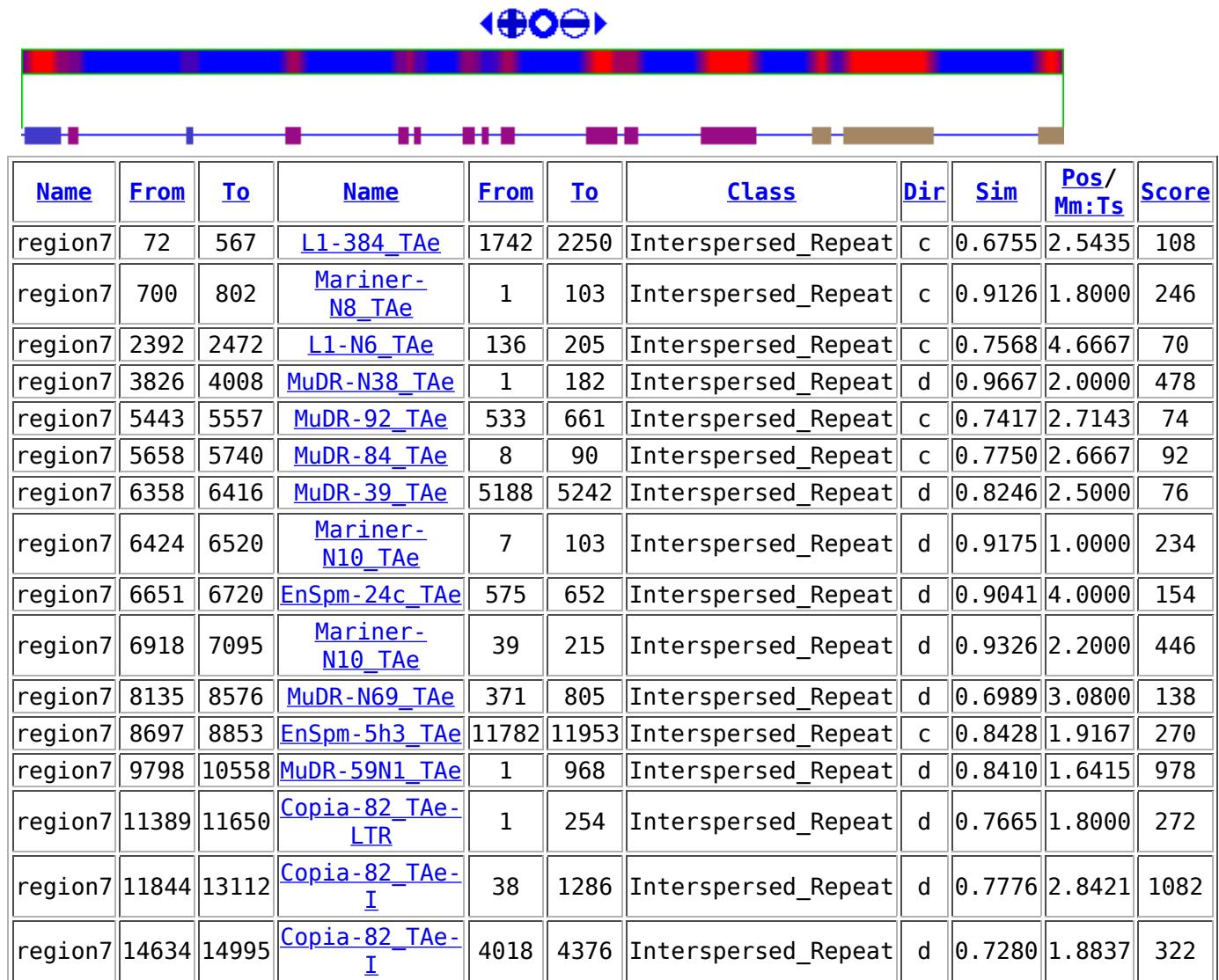


Map of Hits

[SVG viewer](#) is required to view graphical representation of the map as Scalable Vector Graphics (SVG plot).

region7 ([SVG Plot](#); [Alignments](#); [Masked](#))



Masked Sequence

```
>region7
CATGATCTGTGAAGGTCAATTCTGTGACAAGTTGGAGAACCATTAATTGTGCAAATGCCTCTT
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXTTTAGAAAAAGAAGAAACTCGTAAGGACGGTGGTAATGAAGATAGGACATCATTGACCGTC
AGCAGCCTCCATCGTAACTCAGGTAGTCAGAGCACACACCGAGTCTTTTGAAATTCCCTCAATAATA
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXTTTAGAAAAAGAAGAAACTCGTAAGGACGGTGGTAATGAAGATAGGACATCATTGACCGTC
AGAGGAGCTGGTTTGATTGTCTAATTGCTTGGCCCCAGAAGCTCTAGAGAAGGAATCAATTAGGAG
TTAAGCTGGGAATTACATTCGTTGCTGTTGTTAGCACAAAGTCATTCCCGAAGACATGTCG
TGTAAATTCCAGTCCCGATAATGCCCTCCCCAAAACAATGGGAATGATAACCTCAGTTCATCGACCG
TCCTTGTCTCTCCACTTTCTAAGGCGGTGAAGTCGTCATGGCTACAGCCAAAGGAGACGACGTAC
TGAATGACCATGTTCTCCCGAAGTTCACATTATTAGGCATTGGTCGGGTCAAGCAGCACGAAC
```


Local Alignments*

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
region7	72	567	L1-384_TAe	1742	2250	c	0.6755	2.5435	108

1742 ggcatcatcaagcaa-ttggAACGAAT-tatgAGACAA-tgcCTTGGAGAGGAA---ttcggatacccc 1806
500 -ag--aatcctcccttg--gcggcaacatgggagctaataatgtaaacttaaagagcggggtgattaggg 436
-||--||||-|||---|||----||| :||| :||:||:||| :||| :||| :||| :|||
1807 taggcaatc-tc--ttgctgcg-----tggacttgtctgcagacctaaggagaaggtggttgggt 1867
435 atcctcaatttacag-ttatgaaacaatag--tctgctgcgaagatgctccataagtttcaatcatca 369
:||: ||||:||| -|| | ||| ||| :||-||| | -||| ||:||||| ||| ||| |||
1868 gttgttaatctgcagcttcagaatcaaggcTTCTTATT--aagcaccttcataagtttcaataaaagc 1935
368 tggatataccatggggccacttggctggaaagcatactatgcaat-----gtcaacatgttgcattgc 305
||| ||| ||| : |||| | ||||: ||||||| ---|||---||| ||| ||| |:-|||
1936 tgatataccctgggtatcTTGTGGAATTcatactatg---atggagtagtcccacaag-cca-ctg 2000
304 -cctgctgctgcttctttggagagattgtc-tcagactaattctatctaaaaa--acatggcca 239
-|||- |||- :||:|||||:|||-:|||-|||---|||---||| |||: |||-||| |||||
2001 tcct-mtg-tggctcTTTGGAAAGA-tatcttca---aat---tagtgcacaattacaggcaca 2060
238 -a--ctgcactgtgctcta-----cctccgttcaattctggactgatacttgg-----atggt- 188
-||-|| :||| ||| -|||----- :||| |||: :||||| |||||:||||| -----|||---|||
2061 tagcctcggtttggg-taataaggggattcggTTTGTGCTGATGCTGGAAACTGGATGGTT 2129
187 ----ca-gccttatactcaaattggcctcatctgcac-----tcctt-tgccaaggctgatcaaatt 131
-----||-||| | ||||---| ||||-|||---|||---||:|||-|||: ||| |||| |:||:
2130 ctaccatgcTTTGGAGACAAA---gactc--c--c-acggttatTTCTATGCTCTGGATGATAAGATC 2191
130 tctattagccag---ttatgg--agccaggat-gatttatcagatTTTCCATCTACCTCTCTC 72
||||:||-|| | |---||| | -|||:|||||:||| :|||-||| ||||| |||: ||| |||||
2192 tctgt--ggctgattttattgacagtgcaggatagagct-tc---ttttttccagctgcctatctc 2250

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
region7	700	802	Mariner-N8_TAe	1	103	c	0.9126	1.8000	246

<u>Name</u>	<u>From</u>	<u>To</u>	<u>Name</u>	<u>From</u>	<u>To</u>	<u>Dir</u>	<u>Sim</u>	<u>Pos/Mm:Ts</u>	<u>Score</u>
region7	2392	2472	L1-N6_TAe	136	205	c	0.7568	4.6667	70

2472 acgacgctggagacggcgttccgtgccggcgctcgagcacctggccgtgcggagccccctgg 2403
 |||:|| | || |: |||-----| |||-|| | ||:|| | || | ||| ||||| |||| | |||
 136 acggcggtgtggcgggggcccttc---ctctc-tcctgcgccatggggcggtgcggagcccccg 196

2402 cgatgttggtg 2392
 ||-||-|||||
 197 cg-tg-tggtg 205

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
region7	3826	4008	MuDR-N38_TAe	1	182	d	0.9667	2.0000	478

3826 gggtgtgtctaggctcagtcacttagacttaacgaagtctcaactcaaatgataatgtatgagaaga 3895
|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
1 gggtgtgtctaggctcagtcactgagacttaaccaggactctcaactcaagtgataatgtatgagaaga 70

3896 a---aaaaaaactgaaaagaaattttgtacgaatcttaatgcaagatcaatggaatataacatcgactc 3961
|---|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:-----||
71 aaaagaaaaactgaaaggaaattttgtacgaatcttaatgcaagatcaatggaatataaca-----tc 135

3962 gactgagacataacgaaagtctaagtgcactgagacgttagcaaaaactc 4008

136 ||||| gactgagacataaacgaagtctaagtgcactgagacgttagcaaaaactg 182

<u>Name</u>	<u>From</u>	<u>To</u>	<u>Name</u>	<u>From</u>	<u>To</u>	<u>Dir</u>	<u>Sim</u>	<u>Pos/Mm:Ts</u>	<u>Score</u>
region7	5443	5557	MuDR-92_TAe	533	661	c	0.7417	2.7143	74

5557 gcgtcgaagctcgccggatctccgccccttccttgctcgccaccgctc-gccgcacatctccgccccttgc- 5490
||||:|||| |||-|| | :||| ||| |||:|||---|||-|||:||| |||||-||| |||| ||-||||||| :|||-
533 ggcgcgcacgc-ctcccgccttcgcgcacccccc--gc-c-ccgcagctccgcacgcctc-ccgccccgcga 596

5489 ---cggctcgccgc-----cttccctcccgagcagc--c-cc----acttccatcttgctc 5443
---| :|||||||-----|||||||-----||-|-||-||:|||||-|| | |
597 cttccactcgccgcagctccggcttcctcccgagcagcatcgccacatgactccatc-tgactc 661

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
region7	5658	5740	MuDR-84_TAe	8	90	c	0.7750	2.6667	92

5740 gataggcgccggcgccggcctaattttcgccggtcacgcctcacccgtccgataacaactttta- 5672
 ||| |||||:|||||:|||: || |||||: |||: | |||||:|----- |||-
 8 gatctgcggccggcgaccggcccaacggttggccggtcgagccgaaccgtccatgc---ggttag 72

5671 ----aaccgtcagatctg 5658
-----|||||||
73 cgccaaaccgtcagatctg 90

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
region7	6358	6416	MuDR-39_TAe	5188	5242	d	0.8246	2.5000	76

```
6358 ttgaaacatcaagttcacccgat-aaatca-tcat-catacaaggattgttcataaataaaa 6416
||:|||||:||||| |||| | | - | | - | | - | | | | - | | - - - | | :| | | |
5188 ttaaacatcaagatcaccagatcaattcattcatacatacaa--at----atagataaaaa 5242
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
region7	6918	7095	Mariner-N10_TAe	39	215	d	0.9326	2.2000	446

```
6918 taggtcgtcaatttaaccacctaatacacaatggcatatattacaaaaaaaaaatataccaaacataaaacttcagag 6987  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
39 taggtcgtcaatttgaccacctaatacacaatggcatatattacaaaaaaaaaatataccaaatataacttcagat 108
```

7058 ggtatacgcgcatgacttgtaaactgaaacggaggtag 7095
||||| ||||| ||||| ||||| ||||| ||||| |||||
178 ggtatacgcgcaggacttgtaaactgaaacggaggtag 215

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
region7	6424	6520	Mariner-N10_TAe	7	103	d	0.9175	1.0000	234

```
6424 ctctctcagttacaaggcatacgcatacccttaagtcgtaattgtacaacctaatacagaatata 6493  
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
7 ctctctcagttacaggcgctgcgcgtacccttaggtcgtaattgtacaacctaatacagaatata 76
```

```
6494 tcacaaaaatataccaaacataaactt 6520
|:|||||||||||||||:|||||||
77 ttacaaaaatataccaatataaactt 103
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
------	------	----	------	------	----	-----	-----	-----------	-------

region7	6651	6720	EnSpm-24c_TAe	575	652	d	0.9041	4.0000	154
---------	------	------	-------------------------------	-----	-----	---	--------	--------	-----

```
6651 gtgagcctctgttcttatcttctttctaaaaaaattctta-t-----tttagatagatactt 6712
      |||||||:|||||||-|-----| ||| |||||||||
  575 gtgagcctctgttcttatcttctttctgaaaggaaaaattcttacttgtatgttakatagatactt 644

6713 gtctaatt 6720
      ||
  645 atataatt 652
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
region7	8135	8576	MuDR-N69_TAe	371	805	d	0.6989	3.0800	138

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
region7	8697	8853	EnSpm-5h3_TAE	11782	11953	c	0.8428	1_9167	270

8853 tactcccttggtcctaataatataaggcttttagagattctaatacgaa--actacatacagaacaaaatg 8786
| |||||: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
11782 tactccctccgttcctaataatataaggcttttagagattccacttaggtggactacatcggaaacaaaatg 11851

8785 actgaatctac-----ctatatacatccgcacgtactccttattgaaatctctaaaaagact 8729
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
11852 aatgaatctacacttaaatgcatctatatacatccgtatgtggttcatgttgcacaaagact 11921

8728 tatatttaaaaacggaggggagtactactttag 8697
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
11922 tatatttaatggaaacggaggaaactactgtataag 11953

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
region7	9798	10558	MuDR-59N1_TAe	1	968	d	0.8410	1.6415	978

9798 cggaaattactaatttggagggtactccttgc aaagatcactccac tctcaggctgtcaca-gtggcgc 9866
|||||:|||||:|||||||:|||||||:|||||||:|||||||-||:||||||:||:||||||:||:|:|||||||:
1 cggaaatcactaatttggagggtactccttgc aaagaacactcc-actttccca ggttcgcqacaatgac 69

9867 gc-tgcgtgtcgccacttgtcacaacacctgtgagttttt- tttttcgtagatccgttattcaaaa 9932
 :|-||||-:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 70 acatgca-gcgcgccacttgtcgcaacctggag--tttccctttcgtagatccgttattcaaaa 136

9933 catttatatttaaccatgcgtccaaatctgaaccgtttcaccgttgaattcctcggtcaagatc 10002
 |:||||| |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 137 cgtttatctcttaaccgtgcgtccaaatctgaaccgtttcaccattggattcctcggtcgagatc 206

10003 tc当地acttagatcccattgttgaagggtttgacgaactttttt-acgaaaaaccgga----- 10062
 |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 207 tc当地acttagatcccattgttgaagggtttgacgaacttttttacgaaaaaccgacgaaaaaa 276

10063 -----cgaaaaactgaacttggaaaggcatggttttccattccgaaagaggcacggccgtgccttc 10127
 -----|:|||||:|||||:|||||:|||||:|||||:|||||:
 277 cgggcaaaaaaccgaaccgggagcacggttt-tttcccttccgaaagaggcacggccgtgccttc 345

10128 gc-----ggaagg-aaaaaaaactggaa-- 10148
 ||-----|:|||||:|||||:|||||:
 346 gcaaattcacaaccgtgcctctcggttgaagcaaaaccgtgactctcggttgaaggaaaaaaac 415

10149 --ttttttttctgattccgagaggcac----ga----g---aggcacggccgtgccttcgcagaa 10202
 -- |:|||||:|-|:|||||:|||||:-----|:|||||:-----|:|||||:
 416 gcgtttttttc-gtttccgagaggcacggccgtgactctcggttgaaggacacaaccgtgccttcgcgaa 484

10203 gcaaattcgt-acttctcggttgaagcaaaaaataatagaaaacacg-ctttttttcattacgagag 10270
 |:|||||:|-||:|||||:|||||:|||||:|||||:|||||:
 485 gcaaaccgtgac-tctcggttgaag-aaaaaa-aaacagaaaacgcgtatTTTCCCTTCCGAGAG 550

10271 gcacgtccgtgcctttcgaaaggcaccaccgtgcgtctcggttgaagcaaaaccgtgccttcgcggaa 10340
 |:|||||:|||||:|||||:|||||:|||||:|||||:
 551 gcacggccgtgactttcggttgaagcacaaccgtgccttcgcggaaaggcaaaaccgtgacttcacgaaag 620

10341 gaaaaaaaaatgttagaaaacacgtttttctttcggtttttagagag--acgg--g-g----- 10391
 |:|||||:---:|||||:|||||:|:|||||:|:|||||:
 621 aaaaaaaaa---cagaaaacgcgttttgcgttttcccttccgagaggcacggccgtgacttcgcgaaagc 687

10392 ----ccgtgcctcttgccc-----aaaaaaaacagaaaac-aattttt 10429
 ----|:|||||:|:|||||:-----|:|||||:|:|||||:
 688 acaaccgtgcctctcggttgaagcaaaaccgtgacttcgcgtttaaggaaaaacagaaaacgcgtttt 757

10430 ttgcgtttcgaaa---a---cgtg---ttt---tttagcaca-----a----- 10462
 |:|||||:|||||:---|:|||||:|:---|:|||||:-----|:-----|:
 758 ttgcgtttcgaaaggcacggccgtgacttcgcgtttaaggcaaaaccgtgccttcgcggaaaggaaaaacc 827

10463 ----tt-----tttttcg-----aatttt---ttgtttcg- 10487
 ----|:|-----|:|||||:|:|||||:|:|||||:-----|:|:|:
 828 tgactttcggtttaaggaaaaaaagaaaacgcgtttttcggtttaaggcaaaaccgtgccttcgcggaaagg 897

10488 tccaaaatctaagaaaaaggccgttggaaaaccaaaaagtcaaaaaaccggtaaaaaaccgtttaaaaag 10557
 |:|||||:|||||:|||||:|||||:|||||:|||||:
 898 tcgaaaagctaagaaagaccggggaaaaccaaaacgcgtcgaaaaaccggaaaaaccgtttaaaaag 967

10558 c 10558
 |
 968 c 968

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
region7	11389	11650	Copia-82_TAe-LTR	1	254	d	0.7665	1.8000	272

```
11389 tgtaggttgcataccaa-tggcccaacggctcattgggacttgacc---cgccctgatc 11453  
|:|||||:|||||||:|-|:||||:|||||:|||:|||:||-||:||-||:|-|||:|||:  
1 tgtaggttgcataccgagttggctcaacggccatggccct-gatctattcgccctgatc 69  
  
11454 gggggcgttcagccaaaggctggggccctgtcgccgactgtctataaaggaggatgggacc 11523  
|:|||||:|||:|| :| ||:|||||||:-| | :| ||| |||-|||:|||:  
70 qqqqccqcccaaccqttctatqttttqqqccctqt-qacctqcqatataqa-qaqqtqqqqcc- 136
```

11524 gggcacggagttacgaggttca--tcaccgcactg-ttcccactcctaaccctatccatccagagg 11590
| | | | | : | | | | | | | - - | : | | | | - - | : | | | | : | | | | : | | | - -
137 gggcacacggtagcgaggttaccgcgcgcca--gactccccaccgatatccccttcgatctag--- 200

11591 aggcaact-gaagcg---atgggaagctccaccgctgccactcatgcacttcaccgtcgacctct 11650
- | | | | - | | | : | - - | : | | | | - - | | | : | - | | | : | | | |
201 -ggcaatcgacgtgctcacggaaag---caccactgcccac----ctctccatc-tcgatctct 254

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
region7	11844	13112	Copia-82_TAe-I	38	1286	d	0.7776	2.8421	1082

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
region7	14634	14995	Copia-82_TAe-I	4018	4376	d	0.7280	1.8837	322

14634 agaa-gtgcaggatcacctgagacac--agatggctt-caaggaatgagaaaaatcagatacttctgattact 14699
| ||||-|||||| | |||||:| -|-||| |||||-||| -| :||| |||:||| ||:|||:| |||
4018 agaatgtgccagaaactgaggcccttagaaggctacaag-accaagaaagttagctattctactgact 4086

14700 ataaagtctatattatgtaaat---tcaaattggagggttgcattttaaagcgctcaatcgagt 14766
|||||:||| :| |||||---||| |||||:| |||||-----||| | |--
4087 ttaaagttataacacagaaaatggtcataatggaaaaagatcccacctcatatgaag----aagcca-- 4149

14767 ttggagaagtgc-ttcttatctaaatg-ataagagactatgagatgaaattggtaattct 14833
--|||||||: -||-|||-||| ||:|||-|||:-|||:| ||: :|||:|||:|||||||:|||:|||:
4150 --tgagaaggcccttattc--atcgaaatggatga-aggcaatgaaagacgagatgaaatcgatgatgtcc 4214

14834 gacgatgttggactcacgagtaattcc-aatggagccaaacagtaggtgtaaa-gagtctacaag 14901
:| |||||:|||:|||-||| ||| -||| |||:|||:|||:|||:|||:|||:|||:|||:
4215 aaagatgttggactta-gagggaaattctaaaggagccaaacagtaggtgtaaaatggctacaaa 4283

14902 gacaa-tgtgactccaaaggaaatatgtaaagggtgtaaaacacgactaaaatcgaaagggtttgcgcatt 14970
: :||-||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
4284 attaagtatgactctaaaggaaatagaaaagtataaagcagcactcgatggccaaagg-atttacaca- 4351

14971 ttacaccgaatagattacaatgag 14995
| | |:|||||:|||||:
4352 aaqagaqaqqgatqattacaatgag 4376

Masked Regions

```
>region7 FRAGMENT 567 -> 72
GGCATTATTACTTAAGTTGACAATATAGGAGACATTGTTTGGGGAGGGAAAGATTGAAAGAAAAGA
ATCCTCCCTTGGCGGAACATGGAGCTAATATGTAACCTTAAAGAGCGGGGTGGATTAGGGATCCTCAA
TTTACAGTTATGAAACAATAGTCTGCTGCGAGATGCTCCATAAGTCTTCATCATCATGATATAACCA
GGGGCCACTTGGTCTGGGAAGCATACTATGCCAATGTCAACATGTTGATCAGCCTGCTGCTGCTTCTT
TTGGTGGAGAGATTGTCTCAGACTAATTCTATCTAAAAAACATGGCCAAGTGCACTGTGCTCACCTCC
GTTCAATTCTGGACTGATACTTGGAATGGTCAGCCTTACTCAAATTGGCCTCATCTGCACTCCTTGC
CCAAGGCTGATCAAATTCTATTAGCCAGTTATGGAGCCAGGATGATTTCAGATTTTCCATCTACC
TCTCTC
```

>region7 FRAGMENT 802 -> 700
CTCCCTCGTTCGGAATTACTTGTCTGAAAGATGGATGTATGTAGACATTTTAGTTAGATACATCC
ATTTTGCGACAAGTAATTGAAACGGAGGGAG
>region7 FRAGMENT 2472 -> 2392
ACGACGCTGGAGACGGCGTCTGTGCCGGCGCTCGAGCACCTGGGGCGTGCAGGAGCCCCCTCGG
CGATGTTGGTG
>region7 FRAGMENT 3826 -> 4008
GGGTGTGCTAGGTCTCAGTCGACTTAGACTTAACGAAGTCTCACTCAAATGATATAGTATATGAGAAGA
AAAAAAAATGAAAAGAAATTGGTACGAATCTAATGCAAGATCAATGGAATATAACATGACTCGACT
GAGACATAACGAAGTCTAAGTCGACTGAGACGTAGCAAACACTG
>region7 FRAGMENT 5557 -> 5443
GCGTCGAAGCTCGCCGGATCTCCGCCCTTCTTGCTGCCACCGCTGCCGATCTCGCCCTTGCG
GCTCGCCGCCCTCCCTCCGAGCAGCCCCACTTCCATTTGCC
>region7 FRAGMENT 5740 -> 5658
GATAGGCGCCGGCGCCGGCTAACCTTCCGGGTACGCCAACCGTCCGATACAAACTTTAA
ACCGTCAGATCTG
>region7 FRAGMENT 6358 -> 6416
TTGAAACATCAAGTTACCCGATAAAATCATCATACATAACAAGCATTGTTCATAAATAAAA
>region7 FRAGMENT 6424 -> 6520
CTCTCTCAGTTACAAGGCATACGCATAACCCCTAACGTCATTTGATCAACCTAACAGTCATATA
TCACAAAAAAATACCAACATAAACTT
>region7 FRAGMENT 6651 -> 6720
GTGAGCCTTGTCTTATCTTCTTCTGAAATAAAAGAATTCTTATTTAGATAGATACATTGCTAATT
>region7 FRAGMENT 6918 -> 7095
TAGGTCGTAATTAAACCAACCTAACAGTCATATATTACAAAAAATACCAACATAAAACTTCAGAG
TTTCTACTTCAAAAGATATTTTTGTGTGTTATAGTTATATTAGGGTATAAAATTGGCACACCTA
GGTATACGCGCATGACTTGTAAACTGAAACGGAGGTAG
>region7 FRAGMENT 8135 -> 8576
CGTGAACACTTTTGAAGAACGTAACATTAGAAAACACGTGGCACATCAAGAAAACATAATTATTC
TATAGTAATATGGAACGCCCTCTAATTATGTGAAGATTAAAAAGCAACACTTTTAATTACAGG
AATATTGACACATATATAACACTTCTCAAATTCTGAAGGTTATTGAATGTAGAACACTTCCTA
CTATAGCAGGAACATTTCGGATATGAAAGCTCTTCAACCTACCTGAATGTTTCCAAATAAGC
ATTTTTAACATTTCGATGACACTATTTAATTGACAATTCTAAATGTACAATATTGAAATATTGA
AATAGGTAATATGTTTCAAATACCCTGAACATTATCCTAAATAAGTAATAAATTAGAATTTC
GTGCCATTATTCTTCTTCAA
>region7 FRAGMENT 8853 -> 8697
TACTCCCTGGTCTAAATATAAGTCTTTAGAGATTCTAATAGAAAACATACAGAACAAAATGAC
TGAATCTACCTATATACATCCGACGTACTCCTATTGAAATCTCTAAAGACTTATTTAAAAACGG
AGGGAGTACTCTTAG
>region7 FRAGMENT 9798 -> 10558
CGAAATTACTAATTGAGGAGTACTCCTTGTCAAAGATCACTCCCACCTCTCAGGCTGTACAGTGGCG
CTGCATGTGCGCCACTGTACAACCTGTGAGCTTTTTCTGAGATCTCGTTATTCAAACATTT
TATATTAAACCATGCGTCCAAATCTGAACCGTTTACCGTTGAATTCTCGCGTCAAGATCTTCAA
AACTAGATCCCAGTTGAAGGTTTGACGAACCTTTTACGAAAAAACCGGACGAAAAAAACTGAAC
GGAAGCATGGTTCTTCCCCATTCCGAAAGAGGCCAGGGCGTGCCTCTCGCGAAGGAAAAAAACTGGA
ATTTTTCTGATTCCGAGAGGCCAGGAGGCCAGGGCGTGCCTCTCGAGAACAAATCGTACTTC
TCGTGGAAGCAAAAATAAGAAAACACGCTTTTTTACGGTACGAGAGGCCAGTCCGTGCCTTT
GCGAAAGCACCACCGTGCCTCGCGAAGCAGAACCGTGCCTCTCGCGAAGGAAAAAAACTGTTAGAAA
ACACGTTTTCTTCTGTTTGTGAGAGACGGGCCGTGCCTCTGGGAAAAAAACAGAAAACAATT
TTTCGTTTCTGAAACGTGTTTTAGCAGAAATTCTGCAATTGTTCTGCAAAATCT
AAAAAAGGCCGGTGGAAACCAAAAGTCAAAAACCCCGTAAAAAACCGTTAAAAAGC
>region7 FRAGMENT 11389 -> 11650
TGTTAGGTTGATCTCCACCAATGGGCCAACGGCTATTGGCACTTGACCCACGCCGTATCGGGGG
CGTCCAGCCAAGCAAGGCTGGTGGGCCCTGCGCAGTGTCTAAAGAGGAGGTGGGGACAGGGG
ACGGAGTACGAGGTTCATACCGCCACTGTTCCCACCTCTAACCTATCGATCCAGAGGGAGGCACTG
AAGCGATGGGAAGCTCCACCGTGCACACTGCACTTACCGTCGACCTCT
>region7 FRAGMENT 11844 -> 13112
AAAAGAGAAAAGAAAAGCAACACAAATACGATTTGATCTCGGATCGAAGCAGATAGAGAGAAAAGA
CCTCGTGGAAAAGTTGCGCCGCGCAACGGCGCGCCGTTCTCTGATCCGGACGGGACCG
CGAGCCGTTGGAAGAAGAAACTCACCCACAGGGGAAAGGGCACCACAGAGCCATTGACGGCG
CGCTTACCCCTCGAGGTGCTCGCGCACGCCGAAAGGGGTAGCGGGGGCGCCGATCTGGAAACCG
GTCGCTCGCGAAGGGGAGCAGAGGAGGCTCTGCTCGCGCTGCTCGCGTCCCTCTCGCGTGGGGTGG
GGTGGAAAGAAGAGAGGGAAACGGCTCGCGCGCAGTGGCCCTCGCGCCGAGCAGGGGGCG
GAGCGGCCCTACCGAGGCCGCTGCCCTTTACCTGACAGAGAGGGAGCCAGGGACAGAAGAAGAAA
GAAGAAGGGAAAGGGGAAAGAAAGAGAACGGCAGGCTCGCGCGTGGAGCAGGCCGCGCCGAG
GACCGGACAGGCACGGCGCGCCGAGCACGGCGCGTGGCCGAGCAGGGGACATCGTGGCGAGA
GACGAGAGGATGAGAGTTGACCCGAGCTGGTGGGTAGTTGATCCAGCAAAATATGGTGA
GTCGTCGATCGCGTTAACGGCTGGATCAAACCCCTAGCTGCCAACGGCTTTGGGCCGAAAGTGC
AGGGGGCAGCAGCCGCCGGCGCTGCGCTGGGCCGAGGACACAGCCGCGGGGCCAGGCCGGGT
CGAGGCATTTCGCGAGGCACGGCGCGCAGGGCGAGGGCGACTTTTCCGCTGCGGGCCAGCGC

GCTGGGCCAGCTCGTTTCTATTTGTTAGTTTGTTCAGGTTGGGCAGATTCAGATAGA
TTTCTATGCAATTTCAAACGAAAATTTGTTAGAAATAGAAAAGTTAACAGAAAAAGTTCTG
AAAATGAAAATAGAAAATTTCAGAAAAGAAATGTTCATGAATTATAAGAAAATAATAAGTTCAT
GAATTTTTATTGGTCAAAGAAAAGTTCTGTAAGAATAAGAAGTCCATGAATTATTATGTTT
CCGCTGCAAAAATAAAAGAAAAGTGCTTTAAAGAAAATAAAATTCTTATGAATAGAATATT
GTAAAGTT
>region7 FRAGMENT 14634 -> 14995
AGAAGTGCCAGTACCTGAGACACAGATGGTCTCAAGGAATGAGAAAATCAGATACTTCTGATTACTATAA
AGTCTATATTAGTGAATTCAAATGGAGGTTGATCCCACCTCATTTAACGCGCTAACCGAGTTGAGA
AGTGTCTTCTTATCTAAATGATAAGAGACTATATGAGATGAAATGAAATTGGTGAATTCTGACGATGTT
GGGACTCACGAGTAATTCCAATGGAGCCAAACAGTAGGCTGTAAAGAGTCTACAAGGACAATGTGACT
CCAAAGGAAATATGTAAGGTGTAAACACGACTAAAATCGAAAGGTTTGCATTTACACCGAATA
GATTACAATGAG

Annotation of Repbase Sequences

ID Copia-82_TAe-I repbase; DNA; PLN; 5877 BP.
XX
AC .
XX
DT 24-APR-2023 (Rel. 28.08, Created)
DT 24-APR-2023 (Rel. 28.08, Last updated, Version 1)
XX
DE LTR retrotransposon from common wheat: internal portion
DE consensus.
XX
KW Copia; LTR Retrotransposon; Transposable Element; Copia-82_TAe-I;
KW autonomous.
XX
OS Triticum aestivum
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
OC BOP clade; Pooideae; Triticodae; Triticeae; Triticinae; Triticum.
XX
RN [1]
RP 1-5877
RA Bao W.;
RT "LTR retrotransposons from wheat.";
RL Repbase Reports 23(8), 5447-5447 (2023).
XX
DR [1] (Consensus)
XX
CC ~95% identical to consensus.
XX
SQ Sequence 5877 BP; 1859 A; 1141 C; 1440 G; 1432 T; 5 other;

//
ID Copia-82_TAe-LTR repbase; DNA; PLN; 368 BP.
XX
AC .
XX
DT 24-APR-2023 (Rel. 28.08, Created)
DT 24-APR-2023 (Rel. 28.08, Last updated, Version 1)
XX
DE LTR retrotransposon from common wheat: long terminal repeat
DE consensus.
XX
KW Copia; LTR Retrotransposon; Transposable Element;
KW Copia-82_TAe-LTR; autonomous.
XX
OS Triticum aestivum
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
OC BOP clade; Pooideae; Triticodae; Triticeae; Triticinae; Triticum.
XX
RN [1]
RP 1-368
RA Bao W.;
RT "LTR retrotransposons from wheat.";

RL Repbase Reports 23(8), 5534-5534 (2023).
XX
DR [1] (Consensus)
XX
CC ~95% identical to consensus.
XX
SQ Sequence 368 BP; 73 A; 125 C; 97 G; 73 T; 0 other;

//
ID EnSpm-24c_TAe repbase; DNA; PLN; 12587 BP.
XX
AC .
XX
DT 26-APR-2023 (Rel. 29.04, Created)
DT 26-APR-2023 (Rel. 29.04, Last updated, Version 1)
XX
DE DNA transposon from *Triticum aestivum*, consensus.
XX
KW EnSpm/CACTA; DNA transposon; Transposable Element; EnSpm-24c_TAe.
XX
OS *Triticum aestivum*
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
OC BOP clade; Pooideae; Triticodae; Triticeae; Triticinae; *Triticum*.
XX
RN [1]
RP 1-12587
RA Bao W.;
RT "DNA transposons from wheat.";
RL Repbase Reports 24(4), 2131-2131 (2024).
XX
DR [1] (Consensus)
XX
CC ~92% identical to consensus.
XX
SQ Sequence 12587 BP; 3450 A; 2860 C; 3132 G; 3108 T; 37 other;

//
ID EnSpm-5h3_TAe repbase; DNA; PLN; 24019 BP.
XX
AC .
XX
DT 24-FEB-2023 (Rel. 29.04, Created)
DT 26-JUL-2023 (Rel. 29.04, Last updated, Version 1)
XX
DE DNA transposon from *Triticum aestivum*, consensus.
XX
KW EnSpm/CACTA; DNA transposon; Transposable Element; Nonautonomous;
KW EnSpm-5h3_TAe.
XX
OS *Triticum aestivum*
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
OC BOP clade; Pooideae; Triticodae; Triticeae; Triticinae; *Triticum*.
XX
RN [1]
RP 1-24019
RA Bao W.;
RT "DNA transposons from wheat.";
RL Repbase Reports 24(4), 2116-2116 (2024).
XX
DR [1] (Consensus)
XX
CC >97% identical to consensus.
XX
SQ Sequence 24019 BP; 6142 A; 5676 C; 6022 G; 6150 T; 29 other;

//
ID L1-384_TAe repbase; DNA; PLN; 3050 BP.
XX

AC .
XX
DT 18-MAY-2023 (Rel. 28.11, Created)
DT 29-JUN-2023 (Rel. 28.11, Last updated, Version 1)
XX
DE Non-LTR retrotransposon from common wheat: consensus.
XX
KW L1; Non-LTR Retrotransposon; Transposable Element; L1-384_TAe;
KW autonomous.
XX
OS *Triticum aestivum*
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
OC BOP clade; Pooideae; Triticodae; Triticeae; Triticinae; *Triticum*.
XX
RN [1]
RP 1-3050
RA Bao W.;
RT "Non-LTR retrotransposons from wheat.";
RL Repbase Reports 23(11), 7670-7670 (2023).
XX
DR [1] (Consensus)
XX
CC ~92% identical to consensus.
XX
SQ Sequence 3050 BP; 713 A; 647 C; 707 G; 964 T; 19 other;

//
ID L1-N6_TAe repbase; DNA; PLN; 1277 BP.
XX
AC .
XX
DT 18-MAY-2023 (Rel. 28.11, Created)
DT 21-JUL-2023 (Rel. 28.11, Last updated, Version 1)
XX
DE Non-LTR retrotransposon from common wheat: consensus.
XX
KW L1; Non-LTR Retrotransposon; Transposable Element; Nonautonomous;
KW L1-N6_TAe.
XX
OS *Triticum aestivum*
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
OC BOP clade; Pooideae; Triticodae; Triticeae; Triticinae; *Triticum*.
XX
RN [1]
RP 1-1277
RA Bao W.;
RT "Non-LTR retrotransposons from wheat.";
RL Repbase Reports 23(11), 7505-7505 (2023).
XX
DR [1] (Consensus)
XX
CC ~94% identical to consensus.
XX
SQ Sequence 1277 BP; 191 A; 362 C; 458 G; 266 T; 0 other;

//
ID Mariner-N10_TAe repbase; DNA; PLN; 215 BP.
XX
AC .
XX
DT 24-FEB-2023 (Rel. 29.04, Created)
DT 24-FEB-2023 (Rel. 29.04, Last updated, Version 1)
XX
DE DNA transposon from *Triticum aestivum*; consensus.
XX
KW Mariner/Tc1; DNA transposon; Transposable Element; Nonautonomous;
KW Mariner-N10_TAe.
XX

OS Triticum aestivum
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
OC BOP clade; Pooideae; Triticodae; Triticeae; Triticinae; Triticum.
XX
RN [1]
RP 1-215
RA Bao W.;
RT "DNA transposons from wheat."
RL Repbase Reports 24(4), 2108-2108 (2024).
XX
DR [1] (Consensus)
XX
CC >94% identical to consensus,.
XX
SQ Sequence 215 BP; 70 A; 40 C; 39 G; 66 T; 0 other;

//
ID Mariner-N8_TAe repbase; DNA; PLN; 103 BP.
XX
AC .
XX
DT 24-FEB-2023 (Rel. 29.04, Created)
DT 24-FEB-2023 (Rel. 29.04, Last updated, Version 1)
XX
DE DNA transposon from Triticum aestivum; consensus.
XX
KW Mariner/Tc1; DNA transposon; Transposable Element; Nonautonomous;
KW Mariner-N8_TAe.
XX
OS Triticum aestivum
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
OC BOP clade; Pooideae; Triticodae; Triticeae; Triticinae; Triticum.
XX
RN [1]
RP 1-103
RA Bao W.;
RT "DNA transposons from wheat."
RL Repbase Reports 24(4), 2140-2140 (2024).
XX
DR [1] (Consensus)
XX
CC >97% identical to consensus,.
XX
SQ Sequence 103 BP; 28 A; 22 C; 23 G; 30 T; 0 other;

//
ID MuDR-39_TAe repbase; DNA; PLN; 7806 BP.
XX
AC .
XX
DT 13-APR-2023 (Rel. 29.01, Created)
DT 13-APR-2023 (Rel. 29.01, Last updated, Version 1)
XX
DE DNA transposon from Triticum aestivum; consensus.
XX
KW MuDR; DNA transposon; Transposable Element; MuDR-39_TAe;
KW autonomous.
XX
OS Triticum aestivum
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
OC BOP clade; Pooideae; Triticodae; Triticeae; Triticinae; Triticum.
XX
RN [1]
RP 1-7806
RA Bao W.;
RT "DNA transposons from wheat."
RL Repbase Reports 24(1), 239-239 (2024).

XX
DR [1] (Consensus)
XX
CC ~97% identical to consensus.
XX
FH Key Location/Qualifiers
FT CDS join(7436..7362,7116..6967,6696..6241,6111..6096,
FT 5784..5429)
FT /product="MuDR-39_TAe_2p"
FT /translation="MPSWNDGDESSDDSMGGNLMDMEYFDTPDTIPEPLWC
FT GAPMEEVAKCTLHDMKPRKCVAFEGANTGRRFYGCPVQGGVNCGVVQWVDP
FT AWPDVLKNCNLIKLWEMFHEQNGLRIQDKHAYEDEVAKLKDYDHLCTEYHK
FT MVDDVSKMFWDQDGVGKIDYQKAMDAEKFEKQKEELELEMKMEKLRLAKEQ
FT RCILQAQADIIHNTRKAMKEIKVDRDLLAQEKTELEKALQDDVNPIPTLL
FT HPPAAKETLESQGEMDPGEVIDGEEEVPRQARRRDARRRARRQLAEMILAA
FT RNRKDIEQFLEAFPLAPTLVMMISSTGQGGGQISIPFRSLRGGLGFCTHD
FT AAVMFLCS"
FT CDS join(319..641,1010..2586,2665..2876,2964..3914,
FT 4000..4289,4741..5062)
FT /product="MuDR-39_TAe_1p"
FT /translation="MASAAAKPGDGGHSTGGGRGDGGGEFSEVDNWLGSG
SFATQPAAPPPPQRTPQAAALMQAPTPQATPPSPDCQFSLEYRAARSLAS
AVQADPANSQHWASAFGGVELDEIWEVRLFQGRDNMERRFSVSDITFLN
LIALTETEGYGSDDYMYWVKEQGIGQEGFLLLSDSQDAVEEMIDHSDFTVLN
IIVSKANEDRDVECNAHNCEEQIPIGSPVGGPGFVLSLSQDGVVHPLEV
NLNTQQSCNLNISEAHGDDDGQAAGEEDDDIDKSSDFEIDRGDYRGIKM
SYKAWKRGEENIGNEEERDAVEDRPQFEGDSDVSEFWQEEKEADSGEEIVV
EKCRPEKLKPVRRAANPGPTSRAHSQPEIPKFQDFVPEADEYCFPGDVGI
SDSDGETPRLPSGRKRRKKKERWKYDPKVPDAHEQLCKLCFTNVYEFR
KALRNFHVRTLRNFQYHRNEPSRVIVWCPERKNGEFFMTASKVAHEDTFT
IKKCHMDHSCGACGESTKVTAEWVAEAVEDTVRSNVKADVETVLKHTKKF
GVHVPRSLAYRARLMAVDVVQGDHRKQYLRLRDYLQCVLDTNPGSRCIVTT
FEDPLNPAPTPRFKYMFCQLQASKDGFAGCRFIGLDGCFIKLSTGQQIL
AATGRDGNNNVFPIAFGVVDKEDGPSWTFLNQLRVCIGTSNQFGNYTIMS
DRQKGLLKAINEVFPQSPQRYCLRHIYANFQSAGFRAEELKKWVDKASYSF
TEHGHEGMAGLKAACEPAYMWLNGIPKECWARYAMDHVCKTDLVVNNLSE
VFNKMIILDVRSKPIKTMFEGLRTKLMVKYQGIREKTESCRWEITPHYMEKL
EESKKWAKYCEANMAGPNIWQVTSGENTYCVKLDEGSCSRWRDMTGSPCH
HAISAMQKIKVHPEDYVHPFFKKPMYKAAYQHIIYPVPGPEFWPNTNTPDI
EPPVFREKKGKKQTARRKGEFEV PAPKDTSRMGTITCSNCGLQGHRWTMCG
DRLKAKFMTRKNHQENRASYPATSAPTRPPPAPATSSGPAPASGPAPASG
PVRGRKPATASTRATTSASTRATTSTAVSTGGSRKRNPKXPASAPANTRS
SASSPAKNTRSLWXATCRPTPKVASCRPTPKGAKGHFGWLLVDQPQKWL
VDQPPKWPNLATLGGXLSTNPKVATFGHFGLLVDQPQKWLVDQPQRPNL
ATLGGYLSTNPKVAI"
XX
SQ Sequence 7806 BP; 2259 A; 1750 C; 1791 G; 2003 T; 3 other;

//
ID MuDR-59N1_TAe repbase; DNA; PLN; 1112 BP.
XX
AC .
XX
DT 18-MAY-2023 (Rel. 29.01, Created)
DT 18-MAY-2023 (Rel. 29.01, Last updated, Version 1)
XX
DE Nonautonomous DNA transposon from *Triticum aestivum*; consensus.
XX
KW MuDR; DNA transposon; Transposable Element; Nonautonomous;
KW MuDR-59N1_TAe.
XX
OS *Triticum aestivum*
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
OC BOP clade; Pooideae; Triticodae; Triticeae; Triticinae; *Triticum*.
XX
RN [1]
RP 1-1112
RA Bao W.;
RT "DNA transposons from wheat.";

RL Repbase Reports 24(1), 165-165 (2024).
XX
DR [1] (Consensus)
XX
CC ~94% identical to consensus. 9-bp TSDs. 14-bp subterminal TIRs.
CC Termini are similar to those of MuDR-59_TAe (consisting of 3
CC segments: MuDR-59P1_TAe, MuDR-59P2_TAe and MuDR-59P3_TAe).
XX
SQ Sequence 1112 BP; 346 A; 285 C; 251 G; 230 T; 0 other;

//
ID MuDR-84_TAe repbase; DNA; PLN; 9933 BP.
XX
AC .
XX
DT 27-JUN-2023 (Rel. 29.01, Created)
DT 27-JUN-2023 (Rel. 29.01, Last updated, Version 1)
XX
DE DNA transposon from *Triticum aestivum*; consensus.
XX
KW MuDR; DNA transposon; Transposable Element; MuDR-84_TAe;
KW autonomous.
XX
OS *Triticum aestivum*
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
OC BOP clade; Pooideae; Triticodae; Triticeae; Triticinae; *Triticum*.
XX
RN [1]
RP 1-9933
RA Bao W.;
RT "DNA transposons from wheat.";
RL Repbase Reports 24(1), 193-193 (2024).
XX
DR [1] (Consensus)
XX
CC ~98% identical to consensus. 9-bp TSDs.
XX
FH Key Location/Qualifiers
FT CDS join(357..509,880..2597,2714..3620)
FT /product="MuDR-84_TAe_1p"
FT /translation="MDLGSSAAVHGRSPLRRGDPGSSGPVLQRYYNPGVV
FT FQDAARHGRDEIDLNAVEPSIFLDDDMQNVAHEEEYGIDLNDTPQNDSD
FT DSLQLNTDGVPNHGNARVASDNANGNAATLVDEPDEDISSLSPVVFVGMV
FT FDNVEEAQRVYNEYASKMFGFTRIVTSKHSRKSSSDQKRILYRVFECIHS
FT RKNPSKNVGGSIDGAATNECEDVDMSYASNKKSPSKQAGIYMDVSDKRKR
FT NRLERYDCKARMGVNLKGSWVTVFEADHTHQLMLQRGRRRFCRSRKIP
FT DADMQYITSLYRNISTANMMGLGDARCCDPRSLPYVKTDVTNARAKLRR
FT GLSERDLELTIEYFERRQVENPNFFFSSKLQEDGAVRALFWVDRTRALYPK
FT YKDCVFFDTTCTNRYNLPFAPIVGINNHTHTVCLGCALLPDETETFKWV
FT FQQWMLAMNNEHPLNIMTDQDQAMATAISMVFVDSTHRCCWKHVFRVARTK
FT LGRMLGKDEPFAEAFYGCINGSDTVEEFERWKQMVELFGVADKKHLKNMW
FT NSRETWAPVYFRNKFFPFTGTTGRSEGLNSYFKTLNHHGDSVWTFVQQFEL
FT CQEMLMDREDNAGFINEATRPLWGNYNIEKQAADFYTREVFSFKQKLLAK
FT STGYGLQYQLQGNVVWFRLVANDGINPKVYTVRAPEDHTYMCSCNMFEMC
FT GLICPHIIRVMVHLNVQAIIPANYMLPRWSKRATDLAPEPGDGHGRAMHFGVP
FT TTNTLKFNSLCRKFGKLASDACFNDEAYSFVSGLIDQGSVVAAIKARATD
FT GVAGGEEAQGRAANEQVSGGGPSTGQQDPPPVGRLNPPKSAKKGRPKEKEKR
FT RKPLIELREDEMKKKAKKDAAKTKKAPKPMEEKKTPCKYCEDEDHNVKNCQL
FT LAAFLAASASA KAPGVGPILTL"
XX
SQ Sequence 9933 BP; 2928 A; 2126 C; 2293 G; 2585 T; 1 other;

//
ID MuDR-92_TAe repbase; DNA; PLN; 4774 BP.
XX
AC .
XX
DT 14-JUL-2023 (Rel. 29.01, Created)
DT 14-JUL-2023 (Rel. 29.01, Last updated, Version 1)

XX
DE DNA transposon from *Triticum aestivum*; consensus.
XX
KW MuDR; DNA transposon; Transposable Element; MuDR-92_TAe;
KW autonomous.
XX
OS *Triticum aestivum*
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
OC BOP clade; Pooideae; Triticodae; Triticeae; Triticinae; *Triticum*.
XX
RN [1]
RP 1-4774
RA Bao W.;
RT "DNA transposons from wheat.";
RL Repbase Reports 24(1), 71-71 (2024).
XX
DR [1] (Consensus)
XX
CC ~98% identical to consensus. 9-bp TSDs.
XX
SQ Sequence 4774 BP; 1385 A; 974 C; 1131 G; 1284 T; 0 other;

//
ID MuDR-N38_TAe repbase; DNA; PLN; 182 BP.
XX
AC .
XX
DT 27-FEB-2023 (Rel. 29.01, Created)
DT 27-FEB-2023 (Rel. 29.01, Last updated, Version 1)
XX
DE Nonautonomous DNA transposon from *Triticum aestivum*; consensus.
XX
KW MuDR; DNA transposon; Transposable Element; Nonautonomous;
KW MuDR-N38_TAe.
XX
OS *Triticum aestivum*
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
OC BOP clade; Pooideae; Triticodae; Triticeae; Triticinae; *Triticum*.
XX
RN [1]
RP 1-182
RA Bao W.;
RT "DNA transposons from wheat.";
RL Repbase Reports 24(1), 112-112 (2024).
XX
DR [1] (Consensus)
XX
CC >97% identical to consensus. 9-bp TSDs.
XX
SQ Sequence 182 BP; 71 A; 28 C; 40 G; 43 T; 0 other;

//
ID MuDR-N69_TAe repbase; DNA; PLN; 1326 BP.
XX
AC .
XX
DT 02-MAY-2023 (Rel. 29.01, Created)
DT 25-JUL-2023 (Rel. 29.01, Last updated, Version 1)
XX
DE Nonautonomous DNA transposon from *Triticum aestivum*; consensus.
XX
KW MuDR; DNA transposon; Transposable Element; Nonautonomous;
KW MuDR-N69_TAe.
XX
OS *Triticum aestivum*
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
OC BOP clade; Pooideae; Triticodae; Triticeae; Triticinae; *Triticum*.

XX
 RN [1]
 RP 1-1326
 RA Bao W.;
 RT "DNA transposons from wheat.";
 RL Repbase Reports 24(1), 140-140 (2024).
 XX
 DR [1] (Consensus)
 XX
 CC ~93% identical to consensus. 9-bp TSDs.
 XX
 SQ Sequence 1326 BP; 346 A; 237 C; 216 G; 527 T; 0 other;
 //

Summary Table

Repeat Class	Fragments	Length
Transposable Element	16	4718
DNA transposon	11	2248
EnSpm/CACTA	2	227
Mariner/Tc1	3	378
MuDR	6	1643
LTR Retrotransposon	3	1893
Copia	3	1893
Non-LTR Retrotransposon	2	577
L1	2	577
Total	16	4718

* alignment score for local alignment may not always be equal to alignment score in map of hits because of use of heuristics for stitching fragments reported in map section, and use of different [wu-blast](#) parameters on stage of search and stage of producing local alignments.
