Map of Hits
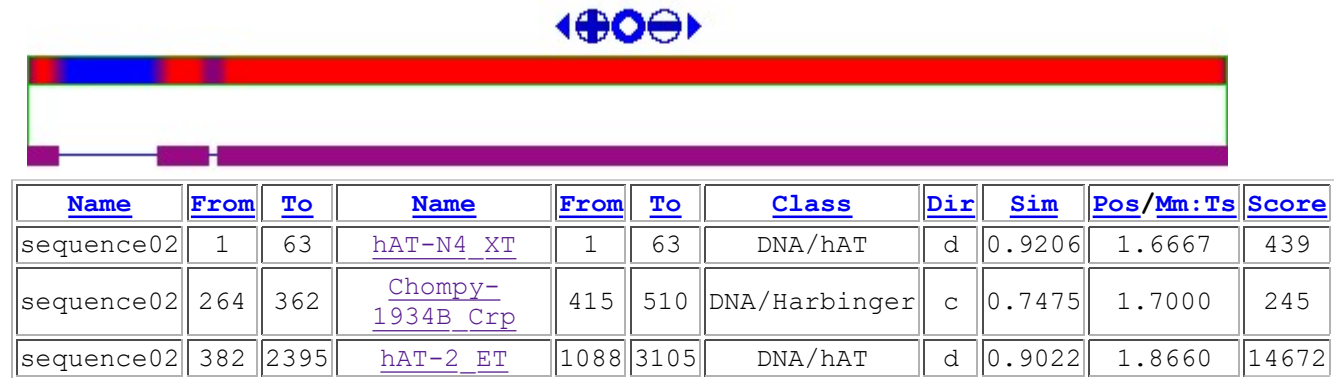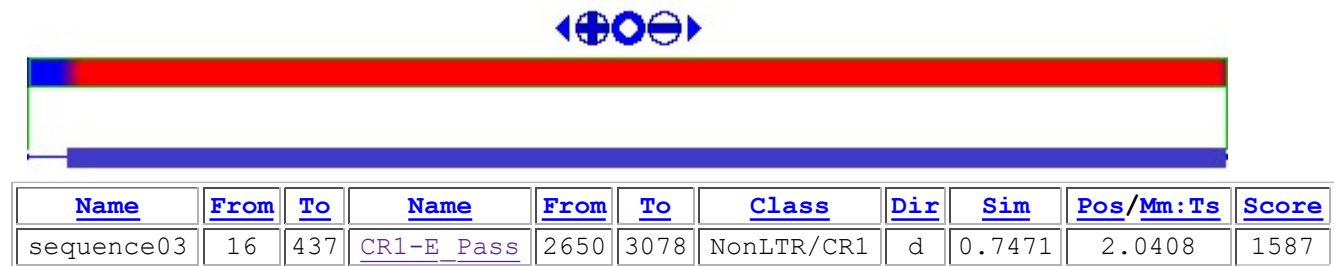
SVG viewer is required to view graphical representation of the map as Scalable Vector Graphics (SVG plot).
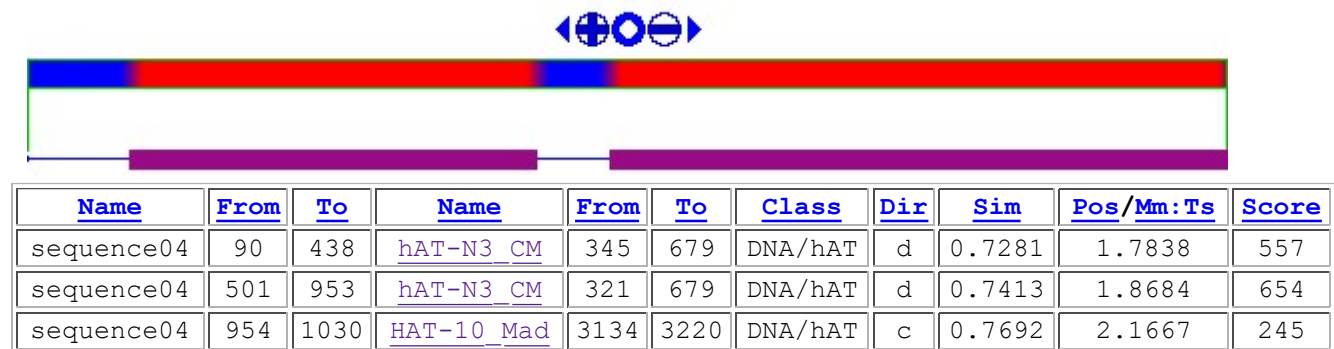
sequence02 (SVG Plot; Alignments; Masked)

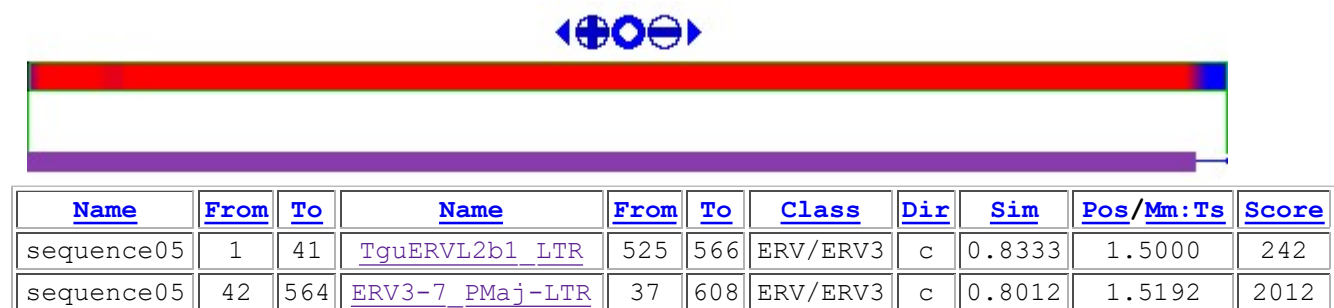| Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
sequence02	1	63	hAT-N4_XT	1	63	DNA/hAT	d	0.9206	1.6667	439
sequence02	264	362	Chompy-1934B_Crp	415	510	DNA/Harbinger	c	0.7475	1.7000	245
sequence02	382	2395	hAT-2_ET	1088	3105	DNA/hAT	d	0.9022	1.8660	14672

sequence03 (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
sequence03	16	437	CR1-E_Pass	2650	3078	NonLTR/CR1	d	0.7471	2.0408	1587

sequence04 (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
sequence04	90	438	hAT-N3_CM	345	679	DNA/hAT	d	0.7281	1.7838	557
sequence04	501	953	hAT-N3_CM	321	679	DNA/hAT	d	0.7413	1.8684	654
sequence04	954	1030	HAT-10_Mad	3134	3220	DNA/hAT	c	0.7692	2.1667	245

sequence05 (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
sequence05	1	41	TguERVL2b1_LTR	525	566	ERV/ERV3	c	0.8333	1.5000	242
sequence05	42	564	ERV3-7_PMaj-LTR	37	608	ERV/ERV3	c	0.8012	1.5192	2012

sequence06 (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
sequence06	1	3910	AviRTE_MUn	14	3958	NonLTR/RTE	d	0.9382	1.3471	30997

sequence07 (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
sequence07	5	78	tRNA-Asp-GAY	1	75	Multicopy_gene/tRNA	d	0.8667	2.2500	431
sequence07	89	144	TguSINE1	77	132	NonLTR/SINE/SINE2	d	0.9821	1.0000	511

sequence08 (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
sequence08	45	809	eBHBV2	421	1192	IntegratedVirus/DNAV	d	0.6849	1.8020	1030
sequence08	1020	1087	L1_AC_10	3950	4020	NonLTR/L1	d	0.7429	1.5000	227
sequence08	1248	2766	eBHBV1	2632	4188	IntegratedVirus/DNAV	d	0.7205	2.0238	3611
sequence08	2807	2896	MER50I	4285	4370	ERV/ERV1	d	0.7356	1.5000	263

sequence09 (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
sequence09	306	378	tRNA-Met_OS	7	77	Multicopy_gene/tRNA	d	0.7500	1.7000	275

sequence10 (SVG Plot; Alignments; Masked)

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

sequence10	29	76	Harbinger-N47_OS	1871	1914	DNA/Harbinger	d	0.8043	1.1667	238
sequence10	252	360	CR1-X1_Pass	4316	4424	NonLTR/CR1	d	0.9725	1.0000	882
sequence10	407	617	Mariner-25_SIn	1071	1281	DNA/Mariner	d	0.6934	2.1852	549

Masked Sequence

```
>sequence01
TTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAG
GGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTT
AGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGG
TTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAG
GGTTAGGGTTAGGGTTAGGG
>sequence02
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGCCGGTA
TTTACAGAACCCCCCCGCCCCCGGGGGGTTGGGGGGGGGAAACCAAGCAGCCGCAGATGACTTCCTGCCACT
TAATCCGCGCGCCGGCCTCCGCAGCCCCCAAGCACCCGCCGGGACTGGGCTGAAACCAGCGCCTCGTCCT
CGAACTGCGCCAAAGTTCCTTCAGTCCCTTCTGGCCACCCTTTCCGGACTGCGXXXXXXXXXXXXXXXXX
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>sequence03
CATGGAGATGCTCCAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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>sequence04
TACGAGGCCGGCCCCCAGGGACACACAAGAGCAGGATACACACACACACGAGAGGCCAGGCTCCAGAGAGA
TGTAGGAGCAGGGGACACAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXAGAGCAGGATACACACACACACGAGAGGCCAGGCTCCAGAGAGATGTAGGAG
CAGGGGACACACXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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>sequence07
AAAAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXGTGGTGCGGTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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>sequence08
AATTCACCTTGCCACCTATAATTCGTTGATATATACTTTGATTCXXXXXXXXXXXXXXXXXXXXXXXXXXX
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CAGAACTTACTTTACAAAGAATGGGTCAAACAATGCCTATCTCAGGAATGAATCCATGGGTACCAACACA
ATATCCCTTCGGCCTGAATGGGCCAGACCTAACGCCATATTACTGGAAAACAGAAATGGAGGAATTAAAG
AAAATGGGCCTCACTCCTGGCAGTCCGGTTGCTCCTCCGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAGCCAGCAGCACTTATCAATCAAGAAACAGAGC
AGATCCTGGCAGAGCTCTGTCGCCGACTGCTCCCGTGTTCAAAAGGCCCACATCAACTTCAACAAATTCT
TCGGCACCAACAGTGAGTTGGGCACTGCCAGCAGTGGTAAAGGAACCACATCCAGTGXXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTTATGAGGTTATACAAGCTTTAGAAAAGGCGGCT
ACAGCTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTAAGTTGCTCCTACCTTACCAATTGAAAATCAAATTGG
>sequence09
TGTAGTGAAATGAGGCAACCAGGTGCCACTAATTGCCAGGGAGTGGGCATGAGCTTGTGTTAAGCCCACC
TGTGCCTGATTAAGGCAGGCCCCAACTGCGCATGAGCAGGATTAGGGGGCCAATAAAAGGTAAGGCCTGA
ACTCACAAGCTCAGCTCACGCTGGAACTCACAACCTCGGCATGCTTGGCTTTTWACTGCTTCTATGAGCA
CCGYGCTAACCTGACTGCRCCCCTGGAGCTTTGTCTCAGCACCGCACTAACTTGGTTGCGCCATCAGAGC
TCTTCACCACTAGGGTGAGGCTCGAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXACCCTAGTGGTGAAGAGCTCTGATGGCGCAACCAAGTTAGTG
CGGTGCTGAGACAAAGCTCCAGGGGCGCAGTCAGGTTAGCGCGGTGCTCATAGAAGCAGTWAAAAGCCAA
GCATGCCGAGGTTGTGAGTTCCAGCGTGAGCTGAGCTTGTGAGTTCAAGCCTTACCTTTTATTGGCCCCC
TAATCCTGCTCATGCGCAGTTGGGGCCCGCCCCTAATCAGGCACAGGTGGGCTTAACACAAGCTCATGCCC
ACTMCCTGGCAATTAGTGGCACCTGGTTGCCTCATTTCACTACA
>sequence10
TGAGGTCCGACACAAAAAACCTGAGACTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXGGTTATAGAACATGTTCTAACCTGTCACAGTGAGACAAGGCTCAACTCGATCGCTTCACTCAGT
ATGAGTGGACACGTGTTCAAATATAGACGTTTTCTTACCCTCGGTTGGAAAATGTCGGTGTGCAAGAGTG
AACAGCGAGTTAACATCACGTTTCTTGTGAAACTGAAGAAAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXGTGACGGAAACTTTTCAATTATTGACTGAGGCTTATGGTGAAGAGAXXXXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAGAGTTACAGGCA
CAGTCTCGKTTTTTTTGTGTCGGACCTCA
```

Local Alignments*

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
sequence02	1	63	hAT-N4_XT	1	63	d	0.9206	1.6667	439

```
1 CAGGGGTCCTCAAACTACGGCCCGCGGGCCGGATACGGCCCCCCAGGGTCCTCAATCCGGCCC 63
  ||||||||||||||||||||||||||||||||||||||||||||||||||:||||  |: |: |:||||||||
1 CAGGGGTCCTCAAACTACGGCCCGCGGGCCGGATACGGCCCCCCAAGGTCATTTACCCGGCCC 63
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
sequence02	264	362	Chompy-1934B_Crp	415	510	c	0.7475	1.7000	245

```
264 CGGCCGGG--CTGAGGAGGGGGCCG--CGGCATCAGCGAGG-GGGGCGGCTCCCCCGTCTCTCCCTCCCT 328
    | ||||||--|| :||:||||||| |--|||-::| ||||||-|||| ||||||---||-||:||| |||:
510 CNGCCGGGGCCTCGGGGGGGGGCGGGCCGG-GCCCGCGAGGCGGGGGGGGCTCC---GT-TCCCCCGCCCC 446
```

```
329 CCCTCCAGCTCCCAGGCAGGACAAGCAAGCCAGC 362
    |||:|||||||||-:|||: |:|||--|||||||||
445 CCCCCCAGCTCC-GGGCGCGGCAA--AAGCCAGC 415
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
sequence02	382	2395	hAT-2_ET	1088	3105	d	0.9022	1.8660	14672

```
 382 ACCATCATGTCAAAAAAAAGAAAAATTTACTCCGAGTGCAGGGTATTCCAAGAAAAGTGGATTTTTGATT 451
     || || ||:|||||:|||:||||||||| |||| |||||:|||:||||| ||||| ||||||:|| |||||
1088 ACAATGATATCAAGAAAGAGAAAAATTGACTCGGAGTGTAGGATATTCAAAGAACAGTGGACTTATGATT 1157
```

```
 452 ATTTTTCCACGGAATACAAAGAAAGAGCTGTTTGTCTGATATGCCAGAATTCAGTGTCTGTGTTCAAGGA 521
     |:||||:||:| |:|||||:|||||||||||| |||:|||||||||||||| :||||||||||||||:||
1158 ACTTTTTCATGCAGTACAAGGAAAGAGCTGTGTGTTTGATATGCCAGAATATAGTGTCTGTGTTCAAAGA 1227
```

```
 522 ATACAATTTGCGTCGACACTACGAAACTCAACATAAAGATAAATATGATTCTTTGGTCGGACAAGTGAGA 591
     ||||||||||||||||||||||||||: |||||||||||||||||||||||| |||||||||| ||||||||
1228 ATACAATTTGCGTCGACACTATCAAACTCAACATAAAGATAAATATGATTGTTTGGTCGGAGAAGTGAGA 1297
```

```
 592 AAAGATAAAATATTAAGACTGAAACATGGATTGACAACTCAGCAAAATACTTCTGTGAAGCAAAAGCAGC 661
     |||||||||||||||:||||||| ||: |||||||||||||||||||||||:|||||||||:||||||||
1298 AAAGATAAAATATTAAAACTGAAAAATACATTGACAACTCAGCAAAATACTTTTGTGAAGCAGAAGCAGC 1367
```

```
 662 TCAATATATCATCACTTSGAGCAAGCTATCAAGTTGCCAAGCTCATAGCGCGCACTTGMAGAGCATTCAT 731
     | |||||| ||||||||  ||||||:| |||||||||||||||||| ||||||:||||| | ||| ||||:|
1368 TAAATATTTCATCACTGCGAGCAAGTTTTCAAGTTGCCAAGCTAATAGCGTGCACTGGCAGACCATTCGT 1437
```

```
 732 AGAGGGAGAATTTGTTAAAGAATGCCTTCTTTCTGTTGCCAAAGAGATGTGTCCAGAGAAGGCGGATTTA 801
     :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
1438 GGAGGGAGAATTTGTTAAAGAATGCCTTCTTTCTGTTGCCAAAGAGATGTGTCCAGAGAAGGCCGATTTA 1507
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 802 TTTAGTACAGTGAGTTTTTCAGGACCTACAATTACACGAAGGATTGAAGAAATGGGGGAAAATTTGAATC 871
     ||||||||||||||||:|||||||||||||||||||||||:||||||||||||||||||:|| |||||| |||
1508 TTTAGTACAGTGAGTCTTTCAGGACCTACAATTACACAAAGGATTGAAGAAATGGGAGACAATTTGCATC 1577
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 872 TGCAGTTGCAAAACTCCTCGAAAAAACTTTGCTATTTCTCATTGGCACTCGACGAAAGCAATGATGTTCG 941
     ||| ||||||||||| |:|||||||||| |||||||:|| ||||||||||||||||||||:|||||||||||
1578 AGCATTTGCAAAACTCCGCAAAAAAACTTTCCTATTTTTCCTTGGCACTCGACGAAAGTAATGATGTTCG 1647
```

```
 942 TGATTCTGCACAACTTCTAATTTTTCATTCGTGGGACAAATGATTCTTT-TGAAGTCACAGAGGAGCTTGC 1010
     ||||||||||||||||||||||||||:|||||||||::||||||:| |||--|||||||||||:||||||||
1648 TGATTCTGCACAACTTCTAATTTTTATTCGTGGGATGAATGACTATTTB-GAAGTCACAGAAGAGCTTGC 1716
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1011 TGCACTGAAAAGCATCAAAGGAACAACTACAGGAGAGGATATCTATGAGAAAGTTTGCCAAACTATGAAT 1080
     |||||||| |||||||||||||||||||||||||||||||||||||||||:||:||||||||||||:|||||
1717 TGCACTGCAAAGCATCAAAGGAACAACTACAGGAGAGGATATCTATGAAAAGGTTTGCCAAACTGTGAAT 1786

1081 GATTTGGAGCTGGACTGGGGTAAACTATTCAGTGTGACAACTGATGGTGCTCCTAGCATGGTGGGGTCCA 1150
     |:|||||||||||||||||| ||||||| :|||||||||||||||||||||||||||||||||||||||:|
1787 GGTTTGGAGCTGGACTGGGCTAAACTAGCCAGTGTGACAACTGATGGTGCTCCTAGCATGGTGGGGTCTA 1856

1151 TGAAAGGAGTGGTTGCACGCATTAACAAAGAGATGGACAAACGCAACCATTCACATCCAATAGCCATACA 1220
     |||||||||::||||| ||||||||| ||||||||||||||||::||||||| ||||||||||||||||||
1857 AGAAAGGAGTAATTGCTCGCATTAACCAAGAGATGGACAAACATAACCATTCTCATCCAATAGCCATACA 1926

1221 CTGCATCATCCACCAACAAGCACTGTGTTGTAAATCACTGAAGCTGGACTCTGTCATGAAAATTGTAGTT 1290
     |||| |||||||||||||||||:|||||| |||||||||||||||: |||||||||:||||||||||:||
1927 CTGCCTCATCCACCAACAAGCGCTGTGTAGTAAATCACTGAAGTGGGACTCTGTTATGAAAATTGTGGTA 1996

1291 TCTTGTGTTAACTTCATTAGAGCTCATGCACTAAACCACAGACAGTTTCAGGAATTTCTGTCTGAGCTAA 1360
     ||||||||||||||||||||||||| |||||||||||||||||||:|||||||||||||||||||||||||
1997 TCTTGTGTTAACTTCATTAGAGCTAATGCACTAAACCACAGACAATTTCAGGAATTTCTGTCTGAGCTAA 2066

1361 ATGTTGCCTATGAAGATATTCTGTACCACACAGAAGTCCGTTGGCTGAGTCGAGGGAGAGTTTTTGAAAT 1430
     ||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||-||||:
2067 ATGTTGCCTATGAAGATGTTCTGTACCACACAGAAGTCCGTTGGCTGAGTCGAGGGAGAGTTTT-GAAAC 2135

1431 GATTTTATGACTTACTTCCACAGGTTTATGATTTTATGCTTTCTAAAAACAAAGAAGTACCAGAGCTCAA 1500
     : ||:|||||||||||||||:|| | |||| ||||||||||||||||||||||||||||||||||
2136 ATTTCTATGACTTACTTCCACAGATTACAGCTTTTCTGCTTTCAAAAAACAAAGAAGTACCAGAGCTCAA 2205

1501 AGATGCAGAATGGAAATGGCACCTTGCGTTTCTGACAGATGTAACAGAGCTACTCAACAATTTCAATGTC 1570
     ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||:||||||||||
2206 TGATGCAGAATGGAAATGGCACCTTGCCTTTCTGACAGATGTAACAGAGCTACTCAACAGTTTCAATGTG 2275

1571 CAACTTCAAGGAAAGGGGAAGCTCATCTGTGATATGTATTCACATGTGAAAGCATTTCAAGTCAAATTAG 1640
     |||||||||||||||||||||||||||||||||||||:| |||||||||||||||||| |||| |||||||
2276 CAACTTCAAGGAAAGGGGAAGCTCATCTGTGATATGCAATCACATGTGAAAGCATTTGAAGTAAAATTAG 2345

1641 ACCTGCTCATTAACCAAGTAAAGGAGGAAAACTTCTGCCATCTCCCCACAACTCAAAACCTGTCTGCAGA 1710
     :||| ||||||:|| |||||:|||||||||:||||||||||||||||||||||||||:||||: ||:||
2346 GCCTCCTCATCAAACAAGTGAAGGAGGAAAATTTCTGCCATCTCCCCACAACTCAAAATCTGTTAGCGGA 2415

1711 AAAACCAGCAGTTGCATTCCCAAACAAAACATGTATGGATGTACTAGAAATGTTGCAAAAGGAGTTTCAA 1780
     ||||||| ::|||||||||||||||||||||:||||| :|||:|||| ||||||||||||||||||:|||
2416 AAAACCATTGGTTGCATTCCCAAACAAAACATGTGTGGATTCACTGGAAAAGTTGCAAAAGGAGTTCCAA 2485

1781 ATTAGATTTAAAGAGCTTCGTCTCCATGAACAGGACATACAGCTTTTCCGGAACCCATTTTCTGTTGACA 1850
     |||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||:||||||
2486 TTTAGATTTAAAGAGCTTCATCTCCATGAACAGGACATACAGCTTTTCCGTAACCCATTTTCTATTGACA 2555

1851 TTGAAACTGTTGATCCGATTTACCAAATGGAATTGGCCGAACTACAGACTTGTGACTCGCTGAAAGATGC 1920
     |||||| ||| ||| |:|||||||||||||||:|||||:|||||:|||| ||||||||| ||||||:||
2556 TTGAAAATGTGGATACAATTTACCAAATGGAACTGGCTGAACTGCAGAATTGTGACTCTCTGAAAGACGC 2625

1921 ATTCAAATCAAGCAGCCTTACTAATTTCTA-TGCATCTCTCCCCTCAGAGACATATCATAATCTCAGGAA 1989
     ||||||:|||||||||||| |||||||||--|||||||||||||| ||||||||||| ||||||||||||
2626 ATTCAAGTCAAGCAGCCTTCCTAATTTCTAB-GCATCTCTCCCCTCTGAGACATATCCTAATCTCAGGAA 2694

1990 CCATGCACTCAAAATTGCAACCATCTTTGGCAGCACCTATGTCTGTGAGCAGACTTTTTCCCGAATGAAA 2059
     |||||||||||||||| |||||||||||||||||||:|||||||||||:|||||||||| |||||||
2695 CCATGCACTCAAAATGGCAACCATCTTTGGCAGCACTTATGTCTGTGAACAGACTTTTTCCAGAATGAAA 2764

2060 CATCTGAAATCTCCAATCAGATCCAGACTAACTGATGAACACTTGCATCACTTGCTACGACTAGCAGTGA 2129
     ||||||||||||||||:||||||:|||||||||||| |||||||||||||||||:||||||||||||||
2765 CATCTGAAATCTCCAACCAGATCTAGACTAACTGATGCACACTTGCATCACTTGTTACGACTAGCAGTGA 2834

2130 CAAATATGGAACCTAACATTGACCATCTCATTAGCCAAAAGCAGGCCCATAGTTCACATTGAAATATTAT 2199
     ||||||||||||: :|||||||||||||||||||||| |||||||||||||||||| ||||||||:|:-
2835 CAAATATGGAACTGGACATTGACCATCTCATTAGCAAAAAGCAGGCCCATAGTTCCCATTGAAATACTG- 2903

2200 TTGT--TTTTGTTGATT--AC---AATTGTTCTTCATTTTAAATATTGCATTCTTTTTCC----TGTTTT 2258
     --||-- |||||||||--||---| ||||||||||||||||||||||||:|||-| ||:||----|||||
```

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2904 --GTAAGTTTGTTGATTTAACTTTACTTGTTCTTCATTTTAAATATTGTATT-TGTTCCCATTTTGTTTT 2970


2259 TTTGTGCACTACTACAAA-TAAAATATGTGCAGTGTGCATAGGAATTCGTTCAT----TTTTTTCCAAAC 2323
     |||------|||| ||||-|||:||||||||||||||||||||||||:||||||----||||||::||||
2971 TTT------TACTTCAAAATAAGATATGTGCAGTGTGCATAGGAATTTGTTCATAGTTTTTTTTTTAAAC 3034


2324 TATAGTCCGGCCCCCGACAGTG-TCTGAGGGACAGTGAACCGGCCCCCTGTTTAAAAAGTTTGAGGACCC 2392
     |||||||:||||||:|--||:||-|||||||||||||||||:||||||||||||||||||||||:|||||
3035 TATAGTCTGGCCCTC--CAATGGTCTGAGGGACAGTGAACTGGCCCCCTGTTTAAAAAGTTTGAAGACCC 3102


2393 CTG 2395
     |||
3103 CTG 3105
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
sequence03	16	437	CR1-E_Pass	2650	3078	d	0.7471	2.0408	1587

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  16 AGGGCTGGAGCCCCTCTGCTCTGGAGCCAGGCTGGGAGAGCTGGGGGTGCTCA-CCTGGAGAGGAGAAGG 84
     |||:||||||| ||||:| || :|:|| |||||||:||:||:||||| ||:|||-||||||||:|||||||
2650 AGGACTGGAGCACCTCCCCTACGAAGACAGGCTGAGAAAGTTGGGGCTGTTCAGCCTGGAGAAGAGAAGG 2719

  85 CTCCAGGGAGAGCTCAGAGCC-CCTKSCAGGGCCTAAAGGGG--CTCCAGGAGAGCTGGAGAGGGACTGG 151
     :| |: ||||| |||| ||| -||| ||| ::||:||||||--|| ||||::|||:||||||||||
2720 TTGCGTGGAGACCTCATAGCAACCTTCCAGTATCTGAAGGGGGCCTACAGGGAAGCCGGAGAGGGACTCT 2789

 152 GGACAAGGGA-TGGAGGGACAGGACACAGGG-AATGGCTCCCA-CTGCCAGAGGGCAGGGCTGGATGGGA 218
        :: |||:|-|| || ||:|||||| :|:|-||||| | | |-||| |||||| |:: :|:|:| :||
2790 TCGTCAGGAACTGTAGTGATAGGACAAGGAGTAATGGGTACAAACTGAAAGAGGGGAAATTTAGGTTAGA 2859

 219 TATTGGGAAGGAATTGTTCCCTGGGAGGGTGGGCAGGCCCTGGCACAGGGTGCCCAGAGCAGCTGTGGCT 288
     ||||:|||||:|||| ||: ||| ||||||||  ||:| |||| ||||| ||||||||:| :|:|||||| |
2860 TATTAGGAAGAAATTCTTTACTGTGAGGGTGGTGAGACACTGGAACAGGTTGCCCAGGGAGGTTGTGGAT 2929

 289 GCCCCTGGATCCCTGGCAGTGCCCAAGGCCAGGCTGGACGGGGCTTGGAGCAGCCTGGGACAGTGGGAGG 358
     |||||---| ||||||||||||::||||||||||:||||::|||:| |||||:||||| :||||||||||
2930 GCCCC---ANCCCTGGCAGTGTTCAAGGCCAGGTTGGATAAGGCCTTGAGCAACCTGGTCTAGTGGGAGG 2996

 359 TGTCCCTGCCCGTGGCAGGGGG---TGGAACGAGATGAGCTTTAACGTCCCTTCCAACCCAAACCATTCT 425
     ||||||||||:||||||||||---|||:|| |||||| |||||| |||| |||||||| | |||||
2997 TGTCCCTGCCCATGGCAGGGGGGGTTGGGACTAGATGATCTTTAAGGTCCNTTCCAACCCTTAACATTCT 3066

 426 GTGATTCTGTGA 437
     :||||||||:|||
3067 ATGATTCTATGA 3078
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
sequence04	501	953	hAT-N3_CM	321	679	d	0.7413	1.8684	654

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501 ACACACACACACACATACGAGGCCGGCCCCAGGGACACACAAGAGCAGGATACACACACACACGAGAGGC 570
    ||||||||| |||||---|||: |:|| || : ||||||-|||--:||:||||||||||| ||||--
321 ACACACACAGACACA---GAGAGAGACCACACACTCACACA-GAG--AGACACACACACACACCAGAG-- 382

571 CAGGCTCCAGAGAGATGTAGGAGCAGGG-GACACACACACACACACACATACGAGGCCGGCCCCAGGGAC 639
    --------|||||||:::| : :|||:|-||||||||||| |||| |||:|-|||---------||:|||
383 --------AGAGAGACACACACAGAGAGACACACACTCACAGACACA-GAG---------AGAGAC 434

640 ACACA-------AGAGCAGGATACACACACACACGAGAGGC-CAGGCTCCAGAGAGATGTAGGAGCAGGG 701
    |||||-------|||| ::||:||||||||| |||---||:|-|||-----|||||||:::|    |||:|
435 ACACACACAAACAGAGAGAGACACACACACTCAC---AGACACAG-----AGAGACACATTCTCAGAG 496

702 GACACACACACACACACACATACGAGGCCGGCCCCAGGGACACACAAGAGCAGGATACACACACACACGA 771
    -| | |||| |||| |||||||-|||---------||:||||||||||---||||---||||| |||||-|
497 -AGAGACACTCACAAACACATA-GAG---------AGAGACACACA----CAGG---CACACCCACAC-A 547

772 GAGGCCAGGCTCCAGAGAGATGTAGGAGCAGGGGACACACACACACACACACATACGAGGCCGGCCCCAG 841
```

```
     ||||---------||||:||------------|||||| |||:|| ||||||| ||:-------|:|--
548 GAGG---------AGAGGGA------------GACACAGACATACTCACACAGACA--------CTC-- 585


842 GGACACACACAAGAGCAGGATACACACACACACGAGAGGCCAGGCTC-CAGAGAGATGTAGGAGCAGGGGAC 910
    --||| |||||||| ::||:|||||||||||||-| ||:|---:|||-||:| : ||:|||:-----|:|||
586 --ACAAACAAGAGAGAGACACACACACAC-ACAGAC---ACTCACAAATGCATATAGA-----GAGAC 644


911 ACACACACACACACACATACGAGGCCGGCCCCAGGGACACACA 953
    |||||||||||||||||| ||:--------| |||:|||||||||
645 ACACACACACACACACAAACA--------CACAGAGACACACA 679
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Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
sequence04	90	438	hAT-N3_CM	345	679	d	0.7281	1.7838	557

```
 90 CACACACACACACATACGAGGCCGGCCCCAGGGACACACAAGAGCAGGATACACACACACACGAGAGGC- 158
    ||||||| |||||| |-|||:| :| |-----|||||| |||| ::|| |||||||||||-|||||:|-
345 CACACACTCACACAGA-GAGACACACAC-----ACACACCAGAGAGAGAGACACACACACA-GAGAGACA 407


159 --CAGGCTC-------CAGAGAGA------TGTAGGAGCAGGG---GACACACACACACACACACATACG 210
    --|| :|||-------|||||||||------:::| :|:|||:|---|||||||||| |||| |||:|-|
408 CACACACTCACAGACACAGAGAGAGAGACACACACACACAAACAGAGAGAGAGACACACACTCACAGACACA-G 476


211 AGGCCGGCCCCAGGGACACACA---AGAGCAGGATACACACACACAC-----GAGAGGC-----CAGGC- 266
    ||---------||:||||||: ---|||| ::||:|| |||| ||||-----|||||:|-----|||||-
477 AG---------AGAGACACATTCTCAGAGAGAGACACTCACAAACACATAGAGAGAGAGACACACACAGGCA 537


267 --TCCAGAGAGATGTAGGAGCAGGGGACACACACACACACACACACATACGAGGCCGGCCCCAGGGACACAC 334
    --:||| | |||----|||| :||:||||||| |||:|| ||||||| ||:-------|:|-----||| ||
538 CACCCACACAGA----GGAGAGGGAGACACAGACATACTCACACAGACA-------CTC-----ACAAAC 591


335 AAGAGCAGGATACACACACACACGAGAGGCCAGGCTC-CAGAGAGATGTAGGAGCAGGGGACACACACAC 403
    ||||| ::||:|||||||||||||-| ||:|---:|||-||:| : ||:|||:-----|:|||||||||||
592 AAGAGAGAGACACACACACACAC-ACAGAC---ACTCACAAATGCATATAGA-----GAGACACACACAC 652


404 ACACACACATACGAGGCCGGCCCCAGGGACACACA 438
    ||||||||| ||:--------| |||:|||||||||
653 ACACACACAAACA--------CACAGAGACACACA 679
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
sequence04	954	1030	HAT-10_Mad	3134	3220	c	0.7692	2.1667	245

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 954 AGAGCAGGATACACACACACACGAGAGGCCAGGCTC-CAGAGAG--------ATGTAGGAGC-----AGG 1009
     ||||||---:|||||||||||||-||| : |: || |-||| | ||--------||||||:| |-----||:
3220 AGAGCA---CACACACACACAC-AGACAGCGCGCACACACACAGTCTTGATAATGTAGAATCCGATGAGA 3155


1010 GGACACACACACACACACACA 1030
     |:||||||||||||||||||
3154 GAACACACACACACACACACA 3134
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
sequence05	1	41	TguERVL2b1_LTR	525	566	c	0.8333	1.5000	242

```
 1 TGTACTGGTTTGAAAACAGA-CCAGTGGGAGGCACCAAGTCA 41
   ||| |||||||||||:||:|-||||||:|||:| |||||||||
566 TGTTCTGGTTTGAAAGCAAAACCAGTGAGAGACTCCAAGTCA 525
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
sequence05	42	564	ERV3-7_PMaj-LTR	37	608	c	0.8012	1.5192	2012

```
42 GAATAACAATT---TATTAGGGAAATTAAAA-ATAAAGGCA-------AGAAAAACC--CCAGTGGGCTA 98
   |||||||||:||---||:|||||:||||||||-| ||| |||-------|:|||||||--|||--------
```

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608 GAATAACAGTTCTTTACTAGGAAAATTAAAATAAAAATGCAGTAGTACAAAAAAACCAACCA-------- 547

 99 AACTAACAGAGTCAGAATACAACCTGGCACCCTGTTAATCAGGGTGGCGTGAGCAGTCCGATGAGATGGT 168
     --||:|||||||||||||||||:|||||||||::|||||||| :|  |||||||||| |:|||||
546 --CTGACAGAGTCAGAATACAACCTGACACCCTGTTGGTCAGGGTGTTGGTAGCAGTCCGATTAAATGGT 479

169 GGCTGTAGTCCTCCTGAAGTGATGGATGTGGCTCTGTCGAAGCAGTGGTCCAGTAGAAAGGTCTGCTCCT 238
     |||||:||||||||||| |||||::|||||||:|||||:|||||||||:||| |||||||:||| |: |::|
478 GGCTGCAGTCCTCCTGSAGTGACAGATGTGGTTCTGTTGAAGCAGTGATCCTGTAGAAGGGTGTAGTTTT 409

239 CCTCAGAAAGTCCAGTGGTGACTATGCAGCT--------CCTGTCCTCTGGGAATCCAGTGGG--AAGGA 298
     |||| |||:|||||||||||:---||:|| |--------:|| |||||||||||||||||||:--||||
408 CCTCTGAAGGTCCAGTGGTGG---TGTAGATGGGTCTGGTCTTTCCTCTGGGAATCCAGTGGAGAAAGGC 342

299 TGCCCGTGGTGTTCAGAGTCCCAGATTATATCCAAGATGGAACGCTTGGTTCCTCCCTCTGGGTGGAGCA 368
     ||||:|||||||||| :|||||:|||||||||||||:|   ||||:||||||:|||||||:|||||||||||
341 TGCCTGTGGTGTTCCAAGTCTCAGATTATATCCAGGTAGGAATGCTTGGCTCCTCCCCCTGGGTGGAGCA 272

369 TCTCACAATRGAATGATG----------AGTCATGAGGCCAGGTGTTGATGGGCTCATTAACAGAAGATA 428
     |||||||||+|:||||||----------||||||| :|: ||::-|::||||-|:|||||||||||||||
271 TCTCACAATGGGATGATGTAATTTTATCAGTCATGCAGTGAGAC-TCAATGG-CCCATTAACAGAAGATA 204

429 GTCC---GGAGGGAGTTATCTCTGAGTCATGCGGCAGGG--------CATTGA----------------- 470
     :||---||||||| ----- ||:||---|:|| ||:|--------||:|| -----------------
203 TCCCCCTGGAGGGAGG-----ATGGGT---GTGGAAGAGATAAAGAACACTGCCMCACCTGGTTTTAACA 142

471 --TGGGCCATTAGCAGAAAGATAGTCC--GGAG----GGAGGA--GGCCA-GGAA----------ACACC 519
     --||| |||||||:|||||-|||| :||--||||----|::|||--||:||-||||----------||||:
141 GCTGGCCCATTAACAGAA-GATATCCCCTGGAGTTATGAGGGATGGGTCATGGAAGAGATAAAGAACACT 73

520 GCCCCACCTGGTTTCAACAGCTCATGAGGATGGTAATAGAATACA 564
     |||||||||||||:|||||---------|||||||||||||||||
 72 GCCCCACCTGGTTTTAACAG---------ATGGTAATAGAATACA 37
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
sequence06	1	3910	AviRTE_MUn	14	3958	d	0.9382	1.3471	30997

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  1 CACCCCCTTGTTGTGGGGAAAGAGCTCACCTGCCCTTGTGAGGTTGGGAGCTATGCTGGTGGTGGCATAT 70
     ||||||||||:|||||||||||||||::| ||||||||||||||||||||||||||||||||||||||||
 14 CACCCCCTTGTCGTGGGGAAAGAGCTTGCGTGCCCTTGTGAGGTTGGGAGCTATGCTGGTGGTGGCATAT 83

 71 GCCTCCAGTAGGGTCTCCCATGCCAGACGAGTCTCAACTGAAGGGTCA----AAGTGTGTCCATTGGCAG 136
     ||||||:||||||||||||||||||||::|||||||||||||||||||----||||||||||||| |||||
 84 GCCTCTAGTAGGGTCTCCCATGCCAGACAGGTCTCAACTGAAGGGTCAGACAAAGTGTGTCCATGGGCAG 153

137 GATGGGCTCACCAGCCTTAGGGCTACCATCCTAGGAGAAGGACAACTCTAACTTCAAACCCAGGCAGATG 206
     |||||||||||:||||||| |||| |||||||||||||||||||||||||||||||||||||||||||||||
154 GATGGGCTCACTAGCCTTTGGGCAACCATCCTAGGAGAAGGACAACTCTAACTTCAAACCCAGGCAGATG 223

207 GAGCTCGTTTAGCCCTGTAAGGCCACCCATCTAAGAGAAGGATACTCTAATTAAACCTACGACCTGAGGA 276
     |||||||||||||||||||||||||||:|||||||||||||||||||||||:|||||||:||||||||||
224 GAGCTCGTTTAGCCCTGTAAGGCCATCCATCTAAGAGAAGGATACTCTAATCAAACCTATGACCTGAGGA 293

277 CCTTGCTGCCACCATCCAAGCTCGCTAGGCCCTGGCAGATAAACCTCAGGTGTAAAGGGTGGGGCCAGTT 346
     |:|||||:||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
294 CTTTGCTGTCACCGTCCAAGCTCGCTAGGCCCTGGCAGATAAACCTCAGGTGTAAAGGGTGGGGCCAGTT 363

347 CCACGCATGCTGTGCTTCACCTAAAAAATCCACTGCACAGGCCTGAAGGGTTTACCCACACTTGCAAAGC 416
     |::|||||||||||:|||||||||||||||||||||||||||:|||||||||||||||||||||||||||
364 CTGCGCATGCTGTGCCTCACCTAAAAAATCCACTGCACAGGCCCGAAGGGTTTACCCACACTTGCAAAGC 433

417 CCTGTAGCGACAGGCGAGGGACAAAACGGCAGGTGATAAGGTGCACTGGAAGCTTCAGACCCAGCCCTGC 486
     ||||||||||||||||||||||:|||||||||||||||||||||||||||||| : |||||||:||||||
434 CCTGTAGCGACAGGCGAGGGACGAAACGGCAGGTGATAAGGTGCACTGGAAGYCGCAGACCCAACCCTGC 503

487 ATGCAGGCAGTTCACGACATTGGTCGCTCGAGACTGACCCAGGAGATGACAGTCTTGTTTGACAGCATCC 556
     ||||||||:|||||| |||||||||||||||||||||||||||||||||||||||||||:||:||||||
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504  ATGCAGGCGGTTCAGGACATTGGTCGCTCGAGACTGACCCAGGAGATGACAGTCTTGTTTGGCAACATCC 573

557  TGAATGATCAAGCAGCCTTTTCTCAAGGAGAGCACTGCTTGCTCCATATGGAGAGAGGTCTAGAAAAGGT 626
     |||||||:|||||||||||:||||||||||||||||||||||||||||||||||||||||:|||||||||||
574  TGAATGACCAAGCAGCCTTTTTTCAAGGAGAGCACTGCTTGCTCCATATGGAGAGAGGCCTAGAAAAGGT 643

627  GGCCTAACCAAAGCTCATCTCCCCCTCCACCTGGTTGGCTAGCTGTGGCCAAAGGGCATCTTCTGTTGCG 696
     |||||||||||||||||||||||||||||||||||||||||||:|:|||||||| |||||||||||||||||
644  GGCCTAACCAAAGCTCATCTCCCCCTCCACCTGGTTGGCTAGCCGCGGCCAATGGGCATCTTCTGTTGCG 713

697  GTCGATCAAAGGCA--GAGACAAAGGCATACACCTGCCTCCAAAGGTGTGTCCAGATTGACACTCACATG 764
     |||||||:|||||:||--|||||||||||||||||||||||||||||||||||||||||||||||:||||
714  GTCGATTAAAGACAAAGAGACAAAGGCATACACCTGCCTCCAAAGGTGTGTCCAGATTGACACTCGCATG 783

765  TTGGAACATCAGAACCATGCTTGATACAGCAAACAGTGGGCGTCCTGAGCGCCGTTCTGCGCTAATTGCC 834
     |||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||
784  TTGGAACATCAGAACCATGCTTGATACAGCGAACAGTGGGCGTCCTGAGCGCCGTTCTGCGCTAATTGCC 853

835  CATGAACTGTCACGACTCAACATCGATATTGCTGCTCTCAGTGAAGTTCGCCTTCATGAGGAAGGTAGCC 904
     ||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
854  CACGAACTGTCACGACTCAACATCGATATTGCTGCTCTCAGTGAAGTTCGMCTTCATGAGGAAGGTAGCC 923

905  TTAAAGAACATGGTGCCGGCTACAAACTCTACTGGTCAGGCAAATCCAAAACTGAAAGTCATCTTTCTGG 974
     |||||||||||||||||||||||||:|| |||||||||||||||||||||||||||||||||||||||||
924  TTAAAGAACATGGTGCCGGCTATACACTCTACTGGTCAGGCAAATCCAAAACTGAAAGTCATCTTTCTGG 993

975  AGATGGCTTCATGATTAAAAACTCCATCATCTCTAAACTTGAAAATTTGCCGACAGGTCAATCCAATCTT 1044
     || |||||||||||||||||||||||||:|||||||||||||||||||||||||:|||||| |||:||| |
994  AGTTGGCTTCATGATTAAAAACTCCATCGTCTCTAAACTTGAAAATTTGCCGATAGGTCATTCCGATCGT 1063

1045 ATTATCTCCTTACGTCTTCCACTACACAATAAGCAACATATTGTTCTTTTCAGCATATGCGCTCCAACTC 1114
     ||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||::||||||||||
1064 ATTATCTCCTTACGTCTTCCACTACACAATAAGCAACATGTTGTTCTTTTCAGCATATATGCTCCAACTC 1133

1115 TGCAAGCTGACCCTGCAGAAAAAGACAAATTCTACTCTGACCTGTGTTGCCTCACCCAAAAGGTTCCTAC 1184
     ||||||||||||||||||||||||||||||||||||:||:|||:||:||||||||:||||||||||||||:
1134 TGCAAGCTGACCCTGCAGAAAAAGACAAATTCTACTCCGATCTGCGTCGCCTCACTCAAAAGGTTCCTAT 1203

1185 AGATGATAAGATCGTAATTCTTGGTGACTTCAACGCCCGGGTAGGTAAGAACTTTGAAGCCTGGAAAGGA 1254
     |||||||||||||:|||||:|||||||||||||||||||::||||||||||||||||||||||||||||||
1204 AGATGATAAGATCATAATCCTTGGTGACTTCAACGCCCAAGTAGGTAAGAACTTTGAAGCCTGGAAAGGA 1273

1255 GTACTAAGCAAGCACAGTGTTGGTAGCTGCAGTGATAATGTTCACCTCTAGCTAGAGTTTTGTGCAGAGC 1324
     ||||||:|||||||||:||||||||||||||||:|||||||:| ||:||||| |||||||||||||||||
1274 GTACTAGGCAAGCACGGTGTTGGTAGCTGCAATGATAACGGTCGCCTCTTGCTAGAGTTTTGTGCAGAGC 1343

1325 AGCAGCTCACCATCACCAATACTATTTTCCAGCAGAAAGACAGCCTGGAGACAACCTGGATGCATCCTTG 1394
     |||||||:|||||||||:||||||||||||||||||||||||||||| |:|||||||||||||||||||:|
1344 AGCAGCTTACCATCACCAACACTATTTTCCAGCAGAAAGACAGCCKGAAGACAACCTGGATGCATCCTCG 1413

1395 ATCTAAATATTGGCACCTTATTGATTATGTCTTAGTGGGCCAGAGAAATGCTCGTGATGTCTGTCACACC 1464
     |||||||:|||||||||||||||||||||||||||||| ||||||||||||:|||||||||||||||||||
1414 ATCTAAACATTGGCACCTTATTGATTATGTCTTAGTGCGCCAGAGAAATGTTCGTGATGTCTGTCACACC 1483

1465 CAAGTGATGCCTAATGCAGAATGTCAATCAGACCACAGCCTTGTGTGTTGCAAGCTTAACCTCCACTTCA 1534
     |:|||||||||||:|||||||||||||| |||||||| ||||||||:|||||||:|||||||:||||||||
1484 CGAGTGATGCCTAGTGCAGAATGTCAAACAGACCACCGCCTTGTGCGTTGCAAACTTAACTTCCACTTCA 1553

1535 AGGCCAAACCTAAGAGGGGCAGCATTCTGAGGAGGAGGCTCAAT----------------AGCTGCAAG 1587
     || |||||||||||||||||||:||||||:|||||||||||||||----------------||||||||-|
1554 AGCCCAAACCTAAGAGGGGCGGCATTCCGAGGAGGAGGCTCAATGTTAATAATCTTCAAATAGCTGCA-G 1622

1588 TGAGGGACAGCTTTCAGGCTAACCTTCAAACTAGGCTTGAAGACCATCTTATAGATTCTTCTCCTGAAGT 1657
     |||||||||||||||||||||||||||||||||||||||||||||+||||||||||||||||||||||||:
1623 TGAGGGACAGCTTTCAGGCTAACCTTCAAACTAGGCTTGAAGACCAYCTTATAGATTCTTCTCCTGAAGC 1692

1658 GCTTTGGTAACATATTAAAAATAGCATCCTGCAGTCCTCTGTAGAACCATTTGAGTTCTCCTTAAAGAAA 1727
     :|||||:|||||||||||||||||||||||||||||||||:|||||||:| ||||:||||||||||||||
1693 ACTTTGGCAACATATTAAAAATAGCATCCTGCAGTCCTCCGTAGAATCCTTTGGGTTCTCCTTAAAGAAA 1762
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1728 AACAAAGACTGTTTTGATGATAACAATCAGGAGGTCCAGGAACTGCTGGCAAAAAAAAGAGATCTGCCCA 1797
     ||||||||||| |||||:|||||||||||||||||||||||:|||||:||||:||--|||||||||||||
1763 AACAAAGACTGGTTTGACGATAACAATCAGGAGGTCCAGGAATTGCTGACAAAGAA--GAGATCTGCCCA 1830

1798 TCAAGCATGCCTTGCTCAGCCACTTTGCCATGTAAGAAATGCAGCCTTTCGTCTTGCATGCAGTAAACTC 1867
     |||||||::|||:||||:|||||||||||||||||||||| |||||||||||||||||||:|||||||||
1831 TCAAGCACACCTCGCTCAGCCACTTTGCCATGTAAGAAAAGCAGCCTTTCGTCTTGCATGYAGTAAACTC 1900

1868 CAACAGAAACTTCGAGACATCCAGAACAAGTGGTGGCTCAACCTAGCAGAAAAGACTCAACTATGGGCAG 1937
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||||| ||||
1901 CAACAGAAACTTCGAGACATCCAGAACAAGTGGTGGCTCAACCTAGCAGAAAAGACTCAATTATGTGCAG 1970

1938 ATTTGGGTGACCACAGAGGATTCTATGAGGCTCTGAAGGCAGTGTATGGACCCACATTTCAGGTTCAAAG 2007
     |||||||||||||||||||||||||||||||||||||:||||||||||||||||||| :|||||||||||
1971 ATTTGGGTGACCACAGAGGATTCTATGAGGCTCTGAAAGCAGTGTATGGACCCACATACCAGGTTCAAAG 2040

2008 CCCCT-A---AGTGCAGATGGCCAAATGCTTCTTATAGATAAAATCTCCATCCTGAATCGTTGGTCTGAA 2073
     |||||-|---||||||||||||||||||:||||||||:|||||||||||||||||||||:|||||||||||
2041 CCCCTTACTTAGTGCAGATGGCCAAACGCTTCTTACAGATAAAATCTCCATCCTGAATCATTGGTCTGAA 2110

2074 CATTTTCAAACACTCTTTAGTGCTAACCGTGTAGTCCAAGGCGTAGGAATCCAGCACATTTTACAACATC 2143
     |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
2111 CATTTTCAAACACTCTTTAGTGCTAACCGTGTAGTCCAAGGCGMAGGAATCCAGCACATTTTACAACATC 2180

2144 TGGTGAAAAATGAACTGGATATAGCCCGTACCATGGGAGAGACTCT-AAGGCTATACAGCAGGTGAAAAC 2212
     ||||||||||:|||:|||||||||||||| |||||||||||||||||-|||||||||||||||||||||||
2181 TGGTGAAAAACGAATTGGATATAGCCCCTACCATGGGAGAGACTCTTAAGGCTATACAGCAGGTGAAAAC 2250

2213 TGGCAAGGCAGCTGGGGTAGGCGGAATCCCACCAGAAAACTGGAATCACGAAGGCCAAGCACTTCATGCT 2282
     |||||||||||||||||| |:|||||||||||| |||| |||||| |||||:||||||||||||||||||
2251 TGGCAAGGCAGCTGGGGTCGACGGAATCCCACCCGAAATCTGGAAGCACGGAGGCCAAGCACTTCATGCT 2320

2283 AAATTTCACGAGCTAGTTGTGCGCTGCTGAGAACAAGGTAAATTACCGTCAGGTTTCTGTGATGGAATCA 2352
     ||||||||||||||||||||||||||:||:|||||||||||||||||||:||||:|||::|||||| |||||
2321 AAATTTCACGAGCTAGTTGTGCGCTGTTGGGAACAAGGTAAATTACCATCAGATTTTCGTGATGCAATCA 2390

2353 TCATCACTCTGTATAAGAAAAAAGGTGTAAAG--------CTCAAGCTACTGAGGTGTAACTCTGACCTC 2414
     |||||||||||||||||||||||||||||||||--------||||||:|||:|||||:|||||| || :|||
2391 TCATCACTCTGTATAAGAAAAAAGGTGTAAAGTCAGACTGCTCAAGTTACCGAGGTATAACTYTGCTCTC 2460

2415 CATTGCTGGAAAAACCCTTGCAAGAATACTATTGAACAGATTAGTATCCACTATCACAGAAGAACTTCTA 2484
     |||||||||||||||::|||||||||||||||||||||||||||||||:||:|||||:|||||||||||||
2461 CATTGCTGGAAAAATTCTTGCAAGAATACTATTGAACAGATTAGTACCCGCTATCGCAGAAGAACTTCTA 2530

2485 CCTGAAAGTCAGTGTGATTTCAGAGCTAATAGAAGTACCACAGACATGGTATTTGTTTTCAAACAACTGC 2554
     ||||||||||||||||:|||||| ||||||||||||||||||||||||||||||||:|||:|||||||||
2531 CCTGAAAGTCAGTGTGGTTTCAGAKCTAATAGAAGTACCACAGACATGGTATTTGTTCTCAGACAACTGC 2600

2555 AAGAGAAGTGTAGAGAACAGAATAAGGGTCTCTGTGTTACTTTTGTTGACCTCACCTAAGTTTTTGACAC 2624
     |||| ||||||||||||||||||||||||||| ||||:|||| |||||:||||||||||| |||:|||||||
2601 AAGARAAGTGTAGAGAACAGAATAAGGGGCTCTATGTAACTTTCGTTGACCTCACCAAAGCTTTTGACAC 2670

2625 TGTGAGCAGAAAAGGCCTGTGGCTGATCTTGGAACGATTAGGTTGTCCCCCCAGGTTCCTCAAAATGATT 2694
     |||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
2671 TGTGAGCAGAAAAGGCCTGTGGCTGATCTTGGAACGATTAGGTTGTCCCCCCAAGTTCCTCAAAATGATT 2740

2695 ATTCTGTTACATGAGGACCAGCAAGGCCAAGTCAGATATGGTGATGCACTCTCTGAACCATTCCCAATAA 2764
     |||||||||||||||:|||||||||||||||||||||||||:|||||||||||||+|| ||||||||||
2741 ATTCTGTTACATGAGGATCAGCAAGGCCAAGTCAGATATGGCGATGCACTCTCTGARCCCTTCCCAATAA 2810

2765 CCAGTGGTGTGAAACAAGGTTGCGTTCTCATACCAATTTTATTTACAATCTTCTTCAGCATGATGCTACA 2834
     ||| |||||||||||||||||||||||||::|||||:||||||:|||||||||||||||||||||||| ||
2811 CCARTGGTGTGAAACAAGGTTGCGTTCTCGCACCAACTTTATTCACAATCTTCTTCAGCATGATGCTYCA 2880

2835 AACGGCTATGGTAGACCTTGACAAACAAAACGGCATTTATATTCGATATCGTACTGATGGGAGCCTATTC 2904
     || ||||||||||||||||:|||:|||||:|||||||||||||||||||||||||||||||||||||||||
2881 AAGGGCTATGGTAGACCTCGACGAACAAAATGGCATTTATATTCGATATCGTACTGATGGGAGCCTATTC 2950

2905 AATCTAAGGCGACTGAAGGCCCACACTAAGACCCTAAATCATCTTGTCCATGAACTGCTTTTTGCTGACG 2974
     ||||||||||||||||||||||||||||||||||| |||||||||||:||||||||||||||||||||:|
```

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2951 AATCTAAGGCGACTGAAGGCCCACACTAAGACCYTAAATCATCTTGTCCGTGAACTGCTTTTTGCTGATG 3020


2975 ATGCCGCCATTGTTGCCCACACAGAAGCAGCTCTGCAGTGCTTAACATCTTGCTTTGCAGAGGCAGCTGA 3044
     ||||||||| ||||||||||||||||||||||||||||||||:|:|||||||||||||||:|||||:|||||
3021 ATGCCGCCCTTGTTGCCCACACAGAAGCAGCTCTGCAGCGTTTAACATCTTGCTTTGCGGAGGCGGCTGA 3090


3045 G-GTTTTGGGCTGGAAGTCAGTTTGAAGAAGACAGTAGTTCTCTGCCAACCTGCACCACAAGAAGATTAT 3113
     |- ||||||||||||||||||:||||||||||||||||||||:||||||||||||||||||||||||||||
3091 GCTTTTTGGGCTGGAAGTCAGCTTGAAGAAGACAGTAGTTCTCTACCAACCTGCACCACAAGAAGATTAT 3160


3114 CATCCTCCCCACATTACCATTGGCGAGTCAGAGCTTAAGTCAGTTCAGCAGTTCAGCTATCTGGGAAGCA 3183
     |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3161 CATCATCCCCACATTACCATTGGCGAGTCAGAGCTTAAGTCAGTTCAGCAGTTCAGCTATCTGGGAAGCA 3230


3184 TTATTTCCTCGGATGCCACAATCTACAAAGGGATAGACAACAGAATAGCAAAGGCTTATAGAGCCTTCAG 3253
     ||||||||||||||||||||:||| ||||||:||||||||||||||||||||||||| |||||||||||:|
3231 TTATTTCCTCGGATGCCACGATCGACAAAGAGATAGACAACAGAATAGCAAAGGCWTATAGAGCCTTCGG 3300


3254 AACACTACATAAAAGAGTCTGGTGCAACAAACACCTGGAGAAAAGTACAAAGATTAGTGTCTATAGAGCT 3323
     || ||| ||||||||||||||||||||||:||||||||:||||||||||||||||||||||||||||||:
3301 AAAACTCCATAAAAGAGTCTGGTGCAATAAACACCTGAAGAAAAGTACAAAGATTAGTGTCTATAGAGCC 3370


3324 ATTGTACTGTCTACTCTTTTATATGGGTCTGAATCATGGGTTATCTACCGTCATCACCTGCAACTCCTCA 3393
     |||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||:|||||||:
3371 ATTGTACTGTCTACTCTTTTATATGGGTCTGAATCATGGGTTATCTACCGCCATCACCTGCGACTCCTCG 3440


3394 GATGCTTTCATCAGCGCTGCCTCCTTACAAT-CTAAACATCCATTGGACTGACTATGTGTCAAATGTAAC 3462
     :|:||||||||||||||||||||| ||||||-|||||||||||||||||||||||||||||||||||| ||
3441 AACGCTTTCATCAGCGCTGCCTCCGTACAATTCTAAACATCCATTGGACTGACTATGTGTCAAATGTTAC 3510


3463 TGTCCTTGAACAGGCAGGGGTCACCAGTATTGAGGCT-TATTGCTGAAATCGCTGCTGCGCTGGGCAGGG 3531
     |||||||||||||||||||||||||||||||||:|||||:-||||||||||||:|| |||||||||||||
3511 TGTCCTTGAACAGGCAGGGGTCACCAGTATCGAGGCCATATTGCTGAAATTGCAGCTGCGCTGGGCAGGG 3580


3532 CACATCTCTAGGATGGAGGATCACCGCCTCCCTAAGATTGTGTTTTATGGTGAACTCGCCACTGGCTGCC 3601
     ||||:|||||||||||:|||||||:|||||||||||||||||||||:|||||||||:|||||:||:||||
3581 CACGTCTCTAGGATGAAGGATCATCGCCTCCCTAAGATTGTGTTTTACGGTGAACTTGCCACCGGTTGCC 3650


3602 GCAAGAGAAGTGCCCCAGAGAAGAGATATATGGATTCCCTGAAACAATACCTCAGCCTTGGCCATACTGA 3671
     ||||||||||||||||||:|||||||||||| |||:||||||||||||||||:||||||||||||:|||
3651 GCAAGAGAAGTGCCCCAAAGAAGAGATATAAGGACTCCCTGAAACAATACCTTAGCCTTGGCCATATTGA 3720


3672 CTACCATCAGTGGTCCACCTTGGTCTCCAATCAGGAGACTTGGAGACACACCATACATAACGCTGTTGTC 3741
     |||||||||||||||||||||:|||||||||||||||||||||||||||||:|||||||||:||||||||
3721 CTACCATCAGTGGTCCACCTTGGCCTCCAATCAGGAGACTTGGAGACACACTATACATAATGCTGTTGTC 3790


3742 TCCTTTGAGAACACACGCAGAATTAGTCTCAAGGAGAAAAGACAAGGTAGAAAGAATTGCACCCTGCCTA 3811
     |||||||||||||||||||||||||||||:|||||||||||||||| |||||||||:|::|||:|||||
3791 TCCTTTGAGAACACACGCAGAATTAGTCTCGAGGAGAAAAGACAACGTAGAAAGAATCGTGCCCCGCCTA 3860


3812 TACCACCTAAAGAGACTTTTCACTGTGCTTTTTTGCAACCGGATTTGCCTATCCCACATTGGCCTTTTTA 3881
     |||||||:||:|||||:|||||:|||||:|||||||||||||-|||||||||||||||||||||||||||
3861 TACCACCCAAGGAGACCTTTCGCTGTGCTTTTT-GCAACCGGATTTGCCTATCCCACATTGGCCTTTTTA 3929


3882 GTCACCAGCACACTTGTAGTAAGCGTGGG 3910
     ||||:||||:|:|||||||||||||||||
3930 GTCATCAGCGCGCTTGTAGTAAGCGTGGG 3958
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Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
sequence07	5	78	tRNA-Asp-GAY	1	75	d	0.8667	2.2500	431

```
5 TCCACTTTAGTACAGTGGTGAGTGTCCCCGCCTCTCATGCGGGAGACCGGGGTTCGATTCCC-GCCAGGG 73
  ||| | ||||||:||||||||||||:|||||| |||:||||||||||||||||||||||-| |:|||
1 TCCTCGTTAGTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCGGGGTTCGATTCCCCGACGGGG 70


74 AGGCA 78
   || ||
```

71 AGCCA 75

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
sequence07	89	144	TguSINE1	77	132	d	0.9821	1.0000	511

```
89 TTAAGAGTTGGACTCGATGATCCTTGTGGGTCCCTTCCAACTCAGAATATTCTGTG 144
   |||||||||||||||:||||||||||||||||||||||||||||||||||||||||
77 TTAAGAGTTGGACTCAATGATCCTTGTGGGTCCCTTCCAACTCAGAATATTCTGTG 132
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
sequence08	45	809	eBHBV2	421	1192	d	0.6849	1.8020	1030

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 45 ATAGGGCTCATAGATTAATGTGGTGGCACATTCAATCTTTAGTCTGGGGAGAAGGTAAGGTAGCTGAATA 114
    |||: ||:|||||||:| ||||||||||: | | | ||||:|:||:||:||| || ||::|||| |:
421 ATAACGCCCATAGACTTTTGTGGTGGCATTGTAATTGTTTAATTTGAGGGGAACCAAACGTGACTGATTG 490

115 TGTGGCTAAATTAAGAACGTGGTTGGCCACTCCTTCTCAGTACAGAGGAAGAGATGCCCCAACCATTGAA 184
    |:|    |: : ||:||||| |||||| |:|||||    |:||:||:|| |||||||||||||||||||||
491 TATTTCCCGCTTGAGAACTTGGTTGTCTACTCCTGAAAAATATAGGGGTAGAGATGCCCCAACCATTGAA 560

185 GCAATCACTTCACCAGTCAGAGTGGCA----CCTCAAAGCCCAAACCAAA---CTCATGCAGCTGGAAGA 247
    ||:||||||: ||||:|: |:||||||----|----|:|||||---||||---|||| : |: |---|||
561 GCGATCACTCGACCAATTCGGGTGGCAAGAGC----AGGCCCA---CAAAGTTCTCAGAAAAAT---AGA 620

248 AGAGCT---AGA-TCAA-CAAAGAAGGAGAAA--TC----CTTCCATTA---------GAAGGAGA---- 293
    |:| ||---:||-||||-|  |||||:|||||--|:----||||:||||---------|||::|||----
621 AAACCTCGTGGACTCAAGCTCAGAAGAAGAAAAGTTAAAACTTCTATTACTTACAGGAGAAAAAGATCTA 690

294 ------GTTGTGCAC-ACC--------AGGACAGTATATGGGACTCCACGATCTTGTGTGGGCTCCCATG 348
      ------|||  |:  ||-|||--------|||: |:-----||||::|:|: | |--|||:||||||| |:
691 AATCCCGTTCTAGACGACCTTCTTCTGAGGGGAA-----GGGATCCTATCAAC--GTGCGGGCTCCCCTA 753

349 AACCACATAATGGATCAGGTTTCTCCAGAGCCTCCACACCCCATAGAGCACAATCTCCTTC--CCAAAAC 416
    :  ||||-------------:||||--||------|||:  |---|||:| | :|||:||:||--|||::|-
754 GCCCAC-------------CTTCT--AG------CACGAC---TAGGGGAGGATCCCCCTCTTCCAGGA- 798

417 CATTAAGGTCAAG------CATACACTGGGAA----AGCTAAAAGGTTTATATTCTAATCATATTTC--- 473
    -: ||| |: :||------||:| |:||||| |----:|||----|| ||||||------||:||:||--
799 -GGTAATGCGGAGGGGCTTCACAAATTGGGTACTTTGGCT----GGATTATAT------CACATCTCAGG 857

474 ---TGATTTTAATATAAACTGGCAAATCTCTGATCTTACAGAAACAAACTTTTCTCTTGAATTAATAAAG 540
    ---||| |||||| :|:||||| ||||::||||| |||||||||| |: | ||  ---||:--||:| ||
858 CTGTGAGTTTAATCCAGACTGGAAAAATTCCTGATATTACAGAAACACATATATCA---GAG--AACACAG 922

541 GAGA------CTCCTGCCAGGACATGGAAATATTTGACCCTGGCCAAATTCTGGCCAAAGGGCATTTCAT 604
    |:||------|||||-| ||:|  ||||||||||| : |::|||||||:||||| |||||||||||| |
923 GGGATGAGATCTCCT-CGAGAAATTGGAAATATTTGTTACCAGCCAAATTTTGGCCCAAGGGCATTTCCT 991

605 ACTATCCTGTTGAAAGC----GGTGTAAAAGTTAATAAGTATCCTGGGTTT-GAAATGG-----AACATT 664
    |:|-|||::---||| |----||::| ||||---|||||||:| |:|| |-||:|| |-----|||||
992 ATT-TCCCA---AAATCTATGGGCATCAAAG---ATAAGTACCAAGAGTATAGAGATTGCCACCAACATA 1054

 665 TATTGTTAACTAAACTTTATTTACAAAAAACTATTCAAGGCA-GGAATTCTATATAGGAGAGAGTCAAAG 733
     || ||:------|::||:||||||-:||||||| ||::- |||-|| ||:||:||||: ||||:|| ||:
1055 TAGTG------AGGCTCTATTTA-GAAAAACTCTTTG-TGCATGGTATCCTGTATAGACGAGAATCTAAA 1116

 734 CACTGT-GTTTCATTTAGAGGCAAATTTT-TTCAGTGGGAGC---AACAGTTCCTTGTC--TCCAGACCA 796
     ||-|||-:| |||||||:||||||||:::|-|||- |||||::---||:|---||||||||--|| | |:||
1117 CA-TGTCATATCATTTAAAGGCAAACCCTATTC-TTGGGAATCTAAATA---CCTTGTCAATCAACATCA 1181

 797 CATGGGACAAGGA 809
     --|||||||||||
1182 --TGGGACAAGGA 1192
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Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score

| sequence08 | 1020 | 1087 | L1_AC_10 | 3950 | 4020 | d | 0.7429 | 1.5000 | 227 |

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1020 CCAATCACAGAAGAAGAGGCAGAGG--CATTGAAAAAGAAATTTCTAGAAGAGCAACAACAACGG--ATA 1085
     ||||||||||||:|||||: |||:|--|-||:| ||||||||:|||||:||::| ||:|  ||:||--|||
3950 CCAATCACAGAAAAAGAGAGAGAAGATC-TTAACAAAGAAATCTCTAAAAAGGAAATACAAATGGCCATA 4018

1086 AA 1087
     ||
4019 AA 4020
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
sequence08	1248	2766	eBHBV1	2632	4188	d	0.7205	2.0238	3611

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1248 CCAATACCTCCTGTTGGGAAAGTGAGGAAGATGTCAGATATATTAGGCCAAATACTCCTTGTCCTAATAG 1317
     || ||| ||||| :|||||:|:| |:||:|||||| |||||| || ||||||||| ||| |||||||| |
2632 CCTATAGCTCCTCCTGGGAGAATCAAGAGGATGTCCTCTATATTCGGACAAATACTACTTTTCCTAATTG 2701

1318 GATTACTGGCTGGGTTTTTCTTGTTGACAAAAATCCTTAAAATACTAAAGAGGCTCAATTGGTGGTGGAC 1387
     |:||||||||:|||||||||||||||||||||||||:||| ||:|:|||||:||:|:||| :|:|||||||:||||
2702 GGTTACTGGTTGGGTTTTTCTTGTTGACAAGAATAGTTGAGATACTGAAAAAGCTAGACTGGTGGCGGAC 2771

1388 TTCTCTCAGTTTTCCAAAGGGAGACACGCTATGTGCTTTCCAAAGTACTGGGCACCCAG---TCACCGTG 1454
     |||||||||||||||||::|||| | ||:  :||| :||||||||||:|||||||-::|||||:---|||||:--
2772 TTCTCTCAGTTTTCCAGGGGGACAAACAAGGTGTCTTTTCCAAAATACTGG-TGCCCAAACCTCACCA-- 2838

1455 CACT-TGCACAGATCTTGCCCATGGACATGCCCATGATTTCCCTGGATGTTTCTCAGGCTTTTTATCATC 1523
     ||||-:|||-:|||:||||||| |||: ||||||| ||||||:|||||||| |||||||| ||||||||||
2839 CACTACGCA-GGATTTTGCCCCTGGGGATGCCCAGGATTTCTCTGGATGTGTCTCAGGCATTTTATCATC 2907

1524 TTCCTCTCAATCCTGCTTCTGCTATGCAGCTTGCTGTTTCTGACGGAAAACTGGTCTACTATTTTCAGAA 1593
     |||||||:||||||||| || | |:|||||||:| |||||||||:||| ||||||||||||||::||
2908 TTCCTCTTAATCCTGCTAGTGGGAGTCGGCTTGCTATATCTGACGGAGAACGCGTCTACTATTTTCGAAA 2977

1594 AGCTCCAATGATA-TCGGTCTCAGCCCTTTTTCTCCTCCATCTCTTCTCAACTGCCCTTGCAGCTGAACTA 1662
     |||| |||||: |-||||| ||||:|||||||:||||||||||||||||| ||||||:||:||||| |||--|
2978 AGCTGCAATGGGAGTCGGTATCAGTCCTTTTTTCCTCCATCTCTTCTCTACTGCTCTCGCAGCAGAA--A 3045

1663 TC--TTGTCACTGGAATATTTGGACTTTTGCTTATAGGGATGACTTCCTCCTCTGCCACACAAGCTCTCG 1730
     ||--| |||:|| |||||||||:|||||||||||| ||||||||||||||||||||||:||| |||:||||:|
3046 TCAGTAGTCGCTTTAATATTTGGGCTTTTGCTTATATGGATGACTTCCTCCTCTGTCACCCAAACTCTTG 3115

1731 TTACCTTAAC----TCAGCCACAGTGTCTGCTGTTTTCTTGAAAGCTTTGGGGTAAGAATAAACTTTGAT 1796
     ||||||||||----|:||||||| ||| |||:|||||||||||::||  |||:|| | | || ||| | |||
3116 TTACCTTAACACAGTTAGCCACTCTGTGTGCCGTTTTCTTGAAGAATTAGGAGTCACTATCAACGTGGAT 3185

1797 AAACGTACTCCATCACCTGTTGAAGAAATCAAATTCTTAGG--ACTGAAATTTACAAGGACTGACATGAT 1864
     |||: ||| ||||||||| :::::||| ||:|| |||:|:||--||:-| ||:  |:||||||: | : |-
3186 AAATCTACACCATCACCGACCAGAGACATTAATTTCCTGGGCTACC-ACATCATCGAGGACTATCTCCA- 3253

1865 GATACCTGAT---------GAAAAAT---GGATTGAAAGTAAACAGGTTATTAAACAAATTGATTGTAAC 1922
     ||| ||||| ---------||  ||||---|||:|| || |:|| ||:|-----||-||||:|:--: |||
3254 GATTCCTGAGACAATGTGGGACAAATTAAGGACTGTAATTGAAAAGAT-----AA-AAATCGG--AGAAC 3315

1923 AAATGTTATGATTTTAAAATCCTGCAAAGATTAATAGGCCACGTAAACTTTGTCATT-CCTTTTACTACT 1991
     ||----|||||:||||||||:  ||||:||||| :|:||:||: ||||:|  ||-|||-|||||||||:|
3316 AA----TATGACTTTAAAATTGTGCAGAGATTTGTGGGTCATTTAAATTGGGT-ATTGCCTTTTACCAGG 3380

1992 TATTCT----AATCATGTGCTACAACCATTGTAT---GC---TGCTGTAATAAACAAAAGGATTTTCAA 2051
      :|| |----|||----||:|||||||:| ||||||---||---|:|||:--:|||||||||----------
3381 GGTTGTGTAGAAT----TGTTACTATCTATGTATCAAGCAATTACTGC--CAAACAAAA---------- 3433

2052 TTTTCTGTTCCATATAAAGCTTTATTGTATAAA-ATGTGTTGT-CAAGGAGTTAAATGGAAAT-TGCAA- 2117
     -|||||| :|:||-::|||:|||-------|||:|:-||||| ||:|-||||| | :||-|||::|-||:|:-
3434 -TTTCTCCTTCA-GCAAAACTT------ATAAGTATGTCTTATACAAGGTGACAA-TGGGGGTCTGTAGG 3494

2118 -------------CCCAAGGACAGTGTTCCTGTTCCTAAGCTTGTGACAGATGGCATGTTGGAAGTTGGA 2174
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              -------------||||  |  ||  :  |  :|||-|  ||  |:|  |||::|||||||  :||||||:  |    |||
3495 CTGGTTCTGGACCCCCATGCACCAAGACCCT-TACCAAGGGTTGCAACAGATGCTATGTTGACACATGGC 3563

2175 GCCATATCCCATATCATCGGTGGGT-TGTCTTCCTTCCATTTTGCAGGACCTAGACCA-ATACACATTCA 2242
        ||  ||||:|||||||||  ||||||||-||:|  |  :||  |:|||  |||--|  |  |  |||  -||  |||||  ||
3564 GCAATATTCCATATCAACGGTGGGTGTGCCGTGTTTACGTTTAGCA--AACAATACCCTATTCACATACA 3631

2243 AGAATTATTGATGGCATTGGTTGCAGTTTCTTTG---ATCAA----ACCGCGGTCTTTGATCTGT----- 2300
        |||||:::||:|||-------|||---||||||||---:|:||----||----:||:|--||  |||-----
3632 AGAATCGCTGGTGG-------TGC---TTCTTTGTAGGTTAATGTTAC----ATCCT--ATATGTATACT 3685

2301 ----GACTCAACATTTGT-CTGCAGACAAAAA---TTCAGCTCTTTGCCATGGAGATTTGC-ACTGTGGG 2361
        ----||:|||||  |||||-||----|||  ||:---||::||||::||||||||||||||||-|::  ||  |
3686 TACAGATTCAACCTTTGTTCT----ACATAAGCGTTTTGGCTCCCTGCCATGGAGATTTGCTATCTTGTG 3751

2362 CCAGGCAAATCTTATCTCAGGTCAAAGTGTAC-----TGGACT-----CCT-TCAAAGTTTAACCCAGCG 2420
        |  |:-|||   |||:----------|||  ||||-----||  |||-----|||-  ||||-|  ||||||  ||
3752 CGAA-CAATGCTTG---------AAGGGTACCCCACTGTACTTTGTACCTAGCAAA-TATAACCCTGCT 3809

2421 GATGGCCCAACACACGGGAGACTATC---TGATTGGAC---TGCATATACTTGCACCCTCCTCAGAAAGC 2484
        ||||||||||||---|:||:|  ||  :|---|||||||||---||:---|  |||:|||  |::|||   :||||
3810 GATGGCCCAAC---CAGGGGTCTCCCCCCTGATTGGACAACTGT---TCCTTACACACCTCTCTTGAAGC 3873

2485 CCTTAAAACTGCCATATC--------------------------------CCAAGCTTGTCAACAA 2518
        |||||||||  |:|||:  ||------------------------------------|  :||||    ||:  |||
3874 CCTTAAAAGTACCACTTCGACTCTGTGGTCGTTAAGATTACACACCTCTCCTTACGGAGCTGCTCGCCAA 3943

2519 GGTATATATTAC-ATCCTTTATTGCTGTTGCTTTCTTGCTGTACTTT--GTCTTAATGAAACAATTTGTA 2585
        |||||-|  ||||-||--||:  ||||||||||  |-||||||||||:||--||----|||  |  |--|:|||
3944 GGTAT-TCTTACGAT--TTCCTTGCTGTTGCTGT-TTGCTGTACCTTTGGT----ATGTACC--TCTGTT 4003

2586 T-TGACTC--TCTT-CATATGGATCCTACTGTTAGAATAGCTCT-TCGAA-ATGTTCATAGTCTGTCTGA 2649
        |-|||:||--|:||-:|||||||  :||  ||:   :||  ||||:|-||:||-|||||--|::|:||:||:
4004 TATGATTCAATTTTATATATGGATATTAATGCACAAAGAGCTTTGTCAAATATGTT--TGATTTGCCTAT 4071

2650 AGATTTCTTTCCACCTGTGCCTGAATTACTTACTTCTGCTGAAGATGTGTTCGAACCTTATTTGC-AAAG 2718
          ||||||||||||:|  :|:   ||  |||  |||   |  |:||:|:||||:   |:|||||--||||:|-||||
4072 TGATTTCTTTCCATCAATAGAAGATTTAATTAGGTATACTAAGGATGCTATTGAACC--ATTTACTAAAG 4139

2719 A--GAT-TCAGAAAATAAACATGTTGTTATTGCAACTAATTTTATGGGTTT 2766
        |--|||-||  --|||  |||||||||  |||  |  ||  |||  |||||  |:|:|||
4140 AAGGATCTCT--AAAGAAACATGTGGTTTTGGCTACTCATTTTTTAGATTT 4188
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Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
sequence08	2807	2896	MER50I	4285	4370	d	0.7356	1.5000	263

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2807 GTAAGATCTC-TGAGGAGCCAGCTGGGAATATAGATTTTTCTGA---AAATTAGGGAGATCCTGACAAAT 2872
        ||||:||  ||-|:||:||  ||--|||||||||||||||||||:||:---|:  |||||||||---:|:|  :|||
4285 GTAAAATATCATAAGAAGGCA--TGGGAATATAGATTTTTTTGGCCTAGTTTAGGGAG---TTAAAGAAT 4349

2873 TATTTGAAACCATTAGAGAAAATA 2896
        |||||  ||:---|||||  |:::|||
4350 TATTTTAAG---TTAGATAGGATA 4370
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Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
sequence09	306	378	tRNA-Met_OS	7	77	d	0.7500	1.7000	275

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306 GTGGCGCAGCCGGTTAGCGCGCGGTACTTATACAGCAAACCCGAGCAATGCTGAGGCCGTGGGTTCGAGC 375
      |||||||||::||:|||||||||::|  ||:|||--||  ||  ||||:::||  ||||||:||  |:||||||||
  7 GTGGCGCAGTTGGCTAGCGCGTAGGTCTCATA--GCTAAAGCGAGTGATCCTGAGGTCGAGAGTTCGAGC 74

376 CTC 378
      |||
 75 CTC 77
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Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
sequence10	29	76	Harbinger-N47_OS	1871	1914	d	0.8043	1.1667	238

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  29 AACCCTATAGCTCAGGAACCAAGAGTGGGAGGGGAGAGACAAAGAGAT 76
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1871 AGCCCTATAGTTCAG---CCAAGAGTGGGGGAAGAGAG-CGACGAGAT 1914
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Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
sequence10	252	360	CR1-X1_Pass	4316	4424	d	0.9725	1.0000	882

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 252 CGGGCACATGGTGTGACTCTTGGGGATGGTCCTGTGCAGGGCCAGGAGTTGGACTCGATGATCCTTATGG 321
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4316 CAGGCACATGGTGTGACTCTTGGGGATGGTCCTGTGCAGGGCCAGGAGTTGGACTCGATGATCCTTGTGG 4385

 322 GTCCCTTCCAACTCAGCATATTCTGTGATTCTGTGATCC 360
     |||||||||||||||||||||||||||||||||||||:|
4386 GTCCCTTCCAACTCAGCATATTCTGTGATTCTGTGATTC 4424
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Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
sequence10	407	617	Mariner-25_SIn	1071	1281	d	0.6934	2.1852	549

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 407 TCCCAAAGATCAAGTTGGTGCTCAAAGGAACCCATTTTTTGTCGGTAGAAGATGTGAAAGCAAAAA-CGA 475
     |:||:|||||||||: |: :| |||||||||||: ||:  ||||:|:|||||| |||||-||:||||-||:
1071 TTCCGAAGATCAAGTCTGCCTTAAAAGGAACCCGGTTCGAGTCGATGGAAGAAGTGAA-GCGAAAATCGG 1139

 476 CGGAGATCCTCAACAGCCTTTCAGAAAATGATCTGTGGAATTGCTTTGAACATTGGCAGCATCGTATGCA 545
     ||||| |||| ||::  :||| ||:||||  ||::|  ||:: ::| ||||||||||| || ||| |: | || ||| |
1140 CGGAGCTCCTAAATGCTCTTACAAAAAAAGACTTCCAGCATTGCTTTGACCAATGGAAAAAACGAATGGA 1209

 546 GCTGTGTGT--CAACTCAGAAGGGAACTATTTTGAAGGTGATCATAGTTGATTTTCT--TAATTTGTTAA 611
     :| ||||||--|:| --:|:||||:| ||: ||||||| || |||--|:|||| |  --|||||| | ||
1210 ACGGTGTGTGGCGAG--GGGAGGGGAGTACATTGAAGGGGAGCAT--TCGATTGTAGAATAATTTTTAAA 1275

 612 ATAAAA 617
     ||||||
1276 ATAAAA 1281
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Masked Regions

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Annotation of Repbase Sequences

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ID    AviRTE_MUn  repbase;    DNA;    VRT; 3999 BP.
XX
AC    .
XX
DT    23-APR-2016 (Rel. 21.05, Created)
DT    24-APR-2016 (Rel. 21.05, Last updated, Version 1)
XX
DE    RTE non-LTR retrotransposon from Melopsittacus undulatus.
XX
KW    RTE; Non-LTR Retrotransposon; Transposable Element; AviRTE_MUn.
XX
OS    Melopsittacus undulatus
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC    Coelurosauria; Aves; Neognathae; Psittaciformes; Psittaculidae;
OC    Melopsittacus.
XX
RN    [1]
RP    1-3999
RA    Suh A., Witt C.C., Menger J., Sadanandan K.R., Podsiadlowski L.,
RA    Gerth M., Weigert A., McGuire J.A., Mudge J. et al.;
RT    "Ancient horizontal transfers of retrotransposons between birds
RT    and ancestors of human pathogenic nematodes.";
RL    nature communications 7, 11396-11396 (2016).
XX
DR    [1] (Consensus)
XX
CC    AviRTE is a novel RTE family present in some birds and nematodes.
CC    Frequent horizontal transfer. Only distantly related to BovB.
CC    Subfamily AviRTE_MUn has 601 copies in Melopsittacus undulatus.
CC    Mean distance to consensus is 6%.
XX
FH    Key           Location/Qualifiers
FT    CDS           695..3958
FT                  /product="AviRTE_MUn_1p"
FT                  /translation="MGIFCCGRLKTKRQRHTPASKGVSRLTLACWNIRTML
FT                  DTANSGRPERRSALIAHELSRLNIDIAALSEVRLHEEGSLKEHGAGYTLYW
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XX
SQ   Sequence 3999 BP; 1129 A; 979 C; 904 G; 973 T; 14 other;

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ID   CR1-E_Pass  repbase;    DNA;    VRT; 3085 BP.
XX
AC   .
XX
DT   08-JAN-2009 (Rel. 14.01, Created)
DT   21-JAN-2009 (Rel. 14.01, Last updated, Version 1)
XX
DE   CR1 Non-LTR Retrotransposon from Passeriformes.
XX
KW   CR1; Non-LTR Retrotransposon; Transposable Element; CR1-E_Pass;
KW   LINE.
XX
OS   Passeriformes
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC   Coelurosauria; Aves; Neognathae.
XX
RN   [1]
RP   1-3085
RA   Smit A.F.;
RT   "CR1-E_Pass - CR1 Non-LTR Retrotransposon from Passeriformes.";
RL   Repbase Reports 9(1), 45-45 (2009).
XX
DR   [1] (Consensus)
XX
CC   18% div. Minor subfamilies ignored. 83% similar to CR1-E in
CC   chicken (consensus starts at poss 1418 in full chicken CR1-E
CC   consensus, at very end of ORF1).
XX
SQ   Sequence 3085 BP; 828 A; 685 C; 968 G; 585 T; 19 other;

//
ID   CR1-X1_Pass repbase;    DNA;    VRT; 4428 BP.
XX
AC   .
XX
DT   08-JAN-2009 (Rel. 14.01, Created)
DT   21-JAN-2009 (Rel. 14.01, Last updated, Version 1)
XX
DE   CR1 Non-LTR Retrotransposon from Passeriformes.
XX
KW   CR1; Non-LTR Retrotransposon; Transposable Element; CR1-X1_Pass;
KW   LINE.
XX
OS   Passeriformes
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC   Coelurosauria; Aves; Neognathae.
XX
RN   [1]
```

```
RP    1-4428
RA    Smit A.F.;
RT    "CR1-X1_Pass - CR1 Non-LTR Retrotransposon from Passeriformes.";
RL    Repbase Reports 9(1), 50-50 (2009).
XX
DR    [1] (Consensus)
XX
CC    subfamily1 17%. gag ORF (full) 311-1453, pol (1 frameshift)
CC    1618-4348, but, like the distantly related R1-YB2_Tgu,  there is
CC    a frameshift that appears tru in the consensus. The frameshift
CC    (2 bp missing) is at 3807, corresponding to pos 3239 of
CC    CR1-YB2_Pass. Notably, this is at a different, later spot then
CC    in CR1-YB2_Pass.With 600 copies of terminal 700 bp, coseg could
CC    find 2 or 3 subfamilies. These are at most 5-6% different from
CC    each other, and I get the impression that recombined copies have
CC    hopped around, so there is only one consensus. Absent at
CC    orthologous sites in chicken.
XX
SQ    Sequence 4428 BP; 1163 A; 1004 C; 1344 G; 899 T; 18 other;

//
ID    Chompy-1934B_Crp repbase;    DNA;    VRT; 1460 BP.
XX
AC    .
XX
DT    29-JAN-2013 (Rel. 18.04, Created)
DT    24-APR-2013 (Rel. 18.04, Last updated, Version 1)
XX
DE    DNA transposon from the crocodile: consensus.
XX
KW    Harbinger; DNA transposon; Transposable Element; Nonautonomous;
KW    Chompy; Chompy-1934B_Crp.
XX
OS    Crocodylus porosus
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Archelosauria; Archosauria; Crocodylia; Longirostres;
OC    Crocodylidae; Crocodylus.
XX
RN    [1]
RP    1-1460
RG    International Crocodilian Genomes Working Group;
RT    "Transposable elements from the crocodilian genomes.";
RL    Direct Submission to Repbase Update (07-FEB-2013).
XX
DR    [1] (Consensus)
XX
CC    3 bp TSDs, cTNAg target. 21% subsr outside CGs. See
CC    CRrnd-5_family-1934_1 for description
CC    CRrnd-5_family-1934_2#DNA/PIF-Chompy.
XX
SQ    Sequence 1460 BP; 178 A; 560 C; 534 G; 175 T; 13 other;

//
ID    ERV3-7_PMaj-LTR repbase;    DNA;    VRT; 741 BP.
XX
AC    .
XX
DT    17-OCT-2018 (Rel. 24.09, Created)
DT    17-OCT-2018 (Rel. 24.09, Last updated, Version 2)
XX
DE    Endogenous retrovirus from the great tit genome, long terminal
DE    repeat consensus.
XX
KW    ERV3; Endogenous Retrovirus; Transposable Element;
KW    ERV3-7_PMaj-LTR.
XX
OS    Parus major
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC    Coelurosauria; Aves; Neognathae; Passeriformes; Paridae; Parus.
```

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      XX
      RN   [1]
      RP   1-741
      RA   Kojima K.K.;
      RT   "Endogenous retroviruses from the great tit genome.";
      RL   Repbase Reports 19(9), 1747-1747 (2019).
      XX
      DR   [1] (Consensus)
      XX
      CC   ~92% identical to consensus. 5-bp TSDs.
      XX
      SQ   Sequence 741 BP; 188 A; 190 C; 144 G; 217 T; 2 other;

      //
      ID   HAT-10_Mad  repbase;    DNA;     PLN; 6710 BP.
      XX
      AC   .
      XX
      DT   20-OCT-2010 (Rel. 15.10, Created)
      DT   20-OCT-2010 (Rel. 15.11, Last updated, Version 2)
      XX
      DE   Autonomous hAT elements, consensus.
      XX
      KW   hAT; DNA transposon; Transposable Element; HAT-10_Mad.
      XX
      NM   HAT-10_Mad.
      XX
      OS   Malus domestica
      OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
      OC   Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae;
      OC   Pentapetalae; rosids; fabids; Rosales; Rosaceae; Maloideae;
      OC   Maleae; Malus.
      XX
      RN   [1]
      RP   1-6710
      RA   Bao W. and Jurka J.;
      RT   "hAT-type DNA transposons from the apple genome.";
      RL   Repbase Reports 10(10), 1626-1626 (2010).
      XX
      RN   [2]
      RA   Velasco R., Zharkikh A., Affourtit J., Dhingra A., Cestaro A.,
      RA   Kalyanaraman A., Fontana P., Bhatnagar S.K. et al.;
      RT   "The genome of the domesticated apple (Malus x domestica
      RT   Borkh).";
      RL   Nat Genet 42(10), 833-839 (2010).
      XX
      DR   [1] (Consensus)
      XX
      CC   TIR is 11-bp long.
      XX
      FH   Key            Location/Qualifiers
      FT   CDS            3409..5058
      FT                  /product="HAT-10_Mad_1p"
      FT                  /translation="MDARDSDSVTDEESVEIIMGTERDLGSESIDNTNSSS
      FT                  TKKKARTINLGKRKLRSPVWNTFTKLDTIFEDSKRRAQCKACKKVMIDDSH
      FT                  HGTGNMKRHLNTCPAKNNVELFMSASELCSQKFDPLVFRGLLVEAIIKHNL
      FT                  PFNFVEHEGIKALFAYVCPDIKLPCRNTIKACVLRMFKTEKQALHNLLGSV
      FT                  EGRICLTSDLWSSQCTDGYLALTAHFVDKDWKLNKRIISFCHMPXPHTGVA
      FT                  LCEKISALVTEWGIEKKLFSITLDNASSNICFVNILRNQLNIRGLLLMNGD
      FT                  FFHVRCCAHILNLIVQDGLKEIDSSVVKIRECIKYVKGSEARKLKFQECVK
      FT                  QVGILDSKRGLRQDVPTRWNSTYLMLDSAIFYRYAFINLGLSDSNFESCXS
      FT                  SEEWDKVVKISKFLGYFYDVTCLFSGTKYPTSNLFFPKVFVIQLQIKAAID
      FT                  DCDSFMNKMGDYMHIKFQKYWSDYSLIMSIAIILDPRYKLHFVDWAYTKLH
      FT                  GVNSMEYXNVHGTLIALFNVYSEISAHLNFSNIPMNSMSNHQTEGEGDALF
      FT                  EVT"
      XX
      SQ   Sequence 6710 BP; 2032 A; 1010 C; 1224 G; 2440 T; 4 other;

      //
      ID   Harbinger-N47_OS repbase;    DNA;    PLN; 2206 BP.
```

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XX
AC    .
XX
DT    05-JUL-2016 (Rel. 21.09, Created)
DT    05-JUL-2016 (Rel. 21.09, Last updated, Version 1)
XX
DE    DNA transposon from Oryza sativa, consensus.
XX
KW    Harbinger; DNA transposon; Transposable Element; Nonautonomous;
KW    DNA; Harbinger-N47_OS.
XX
OS    Oryza sativa
OC    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC    BOP clade; Oryzoideae; Oryzeae; Oryzinae; Oryza.
XX
RN    [1]
RP    1-97
RA    Bao W.;
RT    "DNA transposons from the rice genome.";
RL    Repbase Reports 16(10), 1958-1958 (2016).
XX
DR    [1] (Consensus)
XX
CC    ~98% identical to the consensus.
XX
SQ    Sequence 2206 BP; 625 A; 490 C; 444 G; 643 T; 4 other;


//
ID    L1_AC_10     repbase;      DNA;     VRT; 6848 BP.
XX
AC    .
XX
DT    21-SEP-2012 (Rel. 17.09, Created)
DT    21-SEP-2012 (Rel. 17.09, Last updated, Version -1)
XX
DE    L1 non-LTR retrotransposons - a consensus sequence.
XX
KW    L1; Non-LTR Retrotransposon; Transposable Element; L1_AC_10.
XX
OS    Anolis carolinensis
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Lepidosauria; Squamata; Bifurcata; Unidentata; Episquamata;
OC    Toxicofera; Iguania; Dactyloidae; Anolis.
XX
RN    [1]
RA    Novick P.A., Basta H., Floumanhaft M., McClure M.A.
RA    and Boissinot S.;
RT    "The evolutionary dynamics of autonomous non-LTR retrotransposons
RT    in the lizard Anolis carolinensis shows more similarity to fish
RT    than mammals.";
RL    Mol Biol Evol 26(8), 1811-1822 (2009).
XX
DR    [1] (Consensus)
XX
FH    Key            Location/Qualifiers
FT    CDS            join(1559..1927,1837..2643)
FT                   /product="L1_AC_10_1p"
FT                   /translation="MAYKLRDRDNKDPKMLQKRTSISEEPNIRDMTDTILK
FT                   ELQRMQEKQDAYQKLAQEQMLDFKKEIKEELRTMKQEIGTINQELQDLKLE
FT                   KAEIRSSQEKIRKEVQLLDLETKLNRDKNCWSQKSKLTGKNTKRSTIVGLG
FT                   DKIKSRQELLESKELEYQLRFRNVWEEAKENIRRIIIEIIANILNCSTDEA
FT                   EDRTDRIYRINTNYAKRNKTPRDVIVNFTKKIFRDEILKINNTNTITFKGE
FT                   KIVILKEYPTETLNRRQKYQFLVDELKKHKIRFRWEKTEGLMTTYKGEKYW
FT                   ITSEAKARNFYKKLKKETEEEEKSDEEDQFRTSKSRANVYKKRALDQEFLE
FT                   HQSKLKKGQDNQEEKVEDKEGEEEEEENQITLSEEEEERTEGEKREEAL"
FT    CDS            join(2643..3593,3597..4016,3929..5380,5334..5666,
FT                   5612..6376)
FT                   /product="L1_AC_10_2p"
FT                   /translation="MRRHLKIYTCNVNGLNTPQKRNKIYNSLKKLDYDIIS
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FT                       LQETHIRHGQEKFLTQLKLGQEFHSSYIQKKRGVVTYVNPKLQAQQTFKDM
FT                       DGRILGITINIENLKILVINIYAPNETKSKFVKKLKELMYDKEFDKIILMG
FT                       DFNGVMNCEKDRNPGRKSRDKKYKGLLSKEFKDFKEEYDLDDVWRSHHENE
FT                       RDYTFFSAKYKSWSRIDMVWVSKSLSPLVQKIKILPRLDTDHNPIELILNQ
FT                       KERHWRWKLDSNLLKRKEDIEKNRTLLEEFIKINDNHETPLHIVWEASKAT
FT                       MRGYFIQQGVWKKREKQKHIKSIIDISKIERELKSNPNDLVLLQKLEMTQK
FT                       RREFFELEERAKQMNYIKQTHFESANKPGRWLSRKLRGKKEATNINRIRIG
FT                       EKYHCLEEDILKQFSKYYKQLYGKDSIEREKITSYLGKLKLQSQKKREKIL
FT                       TKKSLKRKYKWPLFGKAKTPITEKEREDLNKEISKKEIQMAIKKFDSSKSP
FT                       GPDGLTAVYYKTFEKELIPYLHKIMNNIRENGKMPDSWKEALITVIHKENS
FT                       DPEEIKNYRPISLLNVDYKIFSNIIAERMKSFLKNWIKEEQSGFLPNRNIK
FT                       DNIRLVVDLLEYYESHNQHEILFLAVDAEKAFDRVNWDFFKLLIQVLDMGY
FT                       YLQNSIEAIYQNQKAKILVNGKETEEFVIEKGTRQGCPLSPLIFIMTLETL
FT                       LINIRSNTELQGANIQGVQYKVQAYADDIICFIEDPVNKGEKWISTIKEYG
FT                       DIAGLKINMSKTKALAKNINKKKQELISKTLGIEITSKIKYLGISISPKNS
FT                       QLLKNNYEKNWKNIKKDLENWKNLEISLLGRISVVKMSILPKMLFLFQCLP
FT                       ILRNQKCFITWNKDLSRFIWQGKNPRIKRINLIDDKRRGGFAMPDLKTYYE
FT                       ASNLIWIKDWIQLKNKKKLTLEGFKSRMAFIFMVRQNRDLRAGWHSYLWYD
FT                       KIKIEKKFGNHFIRSALIKTWNKYKLRMYNKTPTWISPLEAVQRRLLGWSQ
FT                       WPKYEDLIKLQGSEYVLKSQQELKTEYKNITWLQYGQLKNTIKKMKKYNLV
FT                       TVWPIEEYYKKDEIKGFMGKNNLWDKILFSTGHLILRIYKILLEWNTEIEQ
FT                       VKNNMVKWATDIGRPIQMEEWEACWGRKLKYTYSYQLKENWMKMFYRWYIT
FT                       PQKLGMISKTKNYKCWKCGEKERTFHHIWWECKKAKEYWNKIHEIIQNMLN
FT                       IKVKKTPELYLLGIFKESQDINEEKLMTYLTTSARMSYARYSRQKVIPKTE
FT                       EWLTKVAEIKNMDRLTYLIAKNQGRPRKETNWQAIEKYLGTNMATK"
XX
SQ     Sequence 6848 BP; 2822 A; 1080 C; 1389 G; 1557 T; 0 other;

//
ID   MER50I       repbase;    DNA;     PRI; 7205 BP.
XX
AC   .
XX
DT   20-AUG-1998 (Rel. 3.07, Created)
DT   20-APR-2006 (Rel. 5.05, Last updated, Version 3)
XX
DE   Primate MER50I repetitive element - a consensus.
XX
KW   ERV1; Endogenous Retrovirus; Transposable Element; MER4I-group;
KW   MER50; LTR retroelement; MER50I.
XX
NM   MER50I.
XX
OS   Homo sapiens
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-1382
RA   Kapitonov V.V. and Jurka J.;
RT   "MER50I.";
RL   Direct Submission to Repbase Update (AUG-1998).
XX
RN   [2]
RP   1-7205
RA   Smit A.F.;
RT   "MER50I.";
RL   Direct Submission to Repbase Update (FEB-2000).
XX
DR   [2] (Consensus)
XX
CC   MER50I is a class I retrovirus-like element flanked by MER50
CC   LTRs.
CC   It is closely related to other MER4I-group members [1].
CC   A full-length coding regions is present for gag (pos 1732-3083),
CC   matching the HUERS-P3 gag the best (61% similarity). There are
CC   also
CC   partial matches to pol (pos ~3089-3645) and env (pos 6221-6927).
CC   Individual sequences are on average 12% diverged from the
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CC    consensus.
XX
SQ    Sequence 7205 BP; 1968 A; 1691 C; 1537 G; 1892 T; 117 other;

//
ID    Mariner-25_SIn repbase;    DNA;    INV; 1324 BP.
XX
AC    .
XX
DT    10-APR-2012 (Rel. 19.02, Created)
DT    10-APR-2012 (Rel. 19.02, Last updated, Version 1)
XX
DE    Mariner-type transposon sequence - a consensus.
XX
KW    Mariner/Tc1; DNA transposon; Transposable Element;
KW    Mariner-25_SIn.
XX
OS    Solenopsis invicta
OC    Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta;
OC    Pterygota; Neoptera; Holometabola; Hymenoptera; Apocrita;
OC    Aculeata; Vespoidea; Formicidae; Myrmicinae; Solenopsis.
XX
RN    [1]
RA    Wurm Y., Wang J., Riba-Grognuz O., Corona M., Nygaard S.,
RA    Hunt B.G., Ingram K.K., Falquet L., Nipitwattanaphon M. et al.;
RT    "The genome of the fire ant Solenopsis invicta.";
RL    Proc Natl Acad Sci U S A 108(14), 5679-5684 (2011).
XX
RN    [2]
RP    1-1324
RA    Bao W. and Jurka J.;
RT    "DNA transposons from the fire ant genome.";
RL    Repbase Reports 14(2), 341-341 (2014).
XX
DR    [2] (Consensus)
XX
CC    >97% identical to consensus. 30bp TIR.
XX
FH    Key             Location/Qualifiers
FT    CDS             join(194..685,689..1264)
FT                    /product="Mariner-25_SIn_1p"
FT                    /translation="MCDEKHEQRINVKFLVKLKKTPTECYKLLKEAYGENS
FT                    LSRARVFEWYKRFSEGRESTKDDQRPGRPVSVSTPQIVTKINEIVRGDRRM
FT                    SIRMIAETVNADKETVRKILHDELNMKKICAKLVPKNLTPDQKLVRQQICS
FT                    DFLERLDEEPELIENIITCDETWIFYDAETKRQSMHWKTPASPRMKKARMS
FT                    KSKFKAMLIVFFDINGIVMTEWVPEGQTVNQTYYLKVLATLRERVRKKRPE
FT                    LWKNKSWILHQDNAPAHNALSVKRYLASRGTPVLEHAPYSPDLAPCDFFLF
FT                    PKIKSALKGTRFESMEEVKRKSAELLNALTKKDFQHCFDQWKKRMERCVAR
FT                    GGEYIEGEHSIVE"
XX
SQ    Sequence 1324 BP; 415 A; 264 C; 312 G; 333 T; 0 other;

//
ID    TguERVL2b1_LTR repbase;    DNA;    VRT; 566 BP.
XX
AC    .
XX
DT    08-JAN-2009 (Rel. 14.01, Created)
DT    21-JAN-2009 (Rel. 14.01, Last updated, Version 1)
XX
DE    Long terminal repeat of ERV3 Endogenous Retrovirus from
DE    Estrildidae.
XX
KW    ERV3; Endogenous Retrovirus; Transposable Element; ERVL; LTR;
KW    TguERVL2b1_LTR.
XX
OS    Estrildidae
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC    Coelurosauria; Aves; Neognathae; Passeriformes; Passeroidea.
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        XX
        RN   [1]
        RP   1-566
        RA   Smit A.F.;
        RT   "TguERVL2b1_LTR - ERV3 Endogenous Retrovirus from Estrildidae.";
        RL   Repbase Reports 9(1), 181-181 (2009).
        XX
        DR   [1] (Consensus)
        XX
        CC   8-9% 80 Perhaps TguERVL-B_LTR2 LTRs span something quite
        CC   different than TguERVL-B and we may have to rename it.
        XX
        SQ   Sequence 566 BP; 132 A; 137 C; 116 G; 181 T; 0 other;

        //
        ID   TguSINE1     repbase;    DNA;     VRT; 137 BP.
        XX
        AC   .
        XX
        DT   08-JAN-2009 (Rel. 14.01, Created)
        DT   20-MAR-2019 (Rel. 24.03, Last updated, Version 3)
        XX
        DE   tRNA-derived SINE family from Estrildidae.
        XX
        KW   SINE2/tRNA; SINE; Non-LTR Retrotransposon; Transposable Element;
        KW   Nonautonomous; tRNA; TguSINE1; tRNA-CR1.
        XX
        NM   TguSINE1.
        XX
        OS   Estrildidae
        OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        OC   Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
        OC   Coelurosauria; Aves; Neognathae; Passeriformes; Passeroidea.
        XX
        RN   [1]
        RP   1-137
        RA   Smit A.F.;
        RT   "TguSINE1 - tRNA from Estrildidae.";
        RL   Repbase Reports 9(1), 272-272 (2009).
        XX
        DR   [1] (Consensus)
        XX
        CC   tRNA-Ile-ATT/CR1-X 15%.
        XX
        SQ   Sequence 137 BP; 34 A; 29 C; 31 G; 43 T; 0 other;

        //
        ID   eBHBV1       repbase;    DNA;     VRT; 4865 BP.
        XX
        AC   .
        XX
        DT   07-MAR-2017 (Rel. 22.11, Created)
        DT   07-MAR-2017 (Rel. 22.11, Last updated, Version 2)
        XX
        DE   Melopsittacus undulatus endogenous budgerigar hepatitis B viruses
        DE   element 1 (eBHBV1), complete sequence.
        XX
        KW   DNA Virus; Integrated Virus; Hepadnavirus; eBHBV1.
        XX
        OS   Melopsittacus undulatus
        OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        OC   Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
        OC   Coelurosauria; Aves; Neognathae; Psittaciformes; Psittaculidae;
        OC   Melopsittacus.
        XX
        RN   [1]
        RP   1-4865
        RA   Liu W., Pan S., Yang H., Bai W., Shen Z., Liu J. and Xie Y.;
        RT   "The first full-length endogenous hepadnaviruses: identification
        RT   and analysis.";
```

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RL    Journal of Virology 86(17), 9510-9513 (2012).
XX
CC    BK008520.
XX
SQ    Sequence 4865 BP; 1359 A; 1007 C; 1055 G; 1444 T; 0 other;

//
ID    eBHBV2      repbase;    DNA;    VRT; 3856 BP.
XX
AC    .
XX
DT    07-MAR-2017 (Rel. 22.11, Created)
DT    07-MAR-2017 (Rel. 22.11, Last updated, Version 2)
XX
DE    Melopsittacus undulatus endogenous budgerigar hepatitis B viruses
DE    element 2 (eBHBV2), complete sequence.
XX
KW    DNA Virus; Integrated Virus; Hepadnavirus; eBHBV2.
XX
OS    Melopsittacus undulatus
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC    Coelurosauria; Aves; Neognathae; Psittaciformes; Psittaculidae;
OC    Melopsittacus.
XX
RN    [1]
RP    1-3856
RA    Liu W., Pan S., Yang H., Bai W., Shen Z., Liu J. and Xie Y.;
RT    "The first full-length endogenous hepadnaviruses: identification
RT    and analysis.";
RL    Journal of Virology 86(17), 9510-9513 (2012).
XX
CC    BK008521.
XX
SQ    Sequence 3856 BP; 1113 A; 813 C; 787 G; 1143 T; 0 other;

//
ID    hAT-2_ET    repbase;    DNA;    MAM; 3105 BP.
XX
AC    .
XX
DT    21-APR-2009 (Rel. 14.10, Created)
DT    22-APR-2009 (Rel. 14.10, Last updated, Version 1)
XX
DE    hAT-2_ET is a family of autonomous DNA elements in the genome of
DE    Echinops telfairi found also in Tarsius syrichta, Microcebus
DE    murinus, Myotis lucifugus, Monodelphis domestica, Otolemur
DE    garnetii, Anolis carolinensis, Xenopus tropicalis and Schmidtea
DE    mediterranea.
XX
KW    hAT; DNA transposon; Transposable Element; hAT-2_ET.
XX
OS    Echinops telfairi
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Afrotheria; Tenrecidae; Tenrecinae; Echinops.
XX
RN    [1]
RP    1-3105
RA    Novick P.A., Smith J., Ray D. and Boissinot S.;
RT    "Independent and parallel lateral transfer of DNA transposons in
RT    tetrapod genomes.";
RL    Gene 449(1-2), 85-94 (2010).
XX
DR    [1] (Consensus)
XX
FH    Key           Location/Qualifiers
FT    CDS           1091..2896
FT                  /product="hAT-2_ET_1p"
FT                  /translation="MISRKRKIDSECRIFKEQWTYDYFFMQYKERAVCLIC
FT                  QNIVSVFKEYNLRRHYQTQHKDKYDCLVGEVRKDKILKLKNTLTTQQNTFV
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FT                        KQKQLNISSLRASFQVAKLIACTGRPFVEGEFVKECLLSVAKEMCPEKADL
FT                        FSTVSLSGPTITQRIEEMGDNLHQHLQNSAKKLSYFSLALDESNDVRDSAQ
FT                        LLIFIRGMNDYXEVTEELAALQSIKGTTTGEDIYEKVCQTVNGLELDWAKL
FT                        ASVTTDGAPSMVGSKKGVIARINQEMDKHNHSHPIAIHCLIHQQALCSKSL
FT                        KWDSVMKIVVSCVNFIRANALNHRQFQEFLSELNVAYEDVLYHTEVRWLSR
FT                        GRVLKHFYDLLPQITAFLLSKNKEVPELNDAEWKWHLAFLTDVTELLNSFN
FT                        VQLQGKGKLICDMQSHVKAFEVKLGLLIKQVKEENFCHLPTTQNLLAEKPL
FT                        VAFPNKTCVDSLEKLQKEFQFRFKELHLHEQDIQLFRNPFSIDIENVDTIY
FT                        QMELAELQNCDSLKDAFKSSSLPNFXASLPSETYPNLRNHALKMATIFGST
FT                        YVCEQTFSRMKHLKSPTRSRLTDAHLHHLLRLAVTNMELDIDHLISKKQAH
FT                        SSH*"
XX
SQ   Sequence 3105 BP; 911 A; 580 C; 696 G; 901 T; 17 other;

//
ID   hAT-N3_CM   repbase;    DNA;    VRT; 893 BP.
XX
AC   .
XX
DT   06-OCT-2016 (Rel. 21.12, Created)
DT   06-OCT-2016 (Rel. 21.12, Last updated, Version 1)
XX
DE   DNA transposon from the elephant shark - consensus.
XX
KW   hAT; DNA transposon; Transposable Element; Nonautonomous;
KW   hAT-N3_CM.
XX
OS   Callorhinchus milii
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
OC   Chondrichthyes; Holocephali; Chimaeriformes; Callorhinchidae;
OC   Callorhinchus.
XX
RN   [1]
RP   3-183
RA   Bao W.;
RT   "DNA transposons from the elephant shark genome.";
RL   Repbase Reports 16(12), 2239-2239 (2016).
XX
DR   [1] (Consensus)
XX
CC   ~84% identical to consensus. TSDs are 8-bp long.
XX
SQ   Sequence 893 BP; 314 A; 231 C; 214 G; 134 T; 0 other;

//
ID   hAT-N4_XT   repbase;    DNA;    VRT; 328 BP.
XX
AC   .
XX
DT   31-AUG-2006 (Rel. 11.08, Created)
DT   31-AUG-2006 (Rel. 11.08, Last updated, Version 1)
XX
DE   A nonautonomous family of hAT transposons - a consensus.
XX
KW   hAT; DNA transposon; Transposable Element; Nonautonomous;
KW   Interspersed repeat; non-autonomous; hAT-N4_XT.
XX
OS   Xenopus tropicalis
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Pipoidea; Pipidae; Xenopodinae;
OC   Xenopus; Silurana.
XX
RN   [1]
RP   1-328
RA   Kapitonov V.V. and Jurka J.;
RT   "hAT-N4_XT, a family of nonautonomous hAT DNA transposons from
RT   frog.";
RL   Repbase Reports 6(8), 425-425 (2006).
XX
DR   [1] (Consensus)
```

```
XX
CC     The genome contains several thousand copies of hAT-N4_XT-like
CC     elements. These nonautonomous elements have been transposed a
CC     long time ago (~13% divergence from the consensus).
XX
SQ     Sequence 328 BP; 59 A; 108 C; 106 G; 55 T; 0 other;

//
ID     tRNA-Asp-GAY repbase;      DNA;     VRT; 75 BP.
XX
AC     .
XX
DT     29-AUG-2008 (Rel. 13.08, Created)
DT     29-AUG-2008 (Rel. 13.08, Last updated, Version -1)
XX
DE     tRNA from Vertebrata.
XX
KW     tRNA; Multicopy gene; tRNA-Asp-GAY.
XX
OS     Vertebrata
OC     Eukaryota; Metazoa; Chordata; Craniata.
XX
RN     [1]
RP     1-75
RA     Smit A.F.;
RT     "tRNA-Asp-GAY - tRNA from Vertebrata.";
RL     Direct Submission to Repbase Update (05-AUG-2008).
XX
DR     [1] (Consensus)
XX
SQ     Sequence 75 BP; 12 A; 22 C; 25 G; 16 T; 0 other;

//
ID     tRNA-Met_OS repbase;      DNA;     PLN; 87 BP.
XX
AC     .
XX
DT     29-DEC-2015 (Rel. 21.03, Created)
DT     29-DEC-2015 (Rel. 21.03, Last updated, Version 1)
XX
DE     tRNA sequence - consensus.
XX
KW     tRNA; Multicopy gene; tRNA-Met_OS.
XX
OS     Oryza sativa
OC     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC     Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC     BOP clade; Oryzoideae; Oryzeae; Oryzinae; Oryza.
XX
RN     [1]
RP     1-80
RA     Bao W.;
RT     "tRNA sequences from the rice genome.";
RL     Direct Submission to Repbase Update (28-DEC-2015).
XX
DR     [1] (Consensus)
XX
CC     99% identical to the consensus.
XX
SQ     Sequence 87 BP; 16 A; 22 C; 30 G; 19 T; 0 other;

//
```

Summary Table

Repeat Class	Fragments	Length
Integrated Virus	2	2284

```
        DNA Virus                                    2        2284
Multicopy gene                                       2         147
        tRNA                                         2         147
Transposable Element                                16        8533
        DNA transposon                               8        3314
            Harbinger                                2         147
            Mariner/Tc1                              1         211
            hAT                                      5        2956
        Endogenous Retrovirus                        3         654
            ERV1                                     1          90
            ERV3                                     2         564
        Non-LTR Retrotransposon                      5        4565
            CR1                                      2         531
            L1                                       1          68
            RTE                                      1        3910
            SINE                                     1          56
                SINE2/tRNA                           1          56
Total                                               20       10964
```

* 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.