  |||
8016 GTTGAAATTTTCAGGAAAGGTAGAGTATTTAATGGGCTTT CATGTGGAATGGGTTAAATGCGTCGACAAA 7947

141 AAGAAATAGTACTAGAAAAAATA 164
  |||
7946 AAGAAATAGTACTAGAAAAAATA 7923

```

TCsat24

SatDNA	From	To	Rebase	From	To	Dir	Sim	Pos/Mm:Ts	Score
TCsat24	94	122	CerCot-5.769	495	523	d	0.9310	99.0000	226

94 CCAGAGCGCATGCGCATGCGCGTCTGACC 122
 ||||| ||||| |||||
 495 CCAGAGCGCCTGCGCATGCGCGTGTGACC 523

SatDNA	From	To	Rebase	From	To	Dir	Sim	Pos/Mm:Ts	Score
TCsat24	316	397	EnSpm-N2_DaCa	2493	2564	d	0.8108	1.6000	211

```

316 TCACAAAGTCATG--ATTAAAAATTTTAAAGTTTTTTTAACTTAATCGATAGACATGCGCGTAAGATTAA 382
    |:|||||-----|||---|||---|||  || |:-----|::|| |||:|---
2493 TTACAAAGTCATGCAAATTTAA-TTTTAA--TTTTTTAAATTATTT-----CACACGCCTAAAT--- 2550

383 AAAAATA-ATTTTTAT 397
    --|||||---|||
2551 --AAATATATTTTTAT 2564

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TCsat26

SatDNA	From	To	Rebase	From	To	Dir	Sim	Pos/Mm:Ts	Score
TCsat26	68	260	Transib-3_DTa	3053	3197	d	0.7595	1.5625	241

```

68 TTGTAACCATCACTGATTCTAAAAATAACTGAAAAGATTTAAAGTTAAACGTTTTTATCTTCAAAGTAA 137
   |||:||||:|:|---||   ||||:--||||-----|---|:|||:-:|||||:|:|:|:-||
3053 TTGTGACCATTATT---TCAAAAAACA--TGAA-----TA-----TAAAA-ATTTTATTTTAAAA-AA 3106

138 ATATAGCTGTTAAATTTCTCTTTCTTTTTTTTGCAAGTGTCTGCTTAGTTTTCAAAAATTTTAATAAC 207
   |---|:| |--|||||:|:||||:|||||-----|||||:|||||   ||:|
3107 A---AACTTT--AATTTTTTTTTTTTTTTTTT-----TAGTTTTTAAAAATTAAACATA 3158

208 AAAATGCTTTAATAAAAAATTACTAATATAACACATAATTAAACTAAAACAAA 260
   |||-----|||||-----|||:-|:| |:|||| ||--||| |||
3159 AAAA-----AATAAA-----CTAA-ACAAAACGTAATTTAA--AAAAAAA 3197

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SatDNA	From	To	Repbse	From	To	Dir	Sim	Pos/Mm:Ts	Score
TCsat26	285	361	Gypsy-54_MT-I	1445	1515	c	0.7397	1.3333	230

285

TTGTCAACTCGGCGCCTCCACCATTTTAAAT-TTTAGATATCCAACCAATTTACTTTCCTTACTTTTACT

353

|| |||:|:|:| ||::| ||||| |-||:||||:| |-----|:|:|||||:|||||

1515

TTCTCAATTCAATGACTTTGCGATTTTATTCTTTGGATATTCAAC-----ATTCTCCTTATTTTACT

1452

354

GTAAATGA

361

| -|||||

1451

G-AAATGA

1445

TCsat27

SatDNA	From	To	Repbse	From	To	Dir	Sim	Pos/Mm:Ts	Score
TCsat27	21	57	Gypsy-22_DMeI-I	4973	5009	c	0.8649	1.6667	234

21

TTTTTCAAAGTTTTCTTGCTGTTTTTGTCATATTTT

57

|||||:| ||| |||||||||:|||||||:|

5009

TTTTTCGATGTTATCTTGCTGCTTTTGTCATATTCT

4973

TCsat28

SatDNA	From	To	Repbse	From	To	Dir	Sim	Pos/Mm:Ts	Score
TCsat28	99	167	MuDR-18_Cas	1384	1454	c	0.8000	5.0000	209

99

GTACAAAAAATTTTGAACATTATTGTTTGGTAAAATTTTAAA---ATTAACAGAC-GGTTTT-TTATTTT

163

||||| |: |||||||---||||||| | ||||| || |---||||| |:|-|||||-|||||

1454

GTACACAGTATTTTGAA---TATTGTTAGTTAAAAATTACAATGTATTAAGAAACTGGTTTTCTTATTTT

1388

164

TTTT

167

||||

1387

TTTT

1384

SatDNA	From	To	Repbse	From	To	Dir	Sim	Pos/Mm:Ts	Score
TCsat28	216	342	EnSpm-14_RIr	5450	5579	c	0.7460	1.9167	226

216

AATATACAGTTAAATACTTTAATGTG-TTTA---TTATTAAGTACTTGTAAAGAAAAACCTTTTATTTTTG

281

||||| ||||| |:| :||:|-|||---|||-----|::|| ||||| |||---|||||:

5579

AATATACTTTTAAAAATTGCAATATGATTTAAGCTTATT -----TTACAATAAAAAGCTT--ATTTTTA

5518

282

AC-TAA---GCTTAT-----GAAAAATTTATCACTTTTAAGTACAAAGAGTGTTTTATTTTAAAA-AACTT

342

| -|||---|||||---:||||:||||:--|| |:|| |||| |:|||||||---|

5517

AAATAAAAAGCTTATTTTAAAAAGCTTATT--TTTAAAAATAAAAAGCTTATTTTATTTTAAAAAACTT

5450

TCsat33

SatDNA	From	To	Repbse	From	To	Dir	Sim	Pos/Mm:Ts	Score
TCsat33	89	132	Mariner-5_DSuz	1411	1454	d	0.7955	1.8000	209

89

TTATCTTTTTCCAGGTCGAAGCCCAAAACTAATTATTTATGTC

132

||||:||||:| ||| :||:|||||||:||||| ||| |||

1411

TTATTTTTTCCAAGGTAAAAACCCAAAAATTAATCTTTAAGTC

1454

TCsat36

SatDNA	From	To	Repbse	From	To	Dir	Sim	Pos/Mm:Ts	Score
TCsat36	64	132	Helitron-N2_HMM	738	811	d	0.7500	2.1429	205

64

CGATGTTATCCAATCAAGACAGCGGAATTTT--TAACTTGGTGTTTTATTTGA-ATTTTTC--AGAATG

128

||||||| || |:|:|:| || |||||---| |:||| :|||||||---|| |||---|:|

738

CGATGTTATACACTTAAAATATCGTAATTTTAATCATTTGGGATTTTATTTGATATTGTCGCAAAAATT

807

• |||

SatDN

TCsat37	92	204	Mariner-32_RPr	1618	1729	c	0.7455	1.9091	202
---------	----	-----	----------------	------	------	---	--------	--------	-----

| | | | | | | | | - - - | | : | | : | | | : | | | | | | | | : | | : | - - | : | | | | | - - - - | | | | | | | | -

SatDM

Source	From	To	Response	From	To	Lat	Gain	Loss, rms, etc	Notes
TCsat42	10	107	Gypsy-7_TCa-I	872	968	c	0.7113	1.8462	240

||:|:|||||||:|--||| ||||| ||:|:|:|:| |||----||| ||:-||| |||

SatD

Source	From	To	Release	From	To	Size	Size	Pos./Min/Max	Score
TCsat43	60	139	ARNOLDY2	424	501	c	0.7595	1.7500	209

||||:||||| --- ||||-:||||:~:| | |||| ||||||||:||||||| : |||-||||:|

SatDM

Dataset	From	To	Release	From	To	Size	Size	Frequency	Score
TCsat45	190	227	COPIA3-I MT	4552	4589	c	0.8421	1.2000	222

|||:|||||:|:||||| ||||:|:|||||

Sat DM

Substrat	From	To	Rebase	From	To	Dist	Dist	Pos./min/100	Score
TCsat47	6	138	hAT-N20 ALy	185	314	d	0.7597	2.4444	211

| | | : | | | | --- | | | :: | | | - | | | | | | | | | | - | | - | | | | :: ---- | | | | | | ----

69 TTTCTAAATAAGTTGTTACATCTGTTCTTTATTTTTATCAATCATTTTAATAATCTG--AT-TAATAAT 135

|||:| |||| ||:|||---:| |||| |||||:| || |||| || || |||| --|-||| |||||

245 TTTTAAATATTTATTAC---TATTATTTAAATTTATTAATAATTTTATTATCTTTATATAATAAT 311

136 AAT 138
|||
312 AAT 314

TCsat48

SatDNA	From	To	Repbase	From	To	Dir	Sim	Pos/Mm:Ts	Score
TCsat48	57	136	Polinton-2_HM	130	211	d	0.7317	1.3846	216

57 TAAGAAAAGAAAAGCTTAATCTTGTTTTACTCAAA--TGACACTATTTTTATAGAAAAAATGCTTAAAA- 123
|||:||||:|||| | ||||:|-| ||||:|:| | --|:|:-||| : ||||:| ||||| |:| ||||-
130 TAAAAAAAAAAAAAGATTAATTTT-TTTTGTTTAAAGTTAAT-CTAGCGTTATAAAAAAATATATAAAAA 197

124 -GCAAACGATTTTT 136
-||| |:| |||||
198 AGCAAATGCTTTTT 211

TCsat49

SatDNA	From	To	Repbase	From	To	Dir	Sim	Pos/Mm:Ts	Score
TCsat49	47	132	Gypsy-6B_AlBr-I	4605	4687	c	0.8148	3.0000	240

47 TATTGGTTTT---AATTAATTAA-----ATAATTAATTGACGTTGGAAGAGTTATTTTACATTTATAATC 108
||:| |||||---| ||||| |||||----| ||| -||| -||| || |||-----| || | |:| ||| -
4687 TACTTGTTTTGTAAATTAATTAATACTACTATAAG-AATT-ACGTTGTAAGA-----TACTTTTGTAAT- 4628

109 GATATTTTCTTAAGACAAGTAAGC 132
-||| |:| ||||| |||||
4627 -ATAGTCTCTTAAGACTAGTAAGC 4605

SatDNA	From	To	Repbase	From	To	Dir	Sim	Pos/Mm:Ts	Score
TCsat49	175	261	hAT-26_DTa	334	406	c	0.7867	2.8000	219

175 TTAATAAATATTAACAAAAAACAGTTTTTGAGTGAACCTTACACTCGAATTTTGAACAAATAGTAAAC 244
| ||||| -| ||||| |||||----| ||||:| |:| |:| | | ||| | | |:|
406 TTAATAAAT-ATTAACAAAAAA-----ATCTTTATACTTGCATCTGGTTCAAAAAGATAAGC 351

245 AAAAAATTTATTTTTTTT 261
| |||| | |:| |||||
350 AAAAAATATATTCTTTTT 334

TCsat50

SatDNA	From	To	Repbase	From	To	Dir	Sim	Pos/Mm:Ts	Score
TCsat50	12	105	Gypsy-45_PAb-I	3823	3921	d	0.8065	1.8000	215

12 TTTGACAACTTACTATTTAAGAAACA-----TAAATTAA----TCACAATCTGTTATACTTAAAAAAA 72
|||:| |:| | |||||----| ||||-----| |:| |:|----| | -||| | -| |||-----| |||||
3823 TTTAACGAACATACTATT-----AAACAATTGTCAAATTGACATATCA-AATCT-TGATAA-----AAAAAA 3882

73 ATTAAAAAT-GTCCTT----AGGTAACAAA-TTATTTAC 105
| ||||| -| | | -| -:| ||||| -| |||||
3883 TTTAAAAATAGTCATTGGAAAGATAACAAATTATTTAC 3921

TCsat51

SatDNA	From	To	Repbase	From	To	Dir	Sim	Pos/Mm:Ts	Score
TCsat51	59	143	Gypsy-671_AA-I	292	373	d	0.7619	3.0000	211

59 ATAAAAACTTG-GTAAATTGACTTCGCTTATTTAT-TCAGTGAT-ATCTTCGTAATTACTAAGTTTATG 125
| |||| | | | -:| |:| |:| |----| ||| | |||| -| | ||||| -| | | |:| | |----| |||| | | |
292 ATAAAACCGTAAGTAGAATTAA-----GCTTTTTTATATAAGTGATTATCAGAGTGATT--TAAGTGAATG 355

126 ATCAAAATAATAACATAT 143
|||||||:| |||
356 ATCAAAATAACAAATAT 373

SatDNA	From	To	Rebase	From	To	Dir	Sim	Pos/Mm:Ts	Score
TCsat51	170	243	MuDRx-3_TV	699	768	c	0.7639	2.0000	221

170 AGAAAAGCTTAATTTTAACC-CAATTTTATGTTTTATTTTATTAATACAAATTTTCGAATTTATTATTTA 238
||||||| ||||| :|-|||||||:||||:||||| | -| :|||:|||||----| ||:|||| ||
768 AGAAAAGCTTTATTTTTTCTCAATTTTAAATTCATTTTCAGTC-TCTAAACTTTC ----- TTACTATGTA 704
239 AAAAC 243
|||||
AAAAC 699

SatDNA	From	To	Rebase	From	To	Dir	Sim	Pos/Mm:Ts	Score
TCsat51	255	335	Helitron-N60B_CGi	3066	3153	d	0.7765	2.6000	223

255 AGCT-TCAC TTATTTA----TCAACCGATATCTTAAAAAT-TACTCAATTTATGGCTAAACTAA---TTA 315
||||-| |||| | |||----||| ||||| -||||||| -| :|||:||||| |:| |:| |||--- ||
3066 AGCTGTAAC TTTTTTACCTTTCATCCGATAT-TTAAAAATCTTTTCAGTTTATTGTTAGATAAAGAGTA 3134
316 CAGATTTAAAAAATATGATC 335
||-||||||| ||||:|
3135 CA-ATTTAAAAATTATGGTC 3153

TCsat52

SatDNA	From	To	Rebase	From	To	Dir	Sim	Pos/Mm:Ts	Score
TCsat52	4	35	Academ-10_LMi	666	697	c	0.9062	1.5000	225

4 TTTGTAGAGAATTTTATTGTCTTTAATTTTGT 35
||||||| |||||:|:|||||||
697 TTTGTAGACAATTTTGTCTTTAATTTTGT 666

TCsat53

SatDNA	From	To	Rebase	From	To	Dir	Sim	Pos/Mm:Ts	Score
TCsat53	9	140	MuDR-2_GAr	3549	3679	c	0.7405	1.9231	233

9 TTTTTTCAGTTATATTTTATTCTTTTTAGTTTCTCGGGCATTTA--TTGTTTTATTTTCTC--TTAATC 74
|:||||| ||| |||| | |:||||:| :|||-----| |||--||: |||-|||||||--|| ||:
3679 TCTTTTCATTTAAATTTAAATTTTTTCTCATTTTC----- ATTTAAATTAATTT-TTTTCTCATTTTCATT 3617
75 TCGGTT-ATTTTACTTTGCAGTTTTTAAGTTAAACTTCTCAT--GGTTTAGACT--ATTTTTTTCTCATT 139
| :||-|||| | |||-|--||||| ||||:|:||||-- :|||:|:|-- |||||
3616 TAAATTTATTTTCTTT-CA--TTTAAATTTAAATTTTTCATTTTCATTTAAATTTANTTTTTTCTCATT 3550
140 T 140
|
3549 T 3549

TCsat54

SatDNA	From	To	Rebase	From	To	Dir	Sim	Pos/Mm:Ts	Score
TCsat54	12	68	HARB-N1_TC	819	876	c	0.7931	2.0000	209

12 ACAAATA--TTTGATTAATAATGAGAAATAGGTGAAAATCAAGCGAATAAAAAATGAA 68
|:|||||--||| ||||:|||||:| ||||:|-||||||| ||| |||| ||||
876 ATAAATAATTTTTATTGAATAATAATAATAAAT-AAAATCAAGAGAAAAAATTGAA 819

SatDNA	From	To	Rebase	From	To	Dir	Sim	Pos/Mm:Ts	Score
TCsat54	166	264	Gypsy-122_NS-LTR	147	237	c	0.7660	1.7778	232

```

166 CGTACAATTTTTTTATTATTCTTTGGAAATTTTGCAAAACAATCTTGATTGAGTTATTGTAGAAA--- 232
    ||||| | ||||| ||::||:----|||:||||| |||:-||:|:-|||----|||---
237 CGTACATTATTTTATGATTTTTTC----ATTTGTAAAACAACTTA-ATTAAAT-ATT---AAACGC 178

233 AAATAACGACAGTTTTTTGTATTTTTTTTTTAA 264
    |||:-|||| ||||:||||| |||
177 AAATG-CGACATATTTTATATTTTTTATTAA 147

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SatDNA	From	To	Rebase	From	To	Dir	Sim	Pos/Mm:Ts	Score
TCsat54	265	309	Gypsy-27_DW1-I	295	333	c	0.8500	2.5000	201

265 ATTTTGACTTTTATTTTACCAAAAAATATTGTTTCTTATTTAAGA 309
 |||||:| |||||-----|| |:| |||||
 333 ATTTTGATTGTATTTTA-----AATTCGATTCTTATTTAAGA 295

TCsat55

SatDNA	From	To	Rebase	From	To	Dir	Sim	Pos/Mm:Ts	Score
TCsat55	146	309	DNA-1_CQ	1390	1543	d	0.7421	1.6471	275

```

146 AAAATTT--AAGATT-CTAAATTT-CAAAATATGTACCCAAAGTTTTCGAAACTTTAGACTTGAACATGT 211
   |||||---||:|||-|||||||---| ||| |---|:||||--||| |||:|----|||:|:| | |
1390 AAAATTTCTAAATTTCTAAATTTCTAAATTT---CTTAAA--TTTCTAAATTT-----CTTAAATTTCT 1450

212 GAACTT-TGAAACTTCTAAACTTCTAAATAACTAAAACTTGAAGATCTAAAGTTTC-AAAGTTGTTCTAA 279
   :||:|-|:||||:|||||||:||||||| || |||:|-----| |||:||||-||:| |--|||
1451 AAATTTCTAAATTTCTAAATTTCTAAATTTCTTAAATTT-----CTAAATTTCTAAATTT--TCTAA 1512

280 G-TTTC-AAGATTAGGTACAATTTCTAAGATT 309
   :-||||-||:|||- || ||||| |||:||
1513 AATTTCTAAATTT-TCTAAATTTCTAAATTT 1543

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TCsat56

SatDNA	From	To	Rebase	From	To	Dir	Sim	Pos/Mm:Ts	Score
TCsat56	191	244	Harbinger-21_OS	1503	1558	c	0.8182	1.4000	258

191 CATTAAATTATTTTACCAAGCATTTAC---AATAATTTACTCAGAAGATGTCTATT 244
|||:|||||: |||||:| |--|---|||---|||---|||:|||||:|||
1558 CATTGAATTATTCAACCAAGCACTGACCTAAAATA-TTTA-TCAAAAGATGTTTATT 1503

B)

Repeat Class	Fragments	Length (bp)
Transposable Element	37	2955
DNA transposon	27	2267
Academ	2	60
Dada	1	78
EnSpm/CACTA	2	209
Harbinger	2	111
Helitron	2	150
Mariner/Tc1	2	157
MuDR	6	584
Polinton	1	80
Sola	1	66
Sola1	1	66
Transib	2	224
hAT	3	280
piggyBac	1	67
LTR Retrotransposon	9	659
Copia	1	38
Gypsy	8	621
Non-LTR Retrotransposon	1	29
L1	1	29
Total	37	2955

C)

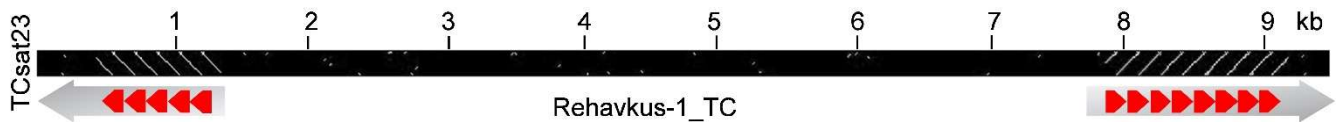


Figure S2. Similarities between *T. castaneum* low-copy satDNAs and Repbase entries (release 27.09) accessed by the software CENSOR. **A)** Alignments of partial sequence segments between *T. castaneum* low-copy satDNAs and Repbase-deposited repetitive elements. **B)** A report classifying all repetitive elements in Repbase with which the *T. castaneum* low-copy satDNAs share partial similarity. **C)** A dot-plot sequence comparison showing TCsat23 monomers (red arrows) repeated in the inverted termini (grey arrows) of Rehavkus-1_TC DNA transposon.