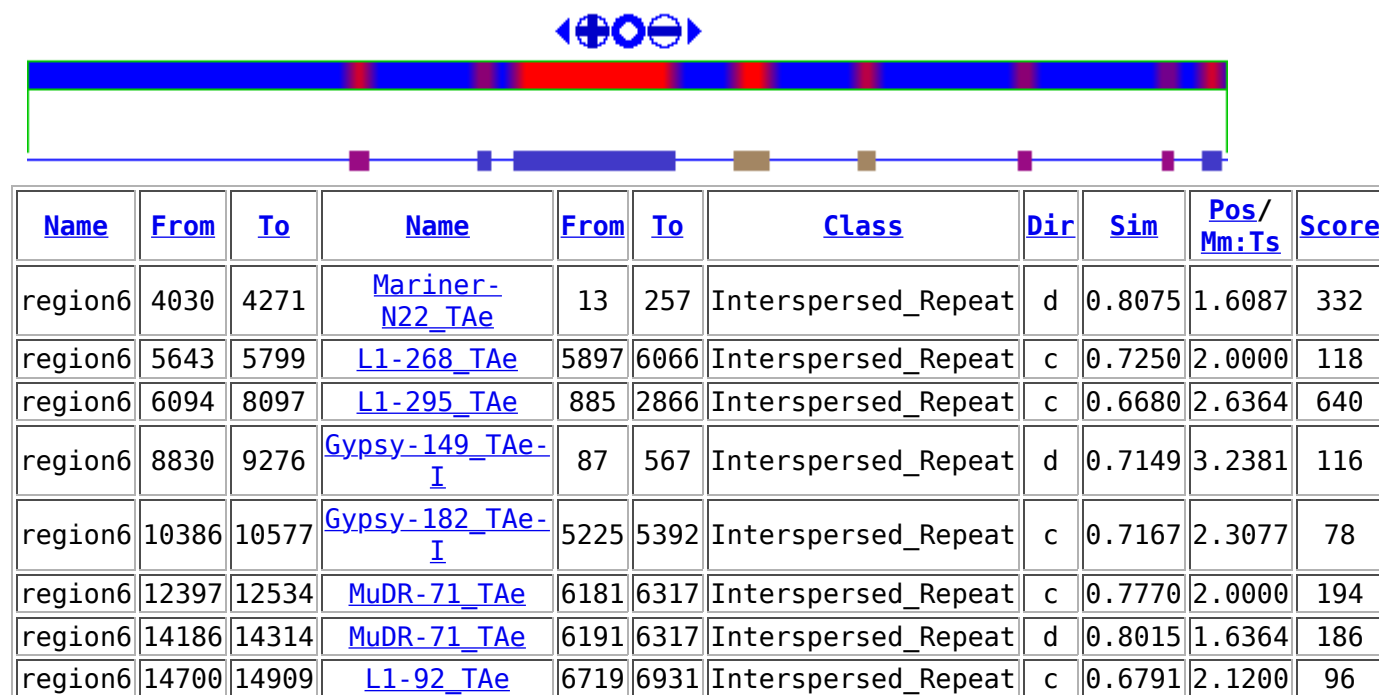


## Map of Hits

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

region6 ([SVG Plot](#); [Alignments](#); [Masked](#))



## Masked Sequence

>region6

```
AGCCGAGCCGACCGACCGACGCTCTGATCCAATCCACCCATCCGTGGACGAGAAAAATACTCCCTCGCCGCA
CAGAAAAAATGGCCGGTGAACGAGACGCAATTTTCAGCGCAGCGAAGGTACAGGATGGGCGGGGACACGG
CTGGTTGGACGTAGTACAGCGAGAGACCGCCGAAACAGGGCCGGTGACACGCGTCGCGCATCGGGGGCCT
CCTCCGAGCCCGACGTGGCCGCGCGCGCGCCCGCGGCCAGCGCACACGTGCGCGTCCCACACGACGCTTC
GAGGCCGGTTCACGCGTCGCGCTCCATTCCAGGCCCGGCCCCGCGCCGCGCGCACCAGCCTCACGT
TGCCTTCACCGGCGGAGACGCGCCACGTCCGCCCCACCGCGCGCGCGCCACCTTTCATCGCCACTATT
TAACCCCATGCCCCCTCCTCATTGTGAGCCCCACCATTTCTTCCCTTCGGTCGAGGAAGGCAGCA
GCAATAAATCTAGGTCCGAGTCGACTCCGTTCCACCATTTCCAGAACCATTCCGACCGGCGAACACA
TTCAATAAACTCCGTTCCCGCGTCCGGTTCTGTGTCACCGGTGATCTGATCTAAGTTGAGCAGCGTCCG
TCGTGCTGCTCCAAGCTCTCCGTCGCACGCGCGCACGTGATCCGGCCAGCCCGTCGTCGTCGTCGTCG
CCACATGGCCCTCAACCTGACCCACCAGACCGGCGCTGCGGCCATCGCGGCCACGCCGGCGCCGGGCGCG
CGCGCTTCGGTGTTCCGGCGGCGCTCGCCCGCGCGCGCGCGCGCGCGCTCCGCCGTGGCGCGGCGCG
AGGCGACGAGCCTGAGGATGCAGACGCGAGCTGGTGGAGCCCGCGCAGCCGAGGCGCGGAGATGTTCCA
GGCCATGGCGCCCGACGACGAGCAGGCGAGGCGCGCGCACCCGGACGCGGCGGCGAGGAGGCACGC
AAGGTGGCGGTGCCGGTGTTCGTGATGATGCCGCTGGACACGGTGCGCAAGGACGGCAGCGCGCTGAACC
GGCGCAAGGCGGTGCAGGCGTCCCTGGCGGCGCTCAAGAGCGCCGGCACGGCCGGCATCATGGTGGACGT
GTGGTGGGGCATCGCCGAGAGCGAGGGCCCCGCGCAGTACAACCTCGCCGGCTACATCGAGCTCATGGAG
ATGGCCAAGAAGGCCGGGCTCAAGGTGACAGGCGTCTGCTTTCCACAGTGCGGCGGCAACGTCGGAG
ACTCAGTCAAGTACGTCGTGCTCTGCTCCCTCTTCTCCATCCAGTCCTCTGTCTATCCAAGTACACATAT
ACGTACATGCATGCTGATCTTGATCATCCTTGCGTACATTCTTGATTTTTCCATGATTCCATGTACCAT
CGCATCTACGGGATGGACGCGTACATGTGACAGTAGAAGCAAAGCCTGAATTAGATAGTGTTATTGGATTT
TGTGGTTCCATGGGCTTGCCATGTGCTGCCACCGCCATTGCCATTAGTTTGTAGCCACTTGCACTAGCA
GGGTATGTGGTAGACAAACGCTATGATGGGTACAGTACTACGTATAGAACTGTGTAGATGAGAGACCAA
GAAAAGAACTTGTTATCTTCTTCATGGCGCTCATGGCAAAGCTTTGTTGGTGATTTGAGTACCCGGGA
AATCGGGATCTCATATGGGGCAACGGGCGACTCGTGACGTAGAAGTGACACGGGCTCGTTTCCACGCAC
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TTTTTTATTTGATGTGAATTGTTACCCTCGCCGAAATTATTTCTTTTCAAGAAACTTTCAATCTATTCAT
CTTCGATCATGATAGTACGACAGACATAAAAAATAATAAAAAATTACATCCAGTAATGTCGCTGAAAAAA
TTATTGTTGCTCTTATACTGTTTCACACTCCACTAATTAGTAATTTGTTTCAATATAATTGATCAAATG
```

[illegible]

[illegible]

AGTCTAGCAGTTATGAGAGCCGCATCGACGAGGACGGCCGCGCCGCCACGGTCTGTATCGGGGAACCTCTA  
CGCCGAGGAGGAGAGGCGTTTTCTTGCTGTCTCTGGCCGTGCCAAGAGCTGAAGCAACAGACGGCGACACC  
GCTACTCTGGTGAAAGTGGTGTTCAGCTACAGAAACGCCGACGACCGGCGCGGACGTGAGCGTGACAACGG  
AGGACACAGTGGTGGCGAGGCGGAGCACGCGCCGAACGCATCGGAGCGGTGGTAGAGGTGGAGCGGGA  
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CCCAGAXXX  
XX  
XXXXTTTTACTCTGTTGACTAGTCAAACACCAAAGAACCCTCTCTCTACCTTACGATGGTCCACCTGTC  
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CGGCCATAATGTGTGAACCTTTGCCATGCTCATATGGTGTCCGCGTTGTGGAGCTAAGGCCTGTGCGGC  
TGCACGTGCATGCCGGTGAATGGGAATATGGCCATGTTCAAGCGAGGACACCGGGCTCAGCTGCTTGTGC  
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GAGTTAACACGTCGGAGAGTCCATGCCCGGTGTTAGGGACTTAGGGTGCCTTAGCTTTGTAGGCTAGCT  
CCTTTATATACTTGTGTACCCTGTGGCCCTGTAATATTTCAATCACATCGATAGAAAGAAAAACAAGAT  
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CTAGCTAGACTGCTTCTTTGTACGTGTATCTCTCGTGTCTATGTTGAGATGGCCGGAACCGATTTAGC  
TCGAAAATTCCTCGAGCTAGCTAGCCTCTAATATGCGTGTATCGATGAAAAGCGCTCAGCTATACCGCCG  
TTGAGGTGCGGACCAGCGCCAACAGCGATGGTGGCCGGGCTCGTCAAAGTGCAGGTGGCGATGGCGTCAGT  
GGGGCGGCGCATCCCCGGGACAGCGAACGTCATATATATGTATTTACGTAACAGGCGTACATACTAGAG  
GTATAAGAATGATCCCGTGGCTGAGTCTGAGTATAAGAATTGTTGTCAATTTTTGTGCTGGGAAAGGGAC  
ACGGAAGGAAAAATGAGTGCCTGAAGAAAGTCGGGAGCTCAGATCATTGCATGCAAGCCCCGTTCCGCC  
CGTATAGCATGCATGCATGCACACATGCGGCGGTACCACACTAAGAAAAATTTGTTGCTATGTGCTGTCCA  
CACATCGATCCAGCGGTCAACTGCATAGCAGGTTTGGCGGTGCTGCGGGAGATCCCTACGTGAAAGCGGC  
GGAGTAGGAGTAGTGTTATTTCTTTTTTTTCTTTCATTGACAGGTGGGTCTTCGTAAGGTAGAGAG  
AGGGTCTATGGTGTGGTACCAGTCAACAAGTGAATACGAAGTXXXXXXXXXXXXXXXXXXXXXXXXXXXX  
XX  
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCATCCAGACCTCCTATTCTTTACTCGTCTTCGTC  
ATTGGATGCCATCAAGTATCCTGGCCCAAATATCTCAATCATGACTTTTGTGTATGTTTTTCAGGAAAA  
AAAAGTAGGACTTTGTTGCGTATTTGTATTGATTTTCAAATAACAAATACAAAGTCAAGTGTTCAAAGG  
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TGGATTTTTTTTTTTCATATCATTGATATCCATCTGTATGGCCTGATATAGAGGAGCTCAGTTGGGATAX  
XX  
XX  
GTAAGTGGTAGAACATCATGCTACCCATGAGAATCTTGATATGTTGTTGACTTTGTAAGTGTTGCACC  
TGCTGGACATTGCCACAAATC

## Local Alignments\*

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
region6	4030	4271	Mariner-N22_TAe	13	257	d	0.8075	1.6087	332

4030 cacaatgtagtgtgtatagatTTTTCTAAAAATCTAactttacaaatTTTaaccAAagttataaagaaaa 4099  
||:|||||||: |||||: |:|:| |||||:|:|:|:|: |:|:|:|  
13 cataatgtagtgccatagatTTTTGagaagtcaaactttacaaactttgaccaagttttagagaaaa 82  
  
4100 ctattttataccgatagtacagtacatactaaatacataaaatgtgaaactactacttcttataatgaatc 4169  
|||||----|- |||----|||:| | :| | |||||----|---|:|:|:|  
83 atatttat----at-ttaca----atacaaaaatatataatgtgaaactac-a--tcttatgatgaatc 140  
  
4170 taataatatatgcttatcattctaaatgtaaatgttttctccaaagatttg--aaaagtttgtgaggtt 4237  
|:|:|:|:|:|:| | |:|:|:|:|:|:|:|:| | |:|:|:|--- |||||  
141 tagtgatatatgtttcgcactctagatgtaaatatttttctccacaaacttggtcaaagtttgtgaggtt 210  
  
4238 tgac---tta-----ct----gcactacagtatggaaggaagggag 4271  
|||---||-----|----| ||||| ||||| |:|:|:|

211 tgacttttttaaaaaatctataggcactacattatggaacggagggag 257

<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>
region6	5643	5799	<u>L1-268_TAE</u>	5897	6066	c	0.7250	2.0000	118

```

5799 aaattcccccacatagattattgtggaataccaaaattcctttaagataaaaagtcttagtgtgattaatt 5730
      |||||:|-|| |:|| :| |||| |:|||:||||| :|||:||||| ||||:|---
5897 aaatttcc-acagaaatacctttggaatatcaaagttcctgcaaaaataaaaagtcttctgtggtta--- 5962

5729 gtgaa-aattagtgatt-----gg---gtct-----aaaaaggatgggaaggtagcaaaacatgt- 5678
      || ||-|| || ||||-----||--|||-----|||:|||:||| :| |||: ||||-
5963 gttaataagaagagtattttgactagggatgtcttactcaaaaagggtggaaggggggaagaatgtg 6032

5677 ccttctagtggggtgtgatgaatttgttgatcatct 5643
      : ||||-|||:||: |||||: :|||:|||||
6033 tgttct-gtggacaagatgaatcaattgatcatct 6066

```

<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>
region6	6094	8097	<a href="#">L1-295_TAE</a>	885	2866	c	0.6680	2.6364	640

8097	ctcccccttcagcacggcggggctgttcggtgaactgaagagcaagtgggggctgcgcggacggctcgact	8028
885	ctgccctacagcaacgagggcctgatcggcgccctaaaaaacaagtggggctctccgtgggtcacctcagct	954
8027	acacacctctccgcaacaaccgcttcattgctcgaattcgagcgtgagggcgatcgtcagca-cgtcctgg	7959
955	acaagccgctcaagaacaactgcttcctcctggagtttsaacgggagggggaccggc-gcttcattcctcg	1023
7958	aaaacggcccatggacacaccgtaaggatgcattcctcattgttccctttgatggacagggcaaggcgctc	7889
1024	acaatggctccgtggacctacaatgggtgatgcttcctgatggttgcgggtggatgg-c--ggccatcccc	1090
7888	gg---acgtaccggtgaacgtcatgccaatctgggcacgcattctatgatgtgccacctctcatgctgtca	7822
1091	gggcgacgtggaggtggcctatatgccaatatgggtccgcattccacgatgtcccccgatcatgttggat	1160
7821	gaagagatcgggtggaagctagggtg---gcctcttgggaaaagtctcagggtagatgcggataagttt	7756
1161	gagggggtggcatggaagctgggtgcaaagc-tc--ggcaagggttctggaggttgacacagacaattgt	1226
7755	gggaatatatttctctgaatttcttt-gtgaagagttgaacataatgtaaacactcctctcctgcgtgag	7687
1227	ggtaaggctctggggtga-tttcattcgggttcgtgtggaacatgatgtagatgaacctctca-----gag	1290
7686	atcag-----tcctagagagtttaggggaga-aa-gagcatatggacctagaggtcaagtatgagagagcc	7624
1291	ataagcttacttctcatga--tagggcaataatgagttgttttcttagagttgaagtatgagagagcg	1358
7623	ccacgattttgtatgtactgtgggcacataggtcatggggaaagggactgcaggctgccgacggatgatc	7554
1359	ccgcgtttttgcggtttttgtggttttctcgggcattggacaacgcgattgtaagttgccggtggacctcc	1428
7553	aagcaga-gagggttcacggggcgatgagagcattgccctataaatcaagcaaaaaca-agtgcggttc	7486
1429	aag-agatgaggtagacacsgcaacaatgcgtgcctccccgtataagaaaagcaatagtagagg-ggatat	1496
7485	gtggtaccagacgcttgtagtgcagacg-cttcctgca-ctttgggtctgagttgga-cggggaggcat	7419
1497	gttgccccggtggctagtagtgcccgtcgtcttc-t-cagcttcgggaaggaggtggctcg---agacag	1561
7418	ggacagccccggccaaattggcctgggagaagctaggcagagacaagaaggtgatgcatgctcgatcaca	7349
1562	aggcagccccatc---a--ggtc--ggagta-cgag--agagtcctgacgagatcc-tgg-cgaacca	1619
7348	ggagatggtgaagatgcagg--gatattccagatgatgtgc---tgctggaccggctgtacaag--cgg	7287

|----| |||-----| ||| | | | -|| | |----| || | | :||| | | -|:|---| |  
 1620 g----tggt-----gcaggcggctattgctgcag-tgagcaaactgcgggtctcgatgg-cgggtcctg 1678  
 7286 ca---at-cgcag-----cggttagcgcgcttagagtgcag-cgaagacactggaatgaaggcaccag 7229  
 ||---||-||| |-----||| | -|||:| | :| | -| | -|||:| |||:| |-----||  
 1679 cactaatacgcaggtgtcctcggt--g-gcgcctactgctattctcatt-actgggaatggag-----ag 1739  
 7228 gaagacgagcatcggcgaga-aca--caaagatggctccggcgaaacccgcgctgaccacggcttctact 7162  
 |:-|||-----|||---||-|||---| ||| ||| :|||----|:||| |-----| | || ||-|||  
 1740 gg-gac-----cgg---gatacatgccaagctggaccgcg----agccctc-----cgaaggatt-tac- 1788  
 7161 ccaaccatagccatggctgacgcggacacctc---gccatctac--acca-----ccgggtacaggggc 7103  
 ---| || |:| -| ||| ||:| | -||| :| |----| |||:| | -| | | |-----|:|---| |||:| |  
 1789 ---agcagaac-akggcagatgct-acagttcagacgccacc-acttascatgaagcca---acagag-c 1848  
 7102 ggggggcgacatcgacaaaaccccgctcgcacacaccatcgaggatgcagcaacccctccctaccgcgcg 7033  
 :|| | -| -| || | -||| |-----| ||||| |-----| | ||-|| | || | -||| |||||  
 1849 aggtg-c-agatag-caaa-----ggacacac-----akgtg-aggaccactg--taccgcgcg 1898  
 7032 ggtttcgagcccgactct--gttaa-----ggcctctcctgtcgctgctactgttaactcagtagagacg 6970  
 |||||:| |:| | | -|||:| |-----||| -| |||| ||| |:| | | |||---|:|---||  
 1899 ggttttgaaccggggtmtcagtcgatcgwtggcg-cggctgtagccccactctgaact---tg---cg 1961  
 6969 g-agacaaagtgcag---ggaa-gt--tgca-----tgcacaaaaggaacaggtctcaaaacc-----aa 6917  
 | -||-||| |||||---||| | :---||| |-----| |||:| | | | |---| |---|  
 1962 gcag-caaagtgcagggggaacgccatgcagaatgctgcactgactggaccgagcctca---cctcgat 2027  
 6916 ggcaaatatattagccagctcaaggaaagaaagg-----aaccagg---gga---gacaaat--- 6865  
 ||| -- :|:| |---| | | :||| |||:| |-----| | | |---| |---| | | |---  
 2028 ggccc--kgtgtt--cc--ctgagaaaaagaagggggcaagaagcatgtcaaggctcctgaaawatcag 2091  
 6864 --tcagtcttagaaaaagaggc-acgggtgacatggcc-acatctactggggct---atggctagtgc 6803  
 --||| ||| |:| | |:|:| | | -| | -|| | | | -| |---|---| | |---| |:| | |  
 2092 catcagtactgggcaagaggggcgaccg-tgagagggaagaga---a---ggcagaaaatggtaagamc 2153  
 6802 --gtctgatgtaa-caggggacatgtataagaa-a-cagagagctgctgta--gaggaagaggatgaga 6741  
 --| ||: |:| | -|| |:| | | | ||| | -| |:| | -| | | | |---| ||||| |---| |---|  
 2154 aaggatggggcaagcagtgatca-gaagaagaagatcaaag-g-tgcaggatctgaggaaga--a--agt 2216  
 6740 g-agctgtaggag-agataggtggtaaggaagctagcgggtattggggctgccggggaactgacgggcgc- 6674  
 | -|| | | |||| | -|:| -| |:|:| ||||| | |||:| | |||||:| | | | |||:| |:| | |  
 2217 gcagcaggaggagcaggc-ggcggtgaggaagcaaccggcataggggctaccggtcaactggcggacgcc 2285  
 6673 gacggagagcgcccgctcaggaggaatgacgatcctatgttggaactgccggggact-gggccaccccggg 6605  
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 2286 gaggaag-gcgcgccaggagccatgacgctgctaagttggaactgtcgaggmctcgggcaacctcgc- 2353  
 6604 acagttcgtgagcttgtgtgcctagtgcgcacgtacc-gccc---ctctgtcgtgttcattctctgagacg 6539  
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 2354 acagttcaggaactcgtgtgccttgtgcacacctacaagcccaagctc-gtc---ttcctttccgagact 2419  
 6538 cggcagtgtaggagagcgtcaaaagaat---aagatggaggctgggcctcaaaaactgcatcaccacg 6472  
 ||||| :|:| | | :||| | |---| |---| | -||| | | | | | | | | | :| |:|:| |:| | |  
 2420 cggcaaaataatmagtacgtcaaaa--atctcaag-tggaggctgggcctccggcattgtatcgcgcaac 2486  
 6471 atggcatgggaaaagggtgctggtatagccctgttttgggatgaaagtgttgaaataaaaattactctccta 6402  
 :||| | | ||||| |:|:| | |||| | |:|:| |:|:| |:|:| |:|:| |:|:| | | :|:| | |  
 2487 ccggcatcggaaaagggtgccggcattgccctctttatgatgagagtatcgaataaaaaagattgccgt 2556  
 6401 tggtttgaggtatattgatgtgcatatgcgtatggatccccatggc--ccgatgtggcgggttacctttg 6334  
 || |:|:| |:|:| |:|:| | :| | | |:|:| |:|:| | |||---| |:|---| | | |:| |||||  
 2557 gggagcgagatacatcgatgtttgatccggttaaacctcttggtgctgcaa--tgagggccacctttg 2624  
 6333 tgtacggcgagcctagagcacatgagaggcataacatgtggaacctgctgaaaagaataaa-----acc 6270  
 | |:|:| | ||| |:| | |||| | |:|:| ||||| |:| | | |:| | | | | |-----| |  
 2625 tttatggggagccgaaagctcatgagcgccaccacatgtggwccttgcgagagaataaaggattcagc 2694  
 6269 aaaatcgattgagccgtggatgatgataggagacttcaatgaaacattatggcaaagt--gaacatttct 6202  
 :| |---| |---| |||| | | |||| | | ||||| |:| | | |:| | |---| |---| |:|:| | |

2695 gaa--c-at---gccgtggctcatgatttggtgacttcaacgaaacatgtggc--agtcggaacacttct 2756

6201 ctgcagcaaaaagatctgaaaggatatgggcaatttcagagatgtactggcatactgtaatctt-catg 6133

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

2757 ctgcttcaaatagatcggagaagaatatggagaattttcgacggttcttgctgactgtaa-ctgtttg 2825

6132 atctgggttaccatgg-ttggtagtggga-aga-aacacccaa 6094

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

2826 acctgggcttcaaaggaccggt-gtggacataataacaacaaa 2866

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
region6	8830	9276	<a href="#">Gypsy-149_TAE-I</a>	87	567	d	0.7149	3.2381	116

8830 ccacctccacctccgcc--gc---cccc---gccggtgcgacctcagccagagactcgtccattcccc 8890

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

87 ccaccgccaccaccgccccgctgtccacaacggccagcgcg-cctccgcccgtgcc-cgtcac---cgcc 151

8891 tccgc-ccg-t---gca-tcat-tctcccgcggcagtcacctcccgtgcatttcgtgcacggtcagcca 8952

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

152 gccgcgcccgtcgccgcccgtcttctctccggaggaggtcaccg---gagcaatccg---cgatct--- 210

8953 ccgccaccgcca-ccacg--a-ccgac-atac-t--cgtggccacgcattc---ccac-gcaggca-cga 9009

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

211 -cgccaccggtccaggcatccgcctatacctggcg-ggcccc---tacgggccaccgcccgtgcgc 275

9010 ca---gccgcccacac--ggcccgtgaatctcgtgc-acggtcagccaccac---cg-----ccgc-- 9061

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

276 caaccgcccgccaccgggcccct---tctcctgccatgg-cagccgcccgtcccgggggcccctccgcgg 341

9062 cgc---cg--ccgccaccgcccctgcgtcccg-tgc---cacc---gccaccacc-----gcc-- 9107

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

342 cgctggtcgggcccgtgcagcccagc-tgcagctgcagccacccccgccaccaccccgcctatggccgc 410

9108 cgtgcgtttcgtgccacggccaccac--taacatcgtcgtggccg-cgcttgcccacgcagctacctcg 9174

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

411 cgtg-g--ccgtccc-cggccaccgcggtttc--cgccgctccggcgcc--cccacgcagctgcagctg 472

9175 ccgcctccaccgccg-ccaccacgcgtgcgtattagccagggtcagccacaatgcagcttcgacg----- 9238

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

473 cagggccaccgccgccagcac-cg-g-----gcc-ggct-----acga--ccgcgcccggggcggt 525

9239 -acga-cgagcaggtt-gg-tccgcctctgggccg--ccagct 9276

- ||| - | ||||| ||| - ||| ||||| - ||| |||| - - |||||

526 tccgatccagcaggttcggttcccgcc-ct-cgcccgcagct 567

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
region6	10386	10577	<a href="#">Gypsy-182_TAE-I</a>	5225	5392	c	0.7167	2.3077	78

10577 ttcgacacgcgcccgcgcac-tcttgacgctcggcctccagcgccatggtcacgggatcg-ccatcgct 10510

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

5225 ttcggcacgctctcacgcaggatctt-cagctcggcctccagcacc-----cggcagcgaccttg-- 5284

10509 cgccgcctctgacagcgccactgcagcgtgccggttcttgagtatcgccaccgcctcctggtgctcgccc 10440

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

5285 -gcggcctc-g---gcgtc-cttca-gc-gccgcctcgcgagca--gctgctgcct---gagct-g--c 5337

10439 cgctccgctgc-cgccctc---gccgcgcga--tgtcctccgccgatccaccgaacg 10386

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

5338 ggct-cgcttctccccctcagaggtcgccgcgacctg-gctcag-cg---ccgccgaacg 5392

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
region6	12397	12534	<a href="#">MuDR-71_TAE</a>	6181	6317	c	0.7770	2.0000	194

12534 tacggagctttgtacgatgaggcagtgaccgtataatcacctcaagtcgtatatagtgatcgtattgacc 12465  
 ||| |-|||: |||||:||||:-||||||| || :|||||:| ||| |:||| |||||  
 6181 taccg-gctcagtagcgtgaa-cagtgaccgtataatcacgtcccatcgtacaaagtkaccgtaatgacc 6248

12464 gtatttttaagtacaatgaccaaagtgagctttcgacacaagttcaatgacatgga-tgcatcttactc 12397  
 |||||:|||||:||||||| :|||||: ||:|:||||||| || || |-|||||:|||||  
 6249 gtatttctaagtagcgtgaccaaaccgagctcgcggcgaagttcaagtacctgtagtgcatcttactc 6317

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
region6	14186	14314	<a href="#">MuDR-71_TAe</a>	6191	6317	d	0.8015	1.6364	186

14186 gtacggtgagacaatgaccgtataatca--tctcaagtcgtatatagtgaccgtattgatcgtattttta 14253  
 ||||| |||-|||:||||| |||||---||:| |--|||:| ||| ||||| |||:|||||:|  
 6191 gtacggtga-acagtgaccgtataatcacgtccca--tcgtacaaagtkaccgtaatgaccgtatttcta 6257

14254 agtacaatgaccaaagtgaggct-tcgacacaaagttcaatgaccgtg-aatgcattttactc 14314  
 |||||:||||||| :||-||- ||:|:-||| |||-||-|:|||||||  
 6258 agtagcgtgaccaaaccga-gctcgcggcgc-aagttcaagtacc-tgtagtgcatcttactc 6317

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
region6	14700	14909	<a href="#">L1-92_TAe</a>	6719	6931	c	0.6791	2.1200	96

14909 aaatgggtttggcacacagct--gccaaat-aaagcat-aagatTTTTTcctggatgctcattaaca 14845  
 || |||:||||:-||-|||---|| |||-||-||-|||:|||| -||| ||| | ||:| :  
 6719 aactggatttggc-ca-agctcttgacacaaatgaaa--atcaaggttttg--cctggatgatgatcatgg 6782

14844 acagactaaacacca-ggcatgttacaacgcaagaattt-cttcctggagaa--atactcttggtgtgt 14780  
 ||||:|:|:|:|:-|| ||| | |: | |:| ||| -| |:|:| | ---||-|||||||:|  
 6783 acaggttgaataactaaggacatggttgagagaaggcattggcatattgaagatgggat-ctctgtgtgtc 6851

14779 tatgtcatctgcatg--agcttgaaca-agagatcacctctttttcgctg-ccccttcgctaggggtt 14714  
 | |||||:|||| |--||---|:| |:-||:|||||||: ||:-|:|:| | |:| || |  
 6852 tctgtcatttgcaggtcag---ggaagatagggatcacctcttttcaattgtctctttagccagcgtgt 6918

14713 gctggtcctacctt 14700  
 |-||| :|||||  
 6919 g-tggaattacctt 6931

## Masked Regions

```
>region6 FRAGMENT 4030 -> 4271
CACAAATGTAGTGTATAGATTTTTCTAAAAATCTAACTTTACAAATTTTAACCAAAGTTATAAAGAAAA
CTATTTATACCGATAGTACAGTACATACTAAATACATAAAATGTGAACTACTACTTCTTATAATGAATC
TAATAATATATGCTTATCATTCTAAATGTAAGTGTCTTCTCCAAAGATTGAAAAGTTGTGAGGTTTG
AATTACTGCACTACAGTATGGAAGGAGGAG
>region6 FRAGMENT 5799 -> 5643
AAATCCCCACATAGATTATTGTGGAATACCAAATTCCTTTAAAGATAAAAGTCTTAGTGTGATTAATT
GTGAAAATTAGTGTATTGGGTCTAAAAAGGATGGGAAGGTAGCAAAACATGTCCTTCTAGTGGGTGTGAT
GAATTTGTTGATCATCT
>region6 FRAGMENT 8097 -> 6094
CTCCCCCTTCAGCACGGCGGGGCTGTTCCGTGAACTGAAGAGCAAGTGGGGCTGCGCGGACGGCTCGACT
ACACACCTCTCCGCAACAACCGCTTCATGCTCGAATTCGAGCGTGAGGGCGATCGTCAGCACGTCCTGGA
AAACGGCCCATGGACACACCGTAAGGATGCATTCTCATTGTTCCCTTTGATGGACAGGGCAAGGCGTCG
GACGTACCGGTGAACGTCATGCCAATCTGGGCACGCATCTATGATGTGCCACCTCTCATGCTGTCAGAAG
AGATCGGGTGAAGCTAGGTGGCCTCTTGGGAAAAGTTCTCAGGGTAGATGCGGATAAGTTGGGAATAT
TTTCTCTGAATTTCTTTGTGTAAGAGTTGAACATAATGTAACACTCCTCTCCTGCGTGAGATCAGTCCT
AGAGAGTTAGGGGAGAAAGACATATGGACCTAGAGGTCAAGTATGAGAGAGCCCCACGATTTTGTATGT
ACTGTGGGCACATAGGTCATGGGAAAGGGACTGCAGGCTGCCGACGGATGATCAAGCAGAGAGGTTAC
GGGGGCGATGAGAGCATTGCCCTATAAATCAAGCAAAAACAAGTGGGCTTCGTGGTACCAGACGCTTGT
AGTGCCAGACGCTTCTGCACTTTGGGTCTGAGTTGGACGGGGAGGCATGGACAGCCCCGCCAAATTGG
CCTGGGAGAAGCTAGGCAGAGACAAGAAGGTGATGCATGCTCGATCACAGGAGATGGTAAGATGCAGGGA
TATTCCAGATGATGTGCTGCTGGACCCGGCTGTACAAGCGGCAATCGCAGCGGTTAGCGCGCTTAGAGTG
```

AGCGAAGACACTGGAAATGAAGGCACCAGGAAGACGAGCATCGGCGAGAACACAAAGATGGCTCCGGCGA  
AACCCGCGCTGACCACGGCTTCTACTCCAACCATAGCCATGGCTGACGCGGACACCTCGCCATCTACACC  
ACCGGGTACAGGGGCGGGGGGCGACATCGACAAAACCCCGCTCGCACACACCATCGAGGATGCAGCAACC  
CCTCCCTACCCGCCGGGTTTCGAGCCCGACTCTGTAAAGGCCTCTCCTGTCGCTGCTACTGTAACTCAG  
TAGAGACGGAGACAAAGTCAGGGAAGTTGCATGCACAAAAGGAACAGGTCTCAAAACCAAGGCAAAATA  
TATTAGCCAGCTCAAGGAAAGAAAGGAACAGGGGAGACAAATTCAGTTCTAGGAAAAAGAGGCACGGGT  
GACATGGCCACATCTACTGGGGCTATGGCTAGTGCGTCTGATGTAACAGGGGACATGTATAAGAAACAGA  
GAGCTGCTGTAGAGGAAGAGGATGAGAGAGCTGTAGGAGAGATAGGTGGTAAGGAAGCTAGCGGTATTGG  
GGCTGCCGGGGAAGTACGGGCGCGACGGAGAGCGCCCGTCAGGAGGAATGACGATCCTATGTTGGAAGT  
GCCGGGGACTGGGCCACCCCGGGACAGTTCGTGAGCTTGTGTGCCTAGTGCACGACGTACCGCCCTCTGT  
CGTGTTCATCTCTGAGACGCGGCAGTGTGAGGAGAGCGTCAAAAGAATAAGATGGAGGCTGGGCCTCAA  
AACTGCATCACCCACGATGGCATGGGAAAAGGTGCTGGTATAGCCCTGTTTTGGGATGAAAGTGTGAA  
TAAATTAATCTCTCTATGGTTTGAGGTATATTGATGTGCATATGCGTATGGATCCCCATGGCCCGATGTG  
GCGGGGTACCTTTGTGTACGGCGAGCCTAGAGCACATGAGAGGCATAACATGTGGAACCTGCTGAAAAGA  
ATAAAACCAAAATCGATTGAGCCGTGGATGATGATAGGAGACTTCAATGAAACATTATGGCAAAGTGAAC  
ATTTCTCTGCAGCAAAAAGATCTGAAAGGTATATGGGAATTTAGAGATGTACTGGCATACTGTAATCT  
TCATGATCTGGGTTACCATGGTTGGTAGTGAAGAAACACCCAA  
>region6 FRAGMENT 8830 -> 9276  
CCACCTCCACCTCCGCGCCCCCGGGTGCACCTCAGCCAGAGACTCGTCCCATTCCCCTCCGCCCCGT  
GCATCATTTCTCCCGCGGCAGTCACTCCCGTGCATTTCTGTGCACGGTCAGCCACCGCCACCGCCACCACG  
ACCGACATACTCGTGGCCACGCATTCCACGCAGGCACGACAGCCGCCGCCACGGCCCGTGAATCTCGTG  
CACGGTCAGCCACCACCGCCGCCGCCGCCGCCACCGCCCTGCGTCCCGTGCCACCGCCACCACCGCCCG  
TGCGTTCGTGCCACGGCCACCACTAACATCGTCGTGGCCGCGCTTGCCACGCAGCTACCTCCGCCGCC  
TCCACCGCCGCCACCACGCGTGCATTAGCCAGGCTCAGCCACAATGCAGCTTCGACGACGACGAGCAG  
GTTGGTCCCGCTCTGGGCCGCCAGCT  
>region6 FRAGMENT 10577 -> 10386  
TTCGACACGCGCCCCGCGCATCTCTTGACGCTCGGCCTCCAGCGCCATGGTCACGGGATCGCCATCGCTCG  
CCGCTCTGACAGCGCCACTGCACGCTGCCGGTCTTGAGTATCGCCACCGCCTCCTGGTGCTCGCCCCG  
CTCCGTGCCGCCCTCGCCGCCGATGTCCTCCGCCGATCCACCCGAACG  
>region6 FRAGMENT 12534 -> 12397  
TACGGAGCTTTGTACGATGAGGCAGTGACCGTATAATCACCTCAAGTCGTATATAGTGATCGTATTGACC  
GTATTTTAAGTACAATGACCAAAGTGAGCTTTGACACACAAGTTCAATGACATGGATGCATCTTACTC  
>region6 FRAGMENT 14186 -> 14314  
GTACGGTGAGACAATGACCGTATAATCATCTCAAGTCGTATATAGTGACCGTATTGATCGTATTTTAA  
TACAATGACCAAAGTGAGGCTTCGACACAAAGTTCAATGACCGTGAATGCATTTTACTC  
>region6 FRAGMENT 14909 -> 14700  
AAATGGGTTTGGCACACAGCTGCCAAATAAAGCATAAGATTTTTTCTGGATGCTCATTAAACAACAGA  
CTAAACACCAGGCCATGTTACAACGCAAGAATTTCTTCTGGAGAAATACTCTTGTGTGTATGTCATCT  
GCATGAGCTTGAAACAAGAGATCACCTTTTTTTCGCTGCCCTTCGCTAGGGTTTGCTGGTCCTACCTT

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## Annotation of Repbase Sequences

ID Gypsy-149\_TAe-I rebase; DNA; PLN; 4911 BP.  
XX  
AC .  
XX  
DT 16-MAY-2023 (Rel. 29.02, Created)  
DT 16-MAY-2023 (Rel. 29.02, Last updated, Version 1)  
XX  
DE LTR retrotransposon from common wheat genome: internal portion  
DE consensus.  
XX  
KW Gypsy; LTR Retrotransposon; Transposable Element; Gypsy-149\_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 1-4911  
RA Bao W.;  
RT "LTR retrotransposons from wheat."  
RL Repbase Reports 24(2), 1108-1108 (2024).  
XX  
DR [1] (Consensus)  
XX

CC ~93% identical to consensus.  
 XX  
 SQ Sequence 4911 BP; 657 A; 1842 C; 1508 G; 870 T; 34 other;

//  
 ID Gypsy-182\_TAe-I rebase; DNA; PLN; 7545 BP.  
 XX  
 AC .  
 XX  
 DT 16-MAY-2023 (Rel. 29.03, Created)  
 DT 21-JUL-2023 (Rel. 29.03, Last updated, Version 1)  
 XX  
 DE LTR retrotransposon from common wheat genome: internal portion  
 DE consensus.  
 XX  
 KW Gypsy; LTR Retrotransposon; Transposable Element; Gypsy-182\_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 1-7545  
 RA Bao W.;  
 RT "LTR retrotransposons from wheat.";  
 RL Repbase Reports 24(3), 1841-1841 (2024).  
 XX  
 DR [1] (Consensus)  
 XX  
 CC ~90% identical to consensus.  
 XX  
 SQ Sequence 7545 BP; 1357 A; 2630 C; 2331 G; 1223 T; 4 other;

//  
 ID L1-268\_TAe rebase; DNA; PLN; 6756 BP.  
 XX  
 AC .  
 XX  
 DT 18-MAY-2023 (Rel. 28.11, Created)  
 DT 24-MAY-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; L1-268\_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 1-6756  
 RA Bao W.;  
 RT "Non-LTR retrotransposons from wheat.";  
 RL Repbase Reports 23(11), 7561-7561 (2023).  
 XX  
 DR [1] (Consensus)  
 XX  
 CC ~95% identical to consensus.  
 XX  
 SQ Sequence 6756 BP; 2298 A; 948 C; 1820 G; 1673 T; 17 other;

//  
 ID L1-295\_TAe rebase; DNA; PLN; 6499 BP.  
 XX  
 AC .

```

XX
DT 18-MAY-2023 (Rel. 28.11, Created)
DT 31-MAY-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; L1-295_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 1-6499
RA Bao W.;
RT "Non-LTR retrotransposons from wheat.";
RL Repbase Reports 23(11), 7586-7586 (2023).
XX
DR [1] (Consensus)
XX
CC ~95% identical to consensus.
XX
SQ Sequence 6499 BP; 1810 A; 1433 C; 1882 G; 1355 T; 19 other;

//
ID L1-92_TAe rebase; DNA; PLN; 7342 BP.
XX
AC .
XX
DT 22-APR-2023 (Rel. 28.07, Created)
DT 22-APR-2023 (Rel. 28.07, Last updated, Version 1)
XX
DE Non-LTR retrotransposon from common wheat: consensus.
XX
KW L1; Non-LTR Retrotransposon; Transposable Element; L1-92_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 1-7342
RA Bao W.;
RT "Non-LTR retrotransposons from wheat.";
RL Repbase Reports 23(7), 4855-4855 (2023).
XX
DR [1] (Consensus)
XX
CC ~93% identical to consensus.
XX
SQ Sequence 7342 BP; 1631 A; 1535 C; 1755 G; 2383 T; 38 other;

//
ID Mariner-N22_TAe rebase; DNA; PLN; 257 BP.
XX
AC .
XX
DT 01-MAR-2023 (Rel. 29.04, Created)
DT 01-MAR-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-N22_TAe.
XX

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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   1-257
RA   Bao W.;
RT   "DNA transposons from wheat.";
RL   Repbase Reports 24(4), 2149-2149 (2024).
XX
DR   [1] (Consensus)
XX
CC   >98% identical to consensus.
XX
SQ   Sequence 257 BP; 88 A; 39 C; 41 G; 89 T; 0 other;

//
ID   MuDR-71_TAe rebase;      DNA;      PLN; 6317 BP.
XX
AC   .
XX
DT   13-JUN-2023 (Rel. 29.01, Created)
DT   13-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-71_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   1-6317
RA   Bao W.;
RT   "DNA transposons from wheat.";
RL   Repbase Reports 24(1), 183-183 (2024).
XX
DR   [1] (Consensus)
XX
CC   ~96% identical to consensus. 9-bp TSDs.
XX
FH   Key          Location/Qualifiers
FT   CDS          join(459..504,914..1962,2034..3034,3134..3686,
FT              3958..4029,4108..4740)
FT              /product="MuDR-71_TAe_1p"
FT              /translation="MAAIRRPDGPAPDYRARSDFSVLFHHGFFFMGQGS
FT              NRSYVNGHEVWYDQVDRLTWSPIMVEHMFVEEIGWEMAGRIKAYYRIPILDI
FT              TRNSLRQIRSDADTDQMMVFLSIGHHFFDIYLDHDDSLHSHKDVDDVVHNP
FT              RAHLPPVFSPSKEKSSTNPASSSSPSHREGEDPIPIQIVYPNNPEVEVDDG
FT              NPFIFARRTENIQSDNLDHVQQUESTIEPQQHESDRVHXDASGADAENNGVE
FT              REEDRRRAKRGKREVLSESDSDSDSDFDPAAGMFSDFEISDGDDDLAD
FT              NVDEDEPVQSKDKVQGGHAGQVKQGPQAKDEAMSDYESEGEDLWAPDSDDDE
FT              TQTKFRAFRKEDLQCPKFHVGQLPVNDKKRVKAVCDEDCTWYLWASYDSRT
FT              KCFMVKKYVEEHTCCKKWKIKAFAPFLARKYLESFRADQDMNLRNFSRVV
FT              QKEWHMTPSRTKLQRRRLAMKIIHGDEEGQYKLLWDYGNEIRRSNPGSSF
FT              FLALDDKARFNKAYMCLDACKRGFLQGCRPVIFIDGCHIKTRYRGQLLVAV
FT              GIDPNNCIFPIAIGVVEVEDMPNWWFLERLKMDLGIINTSPWTIMSDKQK
FT              GLINAVNDVPESHRFCVRHMWKNFQQLYKGDALKNQLWKIARSTTTIKY
FT              EQYMNEMKELNEDAYKWLKELEPETWVRAFQSDIPKCDILLNNLCEVFNKY
FT              ILEARELPILSMFERIKQWTSRHYTKQLEGEKMQGVTCPIKKMVEKLD
FT              LANTCYVYESGDGVFQVGDRTDYIVDIHTKSCSCMRWQKNGVTCIHVIAC
FT              CRNERVDPITLVDNCYSVAMFKKAYSNIIPCKDITWEKMNQGPQYCHQST
FT              QNMWEDLARVEGNQKRSYAVMEGRECPDMNQEEASTQRAPPVDDLMIDS
FT              LEQRPLPRIIQQTPVPESAFLVNAQSMNLNHSQPSSTVTHGDLAKKLLAMK
FT              TQREKELEDKKQAVLAARREAEMKKAEEAARKRHELAEKKAQDAERKKEAA

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FT          A Q K R E A Q A I L K Q A A A E T R Q I I Q E T H R Q I A A E K K E K L A A E K L A Q K E A A A A K K
FT          L A E R Q A A N A K K E Q A R Q A A A A K K M A D K A A A A A K K L G N R T V Q E E H H S S G L E K
FT          N G S M F D I F R D "
XX
SQ  Sequence 6317 BP; 1905 A; 1303 C; 1540 G; 1555 T; 14 other;

//

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## Summary Table

Repeat Class	Fragments	Length
Transposable Element	8	3519
DNA transposon	3	509
Mariner/Tc1	1	242
MuDR	2	267
LTR Retrotransposon	2	639
Gypsy	2	639
Non-LTR Retrotransposon	3	2371
L1	3	2371
<b>Total</b>	<b>8</b>	<b>3519</b>

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\* 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.

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