**Supplementary Information**

# Data Set S1. Fasta alignments of all investigated phylogenetic informative loci.

Tracking marsupial evolution using archaic genomic retroposon insertions.

Maria A. Nilsson, Gennady Churakov, Mirjam Sommer, Ngoc Van Tran, Anja Zemann, Juergen Brosius, and Juergen Schmitz

Data set S1.
Fasta alignments of all investigated phylogenetic informative loci.

| Abbreviation | Scientific name |
|---|---|
| Mdo | *Monodelphis domestica* |
| Dvi | *Didelphis virginiana* |
| Mnu | *Metachirus nudicaudatus* |
| Rra | *Rhyncholestes raphanurus* |
| Cfu | *Caenolestes fuliginosus* |
| Dgl | *Dromiciops gliroides* |
| Nty | *Notoryctes typhlops* |
| Pta | *Phascogale tapatoafa* |
| Dgo | *Dasyurus geoffroii* |
| Scr | *Sminthopsis crassicaudata* |
| Mfa | *Myrmecobious fasciatus* |
| Bil | *Macrotis lagotis* |
| Pgu | *Perameles gunnii* |
| Iso | *Isoodon obesulus* |
| Tro | *Tarsipes rostratus* |
| Ppe | *Pseudocheirus peregrinus* |
| Tvu | *Trichosurus vulpecula* |
| Mro | *Macropus robustus* |
| Ptr | *Potorous tridactylus* |
| Vur | *Vombatus ursinus* |

**MARKER 08**

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**MARKER 14**

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CAAA--------------------------------------------------------
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-------------------CTGGGGAGACCCTAAGGAATGATCTGGTGTCCA-TCAATAC
ATGTGTAACATTGTCAGGTGGAA--TGGTGGCTTTGG---TGTGGAAGATGAGTAGTGTT
CCAGGTAAAGACAAGAGAATGA--ACAGAGGTCCAGAGAGTGAACTCATCTTCA------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------GAGAATGCTCTATAGGATAGA--------------------
----CTGATGACAGAGTATAAAAGGGAAAATAATGGGAGATGAGTTTGGGAATGTAGGGG
TTAGTCAAATTGTGGTGAGCTTT-GGTAAGACGAGCCAAGTAGCTAAGACTTTATTCTG-
CAAA--------------------------------------------------------
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-----TAGTAAGGA---ATCGGTGAAGG---TTTTGCAGCTGGG-AATACCATGATCAAA
TCCATATTT---------TAAAGGCATGATGA--------GATGATGAGG---CTTGCCC
TGTCTGCTTTCTAGTTTTTTTTTAA-----------------------------------
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------------------------------------------------------------
-------------------GTCAA---ATGAGAT--------------------------
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------------------------------------------------------------
---------------------TTTGGAT--------------------------------
----GGGAAAAGGACCATG-----------------AGAGATAGAAAGTACTACACAGAT
GTGAATTTCCTCACTTTTTCTCTCCCCTAG--GAGATGAGTTACCTT
>Rra
TCTCCTACACCAGTGTCCGAAGTAACAGCTCTTACCTGGGCAGTGATGAGATGGGGTCTG
```

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--GTAAGTAGGAGAAGGT------------------------------------------
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-------------------------------------CTCTTTTTC---AAGATGA----
------AAAGGAGAGGATACTAGGGAGACATTTAGGAAACATCTTATATATG-TCCAACT
TTATGTAGTATTACTGGACGGAA--TGGGTCCTTTGA---CTGGCAAGGCAAGTAGCATT
CTAGGTGAGGACAGTAGTATGAATAGAGAAGCCCAGAGGGAGAACTCATTTGCA------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------GGGAAAAGTTTATAGTGTAGT--------------------
----TTGATGAGAGAGT------------------GGAGGTATGGCTGGAAAGGTAAGGG
ATGGTCTATTTGTGGAGAATTTT-GACAAGACAAGCTAAGGAACT--AACTTTGTTCAT-
GAAG--------------------------------------------------------
------------------------------------------------------------
-----TAGTAGGGG---GTCTTTAAAAG---TTTTTAAACGCAG-CGTAACTTGGTCA--
-CCTTATTT---------TAAGGAGACAATA---------GGGAATGATAATACTTGCTC
TGTCTACTTCATAGGGTTGTTGTAAAAACAAA----------------------------
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------------------------------------------------------------
--------------------TCAG---ATGAGAT--------------------------
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------------------------------------------------------------
---------------------ACTGGTT--------------------------------
----GGGAAA-GGACTATG-----------------AGAGCTAGAAAGCACTCTACAAAT
GTGAGATTATACTCTTTTTCTCTCTCCCAG--GAGATGAATTGCCCT
>Nty
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--GTAAGTAGAATAGGGC------------------------------------------
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------------------------------------------------------------
-------------------------------------CA--TTTTC---AAAATGA----
------AAACAAGAGGGCCTTAGGGAGAC----AGGAAAGATATGGTGCACA-TCCATAA
ATGTGTAGCATTGTCAAGTGGAA--GGGGGTCTTTGG---TGGGAAGGATGAATAGCATT
CCAGGCAGAAACAATAGTATGA--ACAGAGGCCCAGAGGGTAGACTGTTTTTCA------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------GGAAACAGTTAA---TGTAGA--------------------
----TTGATGAGAGAATATGCAAGAGAAATTAA-GGGAGATAAAGTTGCGAAGATAGGAC
ACAGTCAGATGGTGAAGAACCTT-GGCAAGACAAGCTAAGGAGCTAAGGCTTTATTCAG-
TTAA--------------------------------------------------------
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-----TAGTAGGGG---GCCATTGAAGG--TTTTCTATTATTTTC-----CATAATCAGA
TTCATATTT---------TAAAGATATGACAG--------GAGA-TGATAATTCTTACCC
TGCCTATGTCATAGGATTCTTGTTAAAAAAAA-------AAAGTCAG----GGGGGCAGC
TAGATAGTGCAGTGGAT-AGAGCACTGACCTTGGACTTAGGAGGACCTGAGTTCAAATCT
AGCCTCAGACATTTGATACTTAGCTGTGTGGCCTTAGGCAAGTCACTTAACCCCAATTGC
CTAGGGGAAAAAA---AAAGTCAG---ATGAGAT--------------------------
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---------------------ATTGGCT--------------------------------
----GAGAAAGGACCAGAA---------------------GTAGAGAGTACTACCTGGAA
GTGAACTTTCTCATTCGTTCTTTCTCCCAG--GAGATGAGTTGCCTT
>Pta
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--GTAAGTAGGATAGGGC------------------------------------------
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-------------------------------------CA--TTTTC---AGGATGA---A
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ATGTGTAGTATTGTCATATGGAA--GGAGGTCTTTGG---TGAAGAG-------AATGTT
CCAGGCAGAGACAATAGTGTGA--AC---TGCCCAGAGGGTGGACTGATTATCA------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------GGGAACAGTT-------------------------------
---------------------------------------------------------GGG
GGGT-------GTGGT-AAGAAA-ATATTAGCAAGCTAAGGAGC-----------TCAGA
CTTA---TAGTAGGGA---CTTTCTTTATCCTGGAAACTACCTGATCCCATCTTTATGTA
TTTAAACCATCTTCCTCTTTGAAAGTCCTTGACCTTTGTCAAGCTTCTCAAAATAGAAAT
CT---TAGTAGGGC---GCTATTGAAGG--TTTTGAAAGTGGGGA--TA---TCATCAGA
TCTTTATTT---------TAAAGAGATGACA---------GAGGATGATAATCCTTGCTC
TGCCAA----CAAGGATTCTTGTTTAAAAAAAA---------------------------
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------------------------------------------------------------
-------------------ATCGG---ATGAGAT--------------------------
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------------------------------------------------------------
---------------------GTTGACT--------------------------------
----GGGAAA-AGACTACC-----------------------------GAAAGTGTGAAC
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>Dgo
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--GTAAGTAGGACAGGGC------------------------------------------
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CCAGGCAGAGACAATAGTGTAA--AC---TGCCCAGAGGGTGCACTGATTTTCA------
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------------------------------------------------------------
------------------------------------------------------------
-------------------GGGAACAGTTAAAGGTATAGA--------------------
----CTG---AGAGAGTTTGCAAGGAAA-TTAATGGGGGATAAAGTT-------------
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CTCC---TAGTAGGGA---CCGTCTTTACTCTGGAAATTACCTGATCCCATCTTTATGTA
TTTAAACCATCTTCCTCTTTGAAAGTCCTTGACCTTTGTCAAGCTTCTCAAAATAGAAAC
TT---TAGTAGGGA---G-----------------------------TA---TCATCAGA
TCTTTATTT---------TAAAGAAATGACA---------GAGGATGATAATCCTTGCTC
TGCCAA----CAAGGATTCTTGTTTAAAAAAA----------------------------
```

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-------------------ATCAG---ATGAGAT--------------------------
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---------------------GCTGACT--------------------------------
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>Scr
TTTCCTACACCAGTGTCCGCAGTAACAGCTCTTACCTGGGCAGTGATGAGATGGGATCTG
--GTAAGTAGGATAGAGC------------------------------------------
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CCAGGTAGAGACACTAGTGTGA--AC---TGCCCAGAGGGTGGACTGATTTTCA------
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------------------------------------------------------------
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------------------------------------------------------------
-------------------TGGGACAGTTAATGGTATAGA--------------------
----TTG---AAAAAGTATGCAAGGGAAATTAATTGAGA-TAAAATT-------GGCGGG
GGGTGGTGGTGGTGGT-AAGAAA-ATGTTGGCAAACTAAGGAGC-----------TCAGA
CTCC---TAGTAGGGA---CCTTCTTTACCCTGGAAACTACCTGACCCCATCTTTATGCA
TTTAAACCATCTTCCTCTTTGAAAGTTCTTGACCTTTGTCAAGTTTCTCAAAATAGAAAC
CT---TACTAGGGA---GCTATTGAGGG---TTTGTAAGTGGGGAGTAA----CACCAGA
TCTATATTT---------TAAAAAGATGACA---------GAGGATGATAATCCTTGCTC
TGCCAA----CAAGGATTCTTGTTTTTTAAAAAAAA------------------------
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-------------------ATCAG---ATGAGAT--------------------------
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>Mfa
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--GTAAGTAGGATAGGGC------------------------------------------
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ATGTGCAGCATTGTCAGGTGGAA--GGGGATCTTTAG---TACGAAGAATGAGTGATGTT
CCAGGCAGGGACAATACGATGA--AC---CTCCCAGAGGGTGGACTAATTTTTA------
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------GGGAACAGTTAATGGTGTANA--------------------
----TTG---ATAGAGTATGCAAGGGAAATTAATGGAAAATAAAGTT-------------
------GGAGGGTGGT-AAGAAA-ATGTTGGCAAGCTAAGGAGC-----------TCANA
```

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CTCC---TAGTAGGGA---CCTTCTTTACCCTGGAAATCACCTGACCCCATCTTTATGCA
TTTAAATCATCTTCCTCTTTGAAAGTCCTTAACCTTTGTCAAGCTTCTCAAAATAGAAAC
CT---TAGTAGGGA---GCTATTTATTGAAGTTATTAGGTGGAAAGTAA-TATGATCAGA
TCCATATTT---------TAAAGAGATGACA---------GAGGATGATAATCCTTGCTC
TGCCTA----CAAGGATTCTTGTTAAAGAATAAATA------------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------ACCAA---AAAAAAC--------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------------CAGGANT---TCTNGTTTTTTTTTTTTTTTTTTTTTTTA
AAGTCAGATG-AGATGCTG------------GCTTGGAAAAGACCATGGAAAGTGTGAAC
TTTCATGTA---CTTTGTTCTCTCTCCCAG--GAGATGAGTTACCTT
>Bil
TTTCCTACACCAGTGTCCGTAGTAATAGCTCTTACCTGGGCAGTGATGAGATGGGATCTG
--GTAAGTAGAATAAGGC------------------------------------------
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------------------------------------------------------------
-------------------------------------CA--TTTTC---AAGATGA----
------AAAGGAGAAGATGCTAGGGAGACATTTAGGAAATATTAGGTGGGTA-TTCATAT
ATGGGTAGCATTGCCTGGTAGAA--GGGGCTCTTCTTAGATGGAGAGGACAAGTGGCATT
CTAGGCAGAGAAAATTGTAAGA--ACAGA--GGCAGAGGATAAACTTATTTTCA------
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-------------------GAGAACAGTTAGTAGTATAGA--------------------
----TTAATGAGAGCATGTGCAAGAGAAATTAATGGGAGATAAAATTGGGAAGGTAGAAG
ACATTTAAACAGTGAATATTCTT-GAAAAGACAAGGTAAAGAGCTAAGACCTTATTCAG-
AAAA--------------------------------------------------------
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-----TAGTAGGGA---GTCATTGAAGA--TTTTGCAGGTGGGGAATGA-CATAATCAGA
TCCATATTT---------TAAAGAGATGAAAA--------GA-GTTGACA------GTGC
TGCCCACTTCATAGGATTCTTGTTAAA---------------------------------
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------------------------------------------------------------
-------------------GTCAA---TTGAGAT--------------------------
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T-------ACTCACTTGTTCTCCCTGGCAG--GGGATGAATTGCCTT
>Pgu
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CTAGGCAGAGAAAATAGTATCA--ATAGA--GGCAGAGAATAGACTCATTTT--------
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```

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------------------------------------------------------------
------------------------CAGCTAATAGTATAGA--------------------
----TTAATGAAAGAATATGCAAGGGAAATTAATGAGAGATAAAATT-------GGGAAG
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AAAA--------------------------------------------------------
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-----TAATAGGGA---GTCATTGAAGA--TTTTGCAGATGGGGAATGA-CATCATCAGA
TCCATGTCT---------TAAGGAGATGAAAA--------GAGA-TGACA------ATGC
TGCCTACTTCATAGGATTCTTGTTAAAAA-------------------------------
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-------------------GTTAG---ATGAGATA-------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------------ACTAGCT--------------------------------
----GGTTAA-GGACAATG-----------AGAAATAGAAAGCAGTACACCAATGTGGTT
T-------ACTCATTTGTTCTCCCTGGCAG--GGGATGAATTGCCTT
>Iso
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--GTAAGTAGGATAGAGC------------------------------------------
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ATAGATAGCATTGTCATGTAGAA--GGGGCC---CTTAGATGGGGAGGATAAGTGGTATT
CTAGGCAGAGAAAATAGTATCA--ATAGA--GGCAGAGACTAGACTCGTTTTCA------
------------------------------------------------------------
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------------------------------------------------------------
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-------------------GAGAACAGCTAATAGTATAGA--------------------
----TTAATGAAAGAATATGCAAGGGAAATTAATGAGAGATAAAATTGGGAAGGTACGAG
ACA-------TTTAAAGATTCTT-GGCAAGATAAGCTTAAGAGCTAAGATTTTATTCAG-
AAAA--------------------------------------------------------
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-----TAATAGGGA---GTCATTGAAGA--TTTTGCAGATGGGGAATGA-CATCATCAGA
TCCATATCT---------TAAGGAGATGAAAA--------GAGA-TGACA------ATGC
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T-------ACTCATTTGTTCTCCCTGGCAG--GGGATGAATTGCCTT
>Ppe
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--GTAAGTAGGACAAAAC---CATTTTC--TTTTTTCTTCTTTTTCTTTTTTCTTTTTGG
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GTGTTAAGTGTG--AGGCTGGATTTGAACTCAGGTCCTCCTGACTCCAGGGCTGGTGCTC
TATTCAGTGAGCCACCTAGCCACCCCAACAGGAC---CA--TTTTC---AAGATGA----
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```
------AAAGGGGAGGACACTAGGGAGACTTTTAGGAAAGATCTGGTGTACATTACATAT
ATATGTAACATTGTCAGGTGGAA--GGGGGTCTTCAG---TGGGGAGGATGAGCAGGATT
CCAGGCAGAGACAGTAGTGTGA--ACAGAGGCCCAGAACGTGGACTAGTTTTCA------
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------------------------------------------------------------
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------------------------------------------------------------
-------------------GGAAACAGTTAATAGTATAGATTGATGAGAGAGTATGCAAG
CAAATTAATGGGAGATAAAGCT-------------------------GGCAAGATAGGAG
GCAGTCAAATAGTGGAGAACCTT-GGCAAGACAAGCTAAGGAGCTAAGACTTTATTCGG-
TAAA--------------------------------------------------------
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-----TAGTAGGGA---GCCACTGAAGA--TTTTGCAGATGGTGAGTAA-CATGATCAAA
TTCATATTT---------TGAAGAGATGACAA--------GAAA-TGATGATGTTTG---
------TTTCATAGAATTCTTGTTTTAAAAAAAAT-------------------------
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-------------------GTCAG---ATGAGAT--------------------------
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-----------------------------------------------------TGTGAAA
T------TACTCACTTGTTCTCTCTTCTAG--GAGATGAGTTGCCTT
>Mro
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--GTAAGTAGGATAGGGC------------------------------------------
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------------------------------------------------------------
-------------------------------------CA--TTTTC---AAGATGA----
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CTGTGTAGCATTGTCAGGTGGAA--GAGGGTCTTTGG---TGGGGAGGATGAGCATCATT
TCAGGCAGAGACAGTAGTATGA--GCAGAGGCCCAGAAGGTGGACTAATTTTCA------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
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-------------------GGGAACAGTTAATAGTATAGA--------------------
----TTGATGAGAGAGTAAGCAAGGAAA-TTAATAGGAGATAAAATTGGGAAGGTAGAAG
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-----TAGTAGGGT---GCTGCTAAAGA--TTTTGTAGGTGGGGAGTAA-CATGATCAGA
TCCATATTT---------TAAAGAGATGACTG--------GAGG-TGACAATGCTTGGCC
TGCCTACTTCTCAGGATTCTTGTT-AAAAAAAAAT-------------------------
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------------------------------------------------------------
-------------------GCCAG---ATGAGAT--------------------------
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------------------------------------------------------------
---------------------ACTGGCT--------------------------------
----GGGAAA-GGACTGTG-----------AGAAGTAGAAGGCACTACACAGATGTGCAC
T------GACTCACTTGTTCTCTCTCCCAG--GAGATGAGTTACCTT
>Ptr
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--GTAAGTAGGATAGGGC------------------------------------------
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-------------------------------------CA--TTTTC---AAGATGA----
------AAGGGAGAGGATGCTAGGCAGACATTTAGGAAAGATCTGGTGTACA-TCCTTTT
ATGTGTAGCATTGTCAGGTGGAA--GGAGGTCTTTGG---TGGGGAGGATGAGCGGCATT
TCAGGCAGAGACAGTAGTGTGA--GCAGAGGCCCAGAAGGTGGACTGATTTTCA------
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------------------------------------------------------------
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-------------------GGGAACAGTTAATAGTATAGA--------------------
----TTGATGAGAGAGTATGCAAGGAAA-TTGATAGGAGATAAAGTTGGGAAGGTAGAAG
ACAGTCAAATGGTGGAGAACCTT-GGCAAGACAAGCTAAGGAGCCAAG-CT--ATTCAA-
TAAA--------------------------------------------------------
------------------------------------------------------------
-----TTGTAGGGT---GCTGCTAAAGA--TTTTGCAGGTGGGGAGTAA-CATGATCAGA
TCCATATTT---------TAAAGAGATGACTG--------GAGG-TGACAATGCTTGCCC
TGCCTACTTCACAAGATTCTTGT--TAAAAAAAAT-------------------------
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---------------------ACTGGCT--------------------------------
----GGGAAG-GGAC--TG-----------AGAAGCAGAAGGCACTAC-CAGATGTGAAC
T----------TACTTGTTCTCTCTCCCAG--GAGATGAGTTGCCTT
>Human
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
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------------------------------------------------------------
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------CAGACTCCACATCCCTTGTGGGTTTGGAGTT--CTGTAGCTGT
ATCCCCCT---------CTTAGGAAAGTGCTGGGGATGG---------------------
------------------------------------------------------------
------------------------------------------------------------
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------------------------------------------------------------
```

```
------------------------------------------------------------
------------------------------------------------------------
------------------------------TGTGAGGTGGGGCAGGAATGACTGATGG-C
T--------GCTGCTTCTACCTCCTGCCAG-GAGATGAGCTGCCCT
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**MARKER 20**

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>Mar1c_Mdo
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--TAAGGCAAACAGAGGTTAAGTGACTTGCCCAGGGTCACACAGCTAGTAAGTGTCTGAG
GCCGGATTTGAACTCAGGTCTTCCTGACTCCAGGCCCGGCGCTCTATCCACTGAGCCACC
TAGCTGCCTCC-------------------------------------------------
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------
>Mdo
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TATCAGCCAATTAAAGGATAAGTGCTTTGCCCAGAGTTGTGTAGCTAGGTTGTATCTGAG
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GCTTAATTGTATGACCATAAGTCATTAAATATAAGCACTTAAAA-------TATTTTTAC
TATGATTTTACTCCATGTCTTTTGGAGCTAATTTATATATTAAAGTTATCTCCATAGGGC
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-AAAGTTTTCTAT-----TGATAAGCATAGAAA----TGTACTTATATTACTGTTTGTTA
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-AAAAG
>Dvi
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-TGGCAAAAATACTAGAATGATTTGCCATTTCCTTTTCCAGCAGATTCACTGGATTCTTT
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-AAAGTTTTCTAT-----TGATAAGTGTTGAAA----TGTAATTATATTACTGTTTGTTA
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T-AAAT
>Mnu
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-ATAGAATATCTAATGTAGAAACTTCATTTCAT---AAAATTGCAAAT---TGTTCAGTT
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TGTCAACCAGTTAAAGGTTAAGTGCCTTGCCAAGAGCTTTGTAGCTAGGTTGTATCTGAG
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AAGATGGT-GGGAGAGAA-GATTC--GTGCTGTATGTTTAATTTATAAATTATTC-----
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TAAAAG
>Cfu
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------------------------------------------------------------
--------------------------------ACTTT-AAACTTT-AAGATAAAATAGAT
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-AAAAG
>Dgl
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--------------------------------ACTTT-AAACTTT-AAGATAAAATAAAT
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TATCATTTTACTCCATGTCTTTTGG----------------AAAATTATCTCCATATGAC
TAGAACTT-GGGAGAAAA-GATTC-TGTGCTATGTATTTCATTTATAA-TGATTA-----
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---AGTTTTCTATTTTATTGAAAAGGGTAGAAA----TGTAATTGTATTACCATTTGCTA
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-AAAAG
>Nty
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AATGGAATATCTAATGTAGAAACTTCATTTCAT---AAAATTGCAGAT------------
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------------------------------------------------------------
--------------------------------ATATT-AAACTTT-AAGATAAAATAAAT
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GCTTAACTATGTGACTATGAGTCATTTAAGATAGACATTTAAAT----TAC-TCTTTTAT
TATGATTT----------------------------------------------------
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-AAAAG
>Dgo
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------------------------------------------------------------
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TATGATTTTACTCCCATATAATTAG-----------------------------------
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CATTAATTTATGATGACTA---TTTTGTTTCTTTTT---AATTAAAGTTTTATTATTTTT
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**MARKER 26**

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CTGACATTTCAGGTCTTATTGCTTCCTTCACCGTTTATTTGGAGATTTTCATGCTTTGAC
CC-CTTGAATCACCTCTCTTGATCCAATCCTTCCTTTCTATTGTCAGTTTGAAGTAAATT
CTACTTGCTCACTTATTCATTCTTTAGTTTTG-ACTTACATCATCA------------CC
CA--CCCCATTTTGTTCC------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------------------------TACAAGG
TAT-------------------AGGA-TGGGGCATCTAAAGTAATTCATAGT-GCTCTTC
TA-AGTCTCCCCATTAT--------------------------GGACACAAGTGTAAAAG
AAATACAGAGAACCAAAAGTGTAAGCAGCTCGTGGAACCCAAACACAGAAATGTTTGCAT
```

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GCTTCCCAAGACTTAC--TTTCCTTT--GTTAAATATGGA
>Ptr
CCACGCATCTTTATGTATAGTTGAC--CTTCAAAAGAAGATAGGGTTATAGTTAGCACAG
AGGTCAAAGCATCCACTGAAATATCTAAATGGCCATTTT---CTTTGATCAAAAAA----
----------------------TTCCTCTTCATTTGGGAG------------------CA
TTTCTAGCCTTAGTAAGCAAAGTAAAA--TGAACTTGAGATTTGGAATAAAATTTTAAAA
GAACATT---TATATAGAATTCTAGTTGAAAGAACTAGTTACATGAAGCCTGGAGAAGGG
AAGACTTGGGGGAGCAAG------CATGACAGTCATCTTCAA-GTATGTGAAGGACCTAT
AGAAAGAAGGGGGA-TTAAATTTGTTCTAATGGACCCTAGAAGGCAGAACCAGAGGTGAT
GGG---TGGATGTTTTGGAGAGGCAGATCATACATATGTAAGAAAATCCCCCTGGACCCA
CCTGGACCCAACTGCAACAGAAAAAGACTCTT----ATCTGTTTCTCAAAG----CTTCC
CTGGCATTTCAGGTCTTATTGCTTCCTTCACCCTTTATTGGGAGATTTTCATGCTCTGAC
CC-CGTGAATTGCCTCTCCTGATCCAATCCTTCCTTTCTATTGTCAGTTTGAAGTAAATT
CTACTTGCTTACTCATTTATTCTTTAGTTTTGACCCTACATCATCA------------CC
CA--CCCCATTTTGTTCC------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------------------------TACAAGG
TAT-------------------AGGA-TGGGGTATCTAAAGTAATTCAGAGT-GCTCTTC
TA-AGTCTCCCCATTAT--------------------------GGACACAAGTGTAAAAG
AAATAATGAGAAACA------------GCTCATGAAACCCAAACACACAGAAA-------
CATTTGCAAGACTTAC--TTTCCTTT--GTTAAATATGGA
>Vur
CCATGCATCTTTGTGTACAGTTGAC--CTTCAAAAGAAGATAGTG---TAGTTAGCAGAG
GGACCAAAGCTTCCATTGAATTATACAGATTGCTCTTTT---CCTTGATCAAAAAAA---
----------------------CTCTACTTCATTTGGGGG------------------CA
TTTCCAGTCTTAGTAAGGAAAGTAAAA--TGAACTCGAGTTTTGAAATGAAATTTTAAAA
GAGCATT---TATATAGCACCCTAGCTGAAAGAACTTGTTATGTGAAGCCTGGAGAAGGG
AAGACTTGAGGGAGGAGG------CATGATAGTCATCTTCAA-GTATGTGAAGGATCTAT
ACAAGGAATAGGGA-CTAGATTTGTTCTAATGGACCCCAGAAGGCAGAACCAGAGGCAAT
GGG---TGGATGTTTTGGAGAGGCAGATCATATATAGATAAGAAAGCCCCCCTGGACCCA
TCTGGCCCCAACTGCAACAGAGAAAGATTATTTCTTATCTGGGTCTCAAAG----CTTCC
TTGAAATTTCAGATCTTACTGCTTCCTTCACCCTTTATTTGGAGATTGCCATGTTCTGAC
TC-CTTGAAGCAACTCTCTTGCCTCCATCCTTCCTTTCTATTGTCAGCTTGAAGTAAATT
CTACTTGCTCACTAACTCATTCTTCAGTTCTGACCATACATCATCAGCCACCTCATCCCT
CA-GCCCCATTTTGTCCC------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------------------------TGCAACG
AAT-------------------AGGA-TGGTGTCTCTAAAGTAATTCTGAAT-GCTCTTC
TA-AATCTCCCAATTAT--------------------------GGACACAAGTGTAAAAG
AAATATAGAAAACCAAAAACATAAGCAACTCATGTAACCCAAACACAGAAAGGTTTGCAT
GCTTCCCAAGACTTAC--TTTCCTTT--ATTAAATATGGA
>human
CCATGCCTTCTTGTGGACCATTGAC--CTTCGAAAA------------------------
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------------------------------------------------------------
---------------------------------------AAGACAAATTTGCCTATTTCT
ATACCCAGTTACTTAC--TTTCCTTT--GTTAAATACTGA
```

**MARKER 38**

```
>Hal1_Opos1_3end
------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------------TTTTTATT-
---ATATACTTAGTA--ACCACCACCACCAACAAAAAA---CATTTAAATAAACAAATGC
ATAAAAAAATTATGTGCAAAACCACAAACTCCACATTGTTTACAATTTGTTTAAAAATAT
GTAAATTATATATGTGTGCTAATATAAACATCCTCTGCTTTTGAGTTCCCTTTGGATTTG
TTTTACTTNGATACTTTTTT-CTCTTGATTTTGTGGC-----TATTTTTNAAATGTAATC
ATAGTATGTATTATTCTTATTCTCTTTTCTTCTCTTTTCATCTCTTCATATATTTCCCTT
ATTTTCTTTATATTTCCAATATTTGTCATTTCTAATAACATAATACAATCCATTACATTC
AAATATCACAATCTATTCAGCCATTTCT--------------------------------
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----------------------------------------------------
>L1_Opos2_3end
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------------------------------------------------------------
---------------------------------TTTTTTTTTTCCCCAATTACATGTAAA
AACAATTTTTAACATT--TTTTTAAAAATTTTGAGTTCCAAATTCT--------------
------------------------------------------------------------
----------------------------------------------------
>Mdo
AAAAT--CTAATGAGAAATAACTGAAGCTATAA------------------------GCA
TTGT----GGGAAGTCACAAAAA----GTGTCTACATGTGTCCCGAAAACAAAG--ATTC
TCGTTTGGGGAAAC-GAGCCATTT------CGTGGT---AGGCTAAAA---CTATTA-TC
TTTTTAAAAATTGTATATTAATAACCACAAACAAAAAATAACATTTAGCCAAACAA----
---------GTATGTGAAAAATCACAAGTTTAACATTGTTTCAAATTTGTTTAAAAGTAT
ATAAAGTATATATGTGTTCTAATGCAACTATTCTCTGCTTTTATGTTTCCTTTAGGTTTT
TT-AATTTGGATACTTTTTTCCTCTTGATTTTGTGGCTGC--TATTTTT--AATGTAAGC
ATAGTATGTATCATT----------CCCATCCTCTTTT-A-TTCTCCATATATTTACCTT
ATTTTCTTTATATTTCCGATATTTGTCATTTCTATTAACACACTA-----CTTTACCTTC
AAATAAT----------------------------------------------GATTGAA
CTCTATAAAATTCCACTAGTGTCCACTTGGTGGTGCACAAGACA---TAC--CTTAT---
------------------------------------------------------------
------------------------------------------------------------
GCTCTTGAATGATCTTTTCACTGCCTTCCTGTAGCACCAACTTGTTCTCTCGACCAAGCT
CAGTTCTGCATTCTTCTACTAAAGCTAGGAACCTGTTTTTTTCCACTTCTAT
>Mnu
AAAAT--CTAATGAGAAATAACCGAAGCTATAA------------------------GTA
TTGT----GGTAAGTCACAAAAA----GGGTCTACATGTGTGCCCAAAACAAAAAGATTC
```

```
TCACATGGGGAAAT-GTGCCATTT------CATGGT---AGGCTAAA----CTGTTATGC
TTTTTAAAAATTGTATATTAATAACCACCAACAAAAAA---CATTTAACTAAACAA----
---------GTATGTGCAAAATCACCAGCTGCGCATTGTTAAAATTTTGTTTCAAATG-T
ATAAATTTTATACATGTGCTAATA------TCTTCTGCTTTTATGTTTCCTTTAGGTTTG
TTTTATTTGGATACTTTTTT-CTCTTGATTTTGTGGCTGCCATATTTT---AATGTAAGT
ATAGTATGTATCATT----------CTTATTCTCTTTTCTCCTCTTTAAATATTTACCTT
ATTTTCTTTATATTTCCGATATTTGTCATTTCTAATCACACAGTAGAATGCTTTACATTC
AAATAAC-----------------------------CAAG-TTTATTACCTTTGAATGAA
CTCTATAAAATTCCACTAGTGTCCACTTGGTGGTGCATAAGACA---TAC--CTTAT---
------------------------------------------------------------
------------------------------------------------------------
GCTCTTGAATGATCTTTTCACTGCCTTCCTGTAGCACCAACTTGTTCTCTCGACCGAGCT
CAGATCTGCATTCTTCTACTGAAGCTAGAAACCTGTTTTTTTCCACTTCTAT
>Rra
AAAAC--CTATTGAGAAAGACCTGAAACTGTAA------------------------GTA
TTAT----GGGAAACCATAAGAA----GTCTCTACATTATTATAGGGGGGAAAAGGATTC
ACACTTGGG-AAATTGAGTTATTTTGTGATTTTGGTCTCAGGCCAAA-------------
------------------------------------------------------------
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------------------GTATCACAA---------------TCAAA
CTCCATAAAATTCCACCAATGTCCATTTGGTGCAACACGAAACA---TAC--CTTAT---
------------------------------------------------------------
------------------------------------------------------------
GCTCTTGAATGATTTTTTCACTGCCTTCCNGTAGCACTAACTTGTTCTCTCGACCAAGCT
CTGATCTGCATTCTTCTATTGAAGCTAGGAATCTATTTTTCTCTACTTCTAT
>Cfu
AAAAC--CTATTGAGAAAGACCTGAAACTATAA------------------------GTA
TTAT----GGGAAACCATAAGAA----GTCTCTAGATTACTATAGAAAAAAAAGG-ATTC
ACACTTGGG-AAATTGAGTTATTTTGTGATTTTGGTCTCAGGCCAAA-------------
------------------------------------------------------------
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------------------GTATAACAA---------------TCAAA
CTCTATAAAATTCCACCAATGTCCATTTGGTGCAACATGAAACA---TAC--CTTAT---
------------------------------------------------------------
------------------------------------------------------------
GCTCTTGAATGATTTTTTCACTGCCTTCCTGTAGCACTAACTTGTTCTCTCGACTAAGCT
CTGATCTGCATTCTTCTATTGAAGCTAGGAATCTATTTTTCTCTACTTCTAT
>Dgl
AAAAC--CTAATGAGAAACAAGTGAAGTTATAA------------------------GTA
TGGT----GGGAAGCCATTAAAAC-----------------------AACAAA--TATTC
TCCCTTGGG-AAATTGAGACATTTTGTGATTTTGGTCTCAGGCCAAA-------------
------------------------------------------------------------
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------------------------------------------------------------
------------------------------------------------------------
-------------------------------CTATCCCAG--TTG---------------
-------AAATTCCACTAGTGTCCGCTTGGTGGTGTATGAGACA---TAC--CTTAT---
------------------------------------------------------------
------------------------------------------------------------
GCTCTTGAATGATCTTTTCACTGCCTTCCTGTAACACCAATTTATTCTCTCGGCCAAGCT
CAGATTCACACTCTTCTACTGAAGCTAGAAACCTGTTTTTCTCCACTTCTAT
>Nty
AAAAT--CTAATGAGAAACATCTGAAGCTGTAA------------------------GTA
TTGTATGCAAGAAACTTCGAAAAG---GTGCTTACATTTGTACAGAAAACAAAAGTATTT
TCCCTTGGG-AAATTGAGTTGTTTTGTGATTTGGGTCTCAGGCCAGA-------------
------------------------------------------------------------
------------------------------------------------------------
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------------------GTATCACAG-TTCATTACCACTGCACTAA
CTTCATGAAATTCTGCTAGTGTCCACTTGGTGGTGCATGAGACA---TAC--CTTAT---
------------------------------------------------------------
------------------------------------------------------------
GCTCTTGAATGATCTTTTCACTGCCTTCTTGTAGCACCAACTTGTTCTCTCTACTAAGCT
CAGATTTGCACTCTTCTACTGAAGCTAGAAATCTGTTTTTTTCCACTTCTAT
>Pta
AAAAT--CTAATGAGAAACAGAAGAAGCTATCA------------------------GTA
TAGTATTTAAGAATCCACAAAAAAA--GTGTCTACATTTGTATAGAAAACAAAAATATTC
TCCCTACAG-AAATTGGGCCATTTTGTCATTCTGGTCTCATGCCAGA-------------
------------------------------------------------------------
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------------------CTATCACAG-GTTGTTACCTTTGG-TGAA
CTTCATGAAATTCCACTAATTTCCACTTGGTGGTGCCTAAGACA---TAC--CTTAT---
ATTTTTTAATTAAATTTTTAAAAATAGGTTTTTGGGTTTTTTTTCCCAGTTACATGCAAT
GAAAATTTTTAGCATTCATTTTTACAAG-------ATCCAAATTCT---TACCTTAT---
GCTCTTGAATGATCTTTTCACTGCCTTCCNGTAGTACCAATTTGTTCTCTCGACCCAGTT
CAGATTTGCACTCTTCTACAGAATCTAGAAATCTATTTTTCTCCACTTCTAT
>Dgo
AAAAT--CTAATGAGAAACAGATGAAGCTATCA-----------------------AGTA
TTGTATTTAAGAATCCACAAAAAA---GTGTCTACATTTATATGGAAAACAAAAATATTC
TCCTTTGGG-AAATTGGGCCAYTTTGTCATTCCGGTCTCATGCCAGA-------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------------------CTATGACAG-TTTGTTACCTTTGG-TGAA
CTTAATGAAATTCCACTAATGTCCACTTGGTGGTGCATAAGACA---TAC--CTTAT---
ATTTTTTAATTAAATTTTTAAAAA--GTTTTTTTGGCGTTTTTTCCCAGTTACATGTCAT
```

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GAAAATTTTTAGCATTCATTTTTATAAG-------ATCCAAATTCT---TACCTTAT---
GCTCTTGAATGATCTTTTCACTGCCTTCCTGCAGCACCAATTTGTTCTCTCGATCCAGTT
CAGATTTGCACTCTTCTACTGAAGCTAGAAATCTATTTTTCTCCACTTCTAT
>Scr
AAAAC--CTAATAAGAAACAGATGAAGCTAKCA------------------------GTA
TTGTATTTAAGAATCCACAAAAAAAATGTGTCTACAGTTATATAGAAAACAAAAATATTC
TCCCTTGGG-AAATTGGGCCATTTTGACATTCTGGTCTCATGCC----------------
------------------------------------------------------------
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------------------------------------------------------------
--------------------------------AGACATAG-TTTGTTACCTTTAG-TGAA
CTTCATGAAATTCCACTAATGTCCACTTGGTGGTGCATAAGACA---TAC--CTTAT---
ATTTTTAAATTAAATTTTTAAAAA----------------------TAGT--CACGTCAT
GAAAATTTTTAGCATTCATTTTTACAAG-------ATCCAAATTCT---TACCTTAT---
GCTCTTGAATGATCTTTTCACTGCCTTCCTGTAGCACCAATTTGTTCTCTCGACTCAGTT
CAGATTTGCATTCTTCTACTGAAGCCAGAAATCTATTTTTCTCCACTTCTAT
>Mfa
AAAAT--CTAATGAGAAACAGATGAAGTTATCA------------------------GTA
TTGTATTAAAAAATCCACAAAAAG---GTGTCTACATTTGTATAGAAAACAAAAATATTC
TCCCTTGAG-AAATTGGGCCATTTTGTCATTCTGGTCTCATGCCAGG-------------
------------------------------------------------------------
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------------------CTATC--AG-TTTGTTACCTTTGG-CGAA
CTTCATGAAATTCCACTAATGTCCACTTGGTGGTGCATAAGACA---TAA--CTTTT---
----TTAAATTAAATTTTTAAAAA--TAATTTTTTGAGTTTTTTTCCAGTTACATGTCAT
GAAAATTTTTAGCATTCATTTTTACAAG-------ATCCAAATTCT---TACCTTAT---
GCTCTTGAATGATCTTTTCACTGCCTTCCTGTAGCACCAATCTGTTCTCTCGACCCAGTT
CAGATTTGCACTCTTCTACTGAAGCTAGAAATCTATTTTTCTCCACATCTAT
>Bil
AAAAT--CTAATGAGAAACAGCTGAAGCTATAA------------------------ATA
TTGAATAAAGGAAGTCATAAAAAG---GAGTCTACATTTGTAGAGAAAACAAAAACATTC
TCCTTTTCG-AAATTG---CA-----CCTTTTYGGTCTGTCAGACYA-------------
------------------------------------------------------------
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------------------------------------------------------------
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------------------------------------------------------------
----------------------------------TCATAG-TTTGTTACCTTTTCATGAA
TGCCACAAAATTTCATTACTGTCCACTTGGTGGTGCATGAGACA---TAC--CTTAT---
------------------------------------------------------------
------------------------------------------------------------
GCTCTTGAATGATCTTTTCACTGCCTTCCTGTAGTACCAACTTGTTCTCTCGACCCAGTT
CAGATTTGCATTCTTCAACTAAAGCTAGAAATCTATTTTTCTCCACTTCTAT
>Pgu
AAAAT--CTAACGAGAAACAGCTGAAGTTATAA------------------------ATA
```

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TTGAATACTGGAAATCACAAAAAAG--ACTTCTATGTTTGTAGAAAAAAGAAAAACATTC
TCCCTTGGG-AAATTG---CA-----TCATTTTGGTCTCAGTCCAA--------------
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------------------------------------------------------------
-------------------------------CTGTCACAG-TTTGTTACCTTTTCATGAA
TGCCACAAAATTTCATCACTGTCCACTTGGTGGGGCACAAGACA---TAC--CTTAT---
------------------------------------------------------------
------------------------------------------------------------
GCTCTTGAATGATCTTTTCACTGCCTTCCTGTAGTACCAACTTGTTCTCTCGACTCAGTT
CAGATTTGCATTCTTCAACTAAAGCTAGAAATCTATTTTTCTCCACTTCTAT
>Iso
AAAAT--CTAAAGAGAAACAGCTGAAGTTATAA------------------------ATA
TTGAATACTGGAAATCACAWAAAG---ACTTCTATGTTTGTAGAGAAAACAAAAACATTC
TCCCTTGGG-AAATTG---CA-----TCATTTTGGTCTCAGTCCAA--------------
------------------------------------------------------------
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------------------------------------------------------------
-------------------------------CTGTCATAG-TTTGTTACCTTTTCATGAA
TGCCACAAAATTTCATCACTGTCCACTTGGTGGGGCACGAGACA---TAC--CTTAT---
------------------------------------------------------------
------------------------------------------------------------
GCTCTTGAATGATCTTTTCACTGCCTTCCTGTAGTACCAACTTGTTCTCTCGACTCAGTT
CAGATTTGCATTCTTCAACTAAAACTAGAAATCTATTTTTCTCCACTTCTAT
>Tro
AAAAT--CTGATGAGAAACAGCTGAAGCTGTAA------------------------TTA
CTGTATACAGGAAGCCGCAAAAAG---GTGTCTACATTTGTGCTGAAAACAAAAATATTC
TCCCTTGGG-AAATTGAGCCATTTTCTGTTTTTGGTCTCAGGTCAGA-------------
------------------------------------------------------------
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------------------------------------------------------------
-------------------------------CCATCCCA--TTCATTACCTCTGCAGGAA
CTCCATGAAATTCCACTAATGTCCACTTGATGGTGCATGAGACA---TAC--CTTAT---
------------------------------------------------------------
------------------------------------------------------------
GTTCTTGGATGATCTTTTCACTGCCTTCCAGCTGCACCAACTTGTTCTCTCGTCCAAGCT
CTGATTTGCACTCCTCTACCAAAGCTAAAAATCTGTTTTTCTCCACTTCTAT
>Ppe
AAAAT--CTAACGAGAAACAGCTGAAGCTATAA------------------------GTA
TTGTATACAGGAAGCCAC-AAAAC---GTGTCTACATGTGTACAAAAAACAAAAATATTT
TCCCATGGG-AAACTGAGCCATTTTGCGATTTTGGTCTCAAGCCAGA-------------
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------------------------------------------------------------
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------------------------------------------------------------
-------------------------------CAATCATCGATTTGTTACCTTTACATGAA
CTCCATGAAATTCCACTAATGTCCACTTGGTGGTGCATGAGACA---TAC--CTTAT---
------------------------------------------------------------
------------------------------------------------------------
GTTCTTGAATGATCTTTTCACTGCCTTCCAGCAGCACCAACTTGTTCTCTCGACCAAGCT
CTGATTTGCACTCTTCTACTGAAGCTAAAAATCGGTTTCTCTCCACTTCTAT
>Mro
AAAAT--CTAGAGGGAAACAGCTGAAGCTATTA------------------------GTA
ATGTACACAGGAAGTCGCAAAAAA---GTGTCTACATTTGCACAGGAAACAAAAATATTC
TCCTTTGGG-AAACTGAGCCATTTTGTGATTTTGGTCTCAGACCAGA-------------
------------------------------------------------------------
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------------------------------------------------------------
-------------------------------CTATCACAG-ATCTTTATCTTTGTACAAA
CTCGACAAAATTCCACTAACGTCCACTTGGTGGGGCATGAGACA---TAC--CTTAT---
------------------------------------------------------------
------------------------------------------------------------
GCTCTTGAATGATCTTTTCACTGCCCTCCTGTGGCACCAACTTGTTCTCTCGACCAAGCT
CTGATTTGCACTCTTCTATTGAAGATAAAAATCTGTTTTTCTCCACTTCTAT
>Ptr
AAAAT--CTAGAGAGAAACAGCTGAAGCTATAAGTAACATAATAAGTAAATAAAGTAATA
AGTAATATAAGTAAAGTCAAAAAA---GTATCTACATTTGTACAGAAAACAAAAATATTC
TCCTTTGGG-AAACTGAGCCATTTTGTGATTTTGGTCTCAGGCCAGA-------------
------------------------------------------------------------
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------------------------------------------------------------
-------------------------------CTATCACAG-TTCTATATCTTTGTACAAA
CTCGCCAAAATTCCACTTATATCCACTTGGTGGG-CATGAGACA---TAC--CTTAT---
------------------------------------------------------------
------------------------------------------------------------
GCTCTTGAATGATCTTTTCACTGCCTTCCTGTGGCACCAACTTGTTCTCTCGACCAAGTT
CTGATTTGCACTCTTCTATTGAAGATAAAAATCTGTTTTTCTCCACTTCTAT
>Vur
AAAAT--CTAATGAGAAATAGCTGACAGTATAA------------------------GTA
CTGCATACAGGAAGTTGCAAAAAG---GTGTCTACATTTGTACAGAAAACAAAAATATTC
TCCCTTGGG-AAATGGAGCCATTCTGTGGTTTTGGTCTCAGGCCAGA-------------
------------------------------------------------------------
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------------------------------------------------------------
-------------------------------CTATCATAG-TTCATTACYTTTGCATGAA
TTCCACAAAATTCCACTAAGGTCCACTTGGTGGTGCATGAGACA---TAC--CTTAT---
```

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------------------------------------------------------------
------------------------------------------------------------
GCTCTTGAATGATCTTTTCACTGCCTTCCTGTAGCACCAACTTGTTCTCTCGACCAAGTT
CTGATTTGCACTCTTCTACTGAAGCTAGAAATCTGTTTTTCTCCACGTCTAT
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## MARKER 57

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>WSINE1
------------------------------------------------------------
------------------------------------------------------------
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------------------------------------------------------------
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------------------------------------------------------------
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------------------------------------------------------------
----------------------------------------------TTTTTTTTTTTTTT
---GAGGCAATTGGGGTTAAGTGACTTGCCCAGGGTCACACAGCTAGTAAGTGTCTGAGG
CTGGATTTGAACTCAGGTCCTCCTGACTCCAGGGCTGGTGCTCT----------------
-------------------------------------ATCCAC-----------------
--------TGCACCACCTAGCTGCCCCTC-------------------------------
------------------------------------------------------------
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>Mar1b_Mdo
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------------------------------------------------------------
-------------------------------AGGGCAGCTAGGTGGCACAGTGG-ATAGA
GCGCCGGGCCTGGAGTCAGGAAGACCTGAGTTCAAATCTGGCCTCAGACACTTACTAGCT
GTGTGACCCTGGGCAAGTCACTTAACCCTGTTTGCCTCAGTTTCCTCATCTGTAAAATGA
GCTGGAGAAGGAAATGGC--AAACCACTCCAGTATCTTTGCCAA-GAAAACCCCAAATGG
GGTCACGAAGAGTCAGACATGACTGAAAACGACTGAACAACAACAACAA-----------
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>WSINE1
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------------------------------------------------------------
-----------------------------------------------------GAGGGGC
AGCTAGGTGGTGCAGTGGATAGAGCACCAGCCCTGGAGTCAGGAGGACCTGAGTTCAAAT
CCAGCCTCAGACACT-----------TACTAGCTGTGTGACCCTGGGCAAGTCACTTAAC
CCCAA-TTGCCTC-AAAAAAAAAAAAAA--------------------------------
--------------------------------------
>RTE1_Mars
------------------------------------------------------------
---------------------------------TTGGGTGGACCCTCTGTGG-------A
GGATTTATGGGAGGACATGGACAAGAGT--------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---CACACAGGATGAGNAGGCATGGATGGGTTGCGATCTGCATCACTGGAGGGAGT-ACC
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------------------CACATCGATGAGATCACAGATCCATTGA
AGTATTGAAGTA---TTGAA----------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
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------------------------------------------------------------
------------------------------------------------------------
--------------------------------------
>Mdo
TTCACTTTCTCCACATCTTTTCCTTGTCTCTGAAA--CTTAATTTAAAGAGCAAAGTCAA
TGTTAGCAAGAAGAG-CACTCCAACAGCA---TTTTTGAAGACTA--------GGAACAT
```

```
GG-TTTG-GGGAGGGCTTGAACAAGAGT--------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---CACTTGGGACGATGAGGAGTGGAGATGTTACACTTTATGCCACTGAAGGGAGG-ACT
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------------------CAAAACACAGGT-CCA-TG----AAGGA
AGAGATTCCCTA---CTACTTCTTTA---GAATTAAATTATTCACAGAATGCGATGAGAA
CTGAGCAAGCATCAGCTATCAACTCCCAGTTCATTTTT-CTTAAATAACTGGATCCAATT
GGA-GATGATG-CCCCCGAGGAAACCTTTCTGCTGTCCTTGGTGCTACTGTATTAAAAGA
TTATGTGAT--GGGTTTGCTGCTGAAACTTCAAAGCTGTCCAAAGCAAG-----------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------------------CATGTGCCCCCT---AATCCAATTTGGCC
ACGAACGTAC--CTCCCGATTGTCGGCCACGATCACAA
>Dvi
TTAACTTTCTCCACATCTTTTCCTTGTCTCTGAAA--CTAAATTTAAAGAGCAAAGTCAA
TGTTAGCAAGAAGAA-CACTCAAACGGCA---TTTTCGAGGACTA--------GGAACAT
GGGTTTGAGGGAGGGCTCAAACAAGAAT--------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---CACTTAGGAAGGTGAGGCGTGGAGACGTTGCACTTTATGCCACTGAAGGGAGA-ACC
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------------------CATAACAAGGGT-CCACTG----AAGGA
AAAGACTCACAA---CTACTCCTTTA---GAATTAAATTATTCACAGAGTACAAGGAGAA
CTGAGCTAGCATCAGCTATCAACTCCCAGTTCATTTTT-CTTAAATCACTGGACCCAGTT
GGA-GATTCTGGYCCCTGAGGAAACCTTTCTGCTGTCCTTGGTGCTACTGTAGTAGTAGA
TTCTTCGAT-GTGGTTTGCTGCTGAAACTTTGAAGCTGTCCAAAGCAAG-----------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------------------CATGTGCCTCCT---AATCCAATTTGGCC
ACAAACTTAC--CTCCCGATTGTCGGCCACGATCACAA
>Mnu
TTAACTTTCTCCACATCTTTTCCTTGTCTCTGAAA--CTAAATTTAAAGAGCAAAGTCAA
TGTTAGCAAGAAGAA-CACTCAAATGGCA---TTTTCGAGGACTA--------GGAACAT
GGGTTTGAGGGAGGGCTCAAACAAGAAT--------------------------------
------------------------------------------------------------
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------------------------------------------------------------
------------------------------------------------------------
---CACTTAGGAAGGTGAGGCGTGGAGATGTTGCACTTTATGCCACTGAAGGGAGA-ACC
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------------------CATAACAAGGGT-CCACTG----AAGGA
AAAGACTCCCAA---CTACTCCTTTA---GAATTAAATTATTCACAGAGTACAAGGAGAA
CTGAGCTAGCATCAGCTATCAACTCCCAGTTCATTTTT-CTTAAATCGCTGGACCCAGTT
GGA-GATTCTGGTCCCTGAGGAAACCTTTCTGCTGTCCTTGGTGCTACTGTAGTAGTAGA
TTATTTGAT-GTGGTTTGCTGCTGAAACTTTGAAGCTGTCCAAAGCAAG-----------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------------------CATGTGCCTCCT---AATCCAATTTGGCC
ACAAACTTAC--CTCCCGATTGTCGGCCACGATCACAA
>Rra
TTAACCTTCTCCACATCTTTTCCTTGTCTCTGAAA--CTTAATTCAA-----AAAGTCAA
TGTTAGCAATAAGAA-CAATCTAACAGCA---TTTTTGCGGACTGTGGAGTCATAGACAT
GGGTTTGGGGGAAGGAATGGATAAGAAT---GGGGCAGCAGGATGGCACAGGTGAAAAGA
GCCACTGCT---------------------------------------------------
------------ACCACTTGGGCAGTACCATGGATCATCGTAAGGTGATTCACTA-----
---ATGAAAGCAACTACA-AAAACCACTCCAGTATCCTTGTCAAAGAAAACTTG--AAGG
GGGCACCAAGATTTGGACAGCACTAAAAAGT---ACACAACAACCCAAATGGACAGAAAT
---CACTTAGGAAGATGAAAGGTGGAGAGGATACTCT----GCTACTGAAGGGAGAATTC
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------------------ACACCAAGGACT-CCACTACTTCTTCC-
---------------CTACTTCTTAA---TAAT-----------------GGATCAAGAA
TTATTCTAGCATCAGCTATCAAAATCTAACTAATTTTT-CTTAAATAATTAAACCTAACT
TGAAGAA-----TCATTGAGAA-CCCTTTCTGCTGTCCTTAGTGCTACTGTCTACAAAAT
TTGCTTGGT-TTGGCTTATTGCTCCAGTTTCTAAATTGTCCTGAGAAAATGAAGTAACCC
CAAAGTAAGCATGGAGCCCAAATCAAAAAGCAAAAGCT----------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------------------CTAATGGAAGC----ATGAGCATTTGGTC
TGGGACCTAC--CTCCCGATTATCTGCCACGATGACAA
>Cfu
TTAACCTTCTCCACATCTTTTCCTTGTCTCTGAAA--CTTAATTCAA-----AAAGTCAA
TGTGAGCAATAAGAA-CAATCTAACAGCA---TTTTTGAGGACTCTGGAGTCATGAACAT
GGGTTTTGGGGAAGGAATGGACAAGAAT---GGGGCAGCAGGATGGCATAGGTGAAAAGA
GCCACTGCT---------------------------------------------------
------------ACCACTTGGTCAGTTCCATGGGGCATCGTAAGGTGATTCACTA-----
---ATGAAAGAAACTGCA-AAAACCACTCCAGTATACTTGCCAAAGAAAACCTG--AAGG
GGGCACCAAGATATGGACATAACTAAAAAGT---ACACAACAACCCAAATGGACAGAAAT
---CACTTAGGAAGATGAAAGGTGGAGAGGATACTCT----GCTGCTGAAGGGAGAATTC
```

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------------------------------------------------------------
--------------------------------ACACCAAGGACT-CCACTACTTTTTCC-
---------------CTACTCCTTTA---TAAT-----------------GGATCAAGAA
TTATTCTAGCATCAGCTATCAAAATYGAACTAATTTTT-CTTAAATAATTAAACCTAACT
TGAAGAA-----TCATTGAGAA-CCCTTTCTGCTGTCCTTAGTGCTACTGTCTCCAAAAA
TTGCTTGGT-TTGGCKTGTTGCTCCAGTTTCTAAGATGTCCTGAGAGAATGAAGTAACCC
CAAAGTAAGCATGGAGCCCGAATCTTTTG-------CT----------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------------------CCAATGGAAGC----ATGAGAGTTTGGTC
TGGGACCTAC--CTCCCGATTATCTGCCACGATGACAA
>Dgl
TTAACTTTCTCCACATCTTTTCCTTGTCTCTGAAA--CTTAAA-----AAGTAAAGTCAA
TGTTAGCAATAAGAT-TAGTCAAACAGTG---TTTCTGAGGACTCTGGAGTGATGAGCAT
GGGTTTTGGGGAGGGCAGGTACAGGAAT--------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---CACATAGGAAGATGAGGAATGGAGAGATCATACTCTGTGTCACTGAAGGGAGAACGC
------------------------------------------------------------
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------------------------------------------------------------
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------------------------------------------------------------
--------------------------------ACACCAAGGAATTCATGGGTCCACTGCA
GGAAGATTTTC----CTACTTCTGTA---TAATTAAGTTATTCACGGAATGCAATGAGAG
TTAAGCTAGCATCAGCCATCAACTTCCATTTCATTTTT-CTTAAATAAATGAACCCAAGT
AGA-GAGTACAGACACTGAGGAAACCTTTCTGCTGTCCGTGGTGCTACTGTCT-CAGATG
ATTATTTGATGTGGTTTTTTGCTAATGCTCTTCAACTGTTGTGAAAGAATTAAATAACCC
ATGTGTTTACATG-CCTCCAAATCCCTTT-------CT----------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------------------CCAATTTCCTC----ATGGGAGTTTGGCC
ATGAACTTAC--CTCACGATTGTCTGCCACAATCACAA
>Nty
GATTCTTTCTCCACATCTTTTCCTTGTCTCTGAAA--CTTAAT-----GAGTAAAGTCAG
TATTAGCAACAAGAA-TAATCAAACA-TT---TTGGGGGG--CCCTGGGGTCATGAACAT
GAGACTGGAGGAGGGTATGGCTGGGAAT--------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---CACTTGGGAAGATGAGGAGTGGGGAGGTC--ATTCTCTGTCACTGAAGGGAGAACCC
------------------------------------------------------------
------------------------------------------------------------
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------------------------------------------------------------
--------------------------------ACGCCAAGGGGTTCATGGGTC-CGCTGA
AAGAAGACTTTCC--CTACTTCTCTA---GAATCAAATTGTTCACAGAATGCAATGAGAA
GTAAGCTAGCACCAGCTATCAACGTCCACTTCATTTTT-TTTAAGTAACTGAACCCAACT
AGA-GATTATAGTCACCAGGAAAACCTTTCTGCTGTCCTTGGTGCTACTGTCT-CAGATG
ATTACTAGATGTGGTTTGTTGCTGATGCTTTTAAACTCTTGTGAGAGAATGAAATAT-CC
CAAAGCAAACACATGCTCCAAATTCCTTT-------CT---TCAATTTCCTC---GGGGC
AGCTAGATGGCGCAGTGGATAGAGCACTGGCCTTGGACTTAGGAGGACCTGAGTTCAAAT
CCAGCCTCAGACAGACACTTGATATGTTCTATCTGTGTGACCTTGGGCAAGTCACTTAAT
CCCAAATTGCCTCTCCAAAAAAAAGAAG---CCAATTTCCTC----GTGGGAGTTTAGCC
ATGAGCTTAC--CTCGCGATTGTCCGCCACGATCACAA
>Pta
TTAACTTTCTCCACATCTTTTCCCTGCCTCTGAAA--CTGAATTTAAAGAGCAAAGTCAA
TGTTAGCAATCCGAA-TAATCAG----CG---TTCTTTCGGATTTTGGAGTCGTGAACAT
GGATTCAGAGGACGGCACGGACAGGAAT--------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---CACTTAAGAAGTTGAGGAGTGGGGAGGTC----ACTATGTCACTGTAGGAA--GCGC
---CTTTCCCTACTTCTTTATTTTTT-CTCTACTTTTTTTT-------------------
---------------------------------------TTAATTTTTAAAATGTTTTTT
TCTAAGGCAATTAGGATTAAGTGACTTGCCCAGGGTCACAAAACTAG-----------GC
TCATCTTTGAACTCAGGTCCTTCTGATTTCAGAGCTGGTGCTCT----------------
-------------------------------------ATCCAC-----------------
--------TGCGCCATCTAGTTACCCTTCCCC----------------------------
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---------------CTACTTCTTTA---GAATTAACTTGTTCATAGAATGCAATGAGAA
TTAAACTTGCATCAGCTATCAACTTCCAAGTCATTTTT-CTTAAATAATGGAACCCAAAG
AGA-GATTATAGTCACTGAAGAAATTTCCCTGCTGTCCTTGGTGCTACTGTCTTT-----
---------GATGTTTTGCTGTTAATGCCTTTCAACTGTTGGGAGAGAATGAAATAA-CC
T-AAGCAGGCACATGCCCCAGATCCCCTT-------CT----------------------
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>Dgo
TTAACTTTCTCCACATCTTTTCCTTGCCTCTGAAA--CTGAATTTAAAGAGCAAAGTCAA
TGTTAGCAATCTGAA-TAATCAAACAGTG---TTCTTTCGGATTCTGGAGTCATGAACAT
GGATTCAGAGGACGGCACAGACAGGAAT--------------------------------
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---CACTTAGGAAATTGAGGAGTGGGGAGGTC----TCTATGTCACTGTAGGAAGT--GC
---CTTTCCCTACTTCTTTATTTTTTCCTCTACTTTTTT---------------------
-----------------------------------------AATTTTTTAATTTTTTTTT
CGAG------------TTAAGTGACTTGCCCAGGGTCACACTGCTAG-----------AT
CCAGATTTGAACTCAGGTCCTCCTGACTTCAGGGCTAGTGCTCT----------------
-------------------------------------ACCCAC-----------------
--------TGTACCATCTAGCTACCCTTGCCCC---------------------------
```

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---------------CTACTTCTTTA---GAATTAACTTGTTCATAGAATGCAATGAGAA
TTAAATTTGCATCAGCTATCAATTTCCAAGTCATTTTT-CTTAAATAATGGAACCCAAAG
AGA-GATTACACTCACTGAAGAAATTTTCCTG-TGTCCTTGGTGCTACTGTCTAGATGAA
TGTTTG----TTGTGTTGTTATTAATGCCTTTCAACTGTTGGGAGAAAATGAAATAA-CC
TAAAGCAAACACGGCCCCAGA---TCTT-------CT-----------------------
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-------------------------------CTAACGTCCCC----ATGGAACTTTGGCC
ATGAACTTAC--CTCGCGATTGTCCGCCACAATCACAA
>Scr
TTCACTTTCTCCACATCTTTTCCTTGCCTCTGAAA--CTGAATTTAAAGAGCAGAGTCAA
TGTTRGCAATACGAA-TAATTAAA--GTG---TCCTGTCAGATTCCGGAGTCATGAACAT
GGATTCAGAGGACGGCATGGACAGGAAT--------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---CACTTAGGAAGTTGAGGAGAGAGGTCATT-------ATGCCACTGAAGGAA----CC
---CTTTCCCTACTTCTTTATTTTTTCCTCTACTTCTTTTT-------------------
-------------------------------------------------AAATTTTTTTT
CCAGAAGCAATTRGGGTTAAGTGACTTGCCCAGGGTCACACAGCTAG-----------GC
CGAGATTTGAACTCAGGTCCTTCTGACTTCAGGGTCGGTGCTCT----------------
-------------------------------------ATCTAC-----------------
--------TGCACCATCTAGCTGCCCTCC-------------------------------
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---------------CTACTTCTTTA---GAATTAACTTCTTCATAGAATGCAATGAGAA
TTAAGCTTGCATCAGCTATCAACTTCCAAGTCATTTTT-CTTAAATAATGGAACCAAA-G
AGA-GATTACARTCACTGAAGAAATTTTCCTGCTGTCCTTGGTGCTA-TGTCTAGACGAG
TGTTTG----ATGTGTTGTTGTTAATGCCTTTCAACTGTTGGGAGAGAATGAAATAA-CC
TAAAGCAACCATGTGCCCCAGATCCCCTT-------CT----------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------------------CTAATGTCCCC----ATGGAACTTTGGCT
ATGAACTTAC--CTCGCGATTGTCCGCTACAATCACAA
>Mfa
----CTTTCTCCACATCTTTTCCTTGCCTCTGAAA--CTGAATTTCAAGAGCAAAGTCAA
TGTTAGCAAGAAGAA-TAATCAAACAGTG---TTCTTTCGGACTCTGGAGTCACGAACGT
GGATCCGGAGGACGGCATGGATAGGAAT--------------------------------
------------------------------------------------------------
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------------------------------------------------------------
------------------------------------------------------------
---CACTTAGGAAGTTGAGGAGTGGAGAGGTCCCTCTCTATGTGACTGAAGGAA----GC
---CTTTCCCTACTTCTTTATTTTTTCCCTTACTTCTTTTTTTTCTTTTTTATCCTTATT
TTTTATTTTGTGAAAATTCTTAAAAAAAAGAAAATGAGAAGAATTTTAAAATTTCATTTT
C-AGTATAACATCATCAATATAGTGTTGC-TTCTCTCAATAATACAG-------------
-GAAAATTATAGAACCATGCTTTGATTTAAAGCTACCCTCTCTTTTTTTCTTTTTTTTAA
TTAAAAGCTTTTTATTTACAAAACATATGAGTGATTTTTCTACATTGACCTTTGCAAAAC
TTTTTTTTTGTTCCATGCTTTTCCCCTCCTTCCCCCCACCCCCACCCCTAGTACATGCTA
AATATATTAAATTATATGACAAATTTCCC-------------------------------
---------------TTACTTCTTTA---GAATTAACTTGTTCATAGAATGCAATGAGAA
TTAAGTTTGCCTCAGCTAGCAACTTCCAAGTCATTTTT-CTTAAATAATGGAACCCAAAG
```

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AGA-GATTACAGTCACTGAAGAAACTTTCCTGCTGTCCTTGGTGCTGCTGTCT-CAAATG
AGTGTTTGATGTG--TTGTGGTTAATGCCTTTCAACTGTTGTGAGAGAATGAAATAA-TC
TAAAGCAAGCACGTGCCCCAAATCCCCTT-------CT----------------------
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------------------------------------------------------------
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ACGAACTTAC--CTCGCGATTGTC--------------
>Bil
TTAACCTTCTCCACATCTTTTCCTTGTCTCTGAAA--CTTAAA-----AGGTAAAGTCAA
TGTTAGCA-TAAAAAATA-TCAAACA-GT---TTTTTGAGGACTCTAGAGTCATGAACTG
GGGATTGGGGGAGTGCATGGACAGGAAT--------------------------------
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------------------------------------------------------------
------------------------------------------------------------
---CACTTAGGAATATGAAGAATGGAAAGGTC--GTAGTGTGCCATTAAA-------CCC
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------------------------------------------------------------
--------------------------------ACACTGAGGAGTTCATGGGTTCCCAGAA
GGAAGACTTTCT---CTATTTCTTTA---GAATTRAGTTGTTCACAGAATGTAATGAGAA
TAAAGCTAGTATCAACTTCCACTT-------CATTGTT-CTT-AATAGCTGAACCCAACT
AGA-GATTACAGTCATCAAAAAAGCCTTTATGCTGATCTTGGTGATACTGTAA-TAGGTG
GTCATTTAATATGAGTTGCTGCTAATATTTTTAAACTGTTGTGGGAGAATGAAATAA-TC
CAAAGCGAGCACATTCCCCAAA--TCTTT-------CT----------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------------------CCAATTTCCTC----ATGGGAGTTTGACC
ATGAACTTAC--CTCACGGTTGTCTGCCACAATCACAA
>Pgu
TTAACCTTCTCCACGTCTTTTCCTTGTCTCTGAAA--CTTAAA-----GGATAAAGTCAA
TGTTAGCAATAAGAA-----CAAACA-GT---TTTTTGAGGACTCTAGAGTCATGAACCA
GGGATTGGGGGAGCGCATGGACAGGAAT--------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---CAATTAGGAATATGAAGAAGGGAAAGGTC--ATATTGTGTCATTAAA-------CCC
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------------------------------------------------------------
--------------------------------ACATAGAGGAGTTCATGGGTTCACCGAA
GGAAGACTTTCT---CTATTTCTTTA---GAATTAAATTGTTCACAGATTGTAATGAGGA
TTAAGCTAACATCAACTCCCAATT-------CATTTTTTCTTAAATAACTGAACCCGACT
AGA-GATTACAGTCATCAAGAAAACCTTTATGCTGATCTTGGTG-ATTTGTCA-TAGATA
AGTATTTAATGTGATTTATTGCTAATATTTTTAAACTGTTGTGGGAGAATGAAATAA--C
CAAAGCAAGCACATTCCCCAAATCTCTTT-------CT----------------------
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------------------------------------------------------------
-------------------------------CCAATTTGCTC----ATGGGAGTTTGACC
ACGAACTTAC--CTCACGGTTGTCTGCTACAATCACAA
>Iso
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TGTTAGCAATAAGAA-----CAAACA-GT---TTTTCGAGGRCTCTAGAGTCATGAACCA
GGGATTGRGGGAGWCATGGACAGGAAT---------------------------------
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------------------------------------------------------------
---CAATTAGGAATATGAAGAAGGGAAAGGTC--ATATTGTGTCATTAAA-------CCC
------------------------------------------------------------
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------------------------------------------------------------
--------------------------------ACACAGAGGAGTTCATGGGTTTACCGAA
GRAAGACTTTCT---CTATTTCTTTA---GAATTAAATTGTTCACAGATTGTAATGAGAA
TTAAGCTAACATCAACTCCCAATT-------CATTTTT-CTTAAATAACTWSACCCRACT
AGA-GATTRCAGTCATCAAGAAAACCTTTATGCTGATCTTGGTG-ATTTGTCA-TAGATA
AGTATTTAATGTGATTTGTTGCTAATATTTTTAAACTGTTGTGGGAGAATGAAATAA--C
CAAAGCAAGCACATTCCCCAAATCTCTTT-------CT----------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------------------CCAATTTGCTC----ATGGGAGTTTGACC
ACGAACTTAC--CTCACGGTTGTCTGCTACAATCACAA
>Tro
TTAACTTTCTCCACGTCTTTTCCTTGTCTCTGAAA--CTTAATTTCAAGA----------
---------TAAGCA-CAATCAAGCAGTG---TTTTTGAGGACCCTGGAATCATGAATGT
GGGTTTGGGGGGTGCAKGGAYAGAAAT---------------------------------
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------------------------------------------------------------
---GCCTTGGGAAGATG------------------------------------AGAACCT
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------------------------------------------------------------
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------------------------------------------------------------
--------------------------------TCMCCAAGAAGGTCATGGGTCCACTGAA
AGAACACTTTGT---CTACTTC---------ATTAAATTGTTTACAGAATGGAATGAGAA
TTAAGTGGGCACCAGCTATCAATTCCYGCTTCATTTTT-CTTAAATAACAGAACCCAACT
AGA-G-------TCACCTAGGGAAYCTTTCTGCTGTCCATGGTGCTAYSGACT-CAGATG
ATCATATGAT----------------------AAGCTGTTGGGAGAGAAYGAAATAACCC
CAAAGCAAACACATGCTCCAAATCTCTTY-------CT----------------------
------------------------------------------------------------
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-------------------------------CTAATTTCCTC----AGAGGAGT-GGATA
```

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GAGAGCTTAC--CTCCCGATTGTCTGCTACRATCACAA
>Mro
TTAACTTTCTCCACGTCTTTTCCTTGTCTCTGAAA--CTTAATTTAAAGAGTAAAGTCAA
TGTTAGCAATAAGAA-TAATTAAACAGTG---TTTCTGAGGACTCTGGAGCCATGAACAT
GAGTTTGGGGGAGGGCAGGGATAGATAT--------------------------------
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------------------------------------------------------------
---CACTTGGGAAGATAAGGAGAGGAGAGGTCACACTATAT--CACTGAAGGGAGAACCC
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------------------------------------------------------------
--------------------------------CATCAAGGAGCTTGATGGGTCCACTGAA
GGAAGACTTCCT---CTACTTCTTTA---GAATTAAATTGTTTGTAGAATGGAATGAGAA
TTAAGTTAGCATCAGCTCTCAATTCCCAATTCATTTTT-CTTAAATAACTGAACCCAACT
AGA-GAGTATAGTCCT-GAGGAAACCTTTCTGCTGTCCTTGGTGCTACTTCCT-CAGATG
ACTATTTGATGTG----ATTGCTAATGCTTTTAAACTGTTGTGAGAGAATGAAATA-CCC
CCAAGCAAACACATGCCCCAAATCTCTTT-------CT----------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------------------CCAATTTCCCC----TTGGGAGTTTGGCT
GTGAACTTAC--CTCACGATTGTCTGCCACTATCACGA
>Ptr
TTAACTTTCTCCACGTCTTTTCCTTGTCTCTGAAA--CTTAATTTAAAGAGTAAAGTCAA
TGTTAGCAATGAGAA-TAATTAAACAGTG---TTTCTGAGGACTCTGGAGCCATGAACAT
GGGTTTGGGGGAGGACATGGACAGAAAT--------------------------------
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------------------------------------------------------------
---CACTTGGGAAGATAAGGAGATGAGAGGTCATACTGTAT--CACTGAAGGGAGAACCC
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------------------------------------------------------------
--------------------------------CATCAAGGAGCTTGATGGATCCACTGAA
GGAAGACTTCCT---CTTCTTCTTTA---GAGTTAAATTGTTTGCAGAATGGAATGAGAA
TCAAGTTAGCATCAGCTCTCAATTCCCAATTCATTTTT-CTTAAATAACTGAACCCAACT
AGA-GACTATAGTCTT-GAGGAAACCTTTCTGCTGTCCTTGGTGCTACTTCCT-TAGATG
AATGTTTGATGTG----ATTGCTAATGCTTTTAAACTGTTGTGAGAGAATGAAATA-CCC
CCAAGCAAACCCATGCCCCAAATCTCTTT-------CT----------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------------------CCAATTTCCTT----TTGGGAGTTTGGCT
GTGAACTTAC--CTCACGATTGTCTGCCACTATCACGA
>human
TTAACTTTTTCCAGATCTTTTCCTTGCCTCTGAAA--CTTAACAA--TTTTAAATGGCAG
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CATTA-------------------------------------------------------
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---------------------------------------------------AATTTTAAA
AAGTTCTTAC--CTCTCGGTTGTCTGCCACGATCACCA
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**MARKER 85**

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>RTESINE2
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------------------------------CCTGACTTTTGTC----
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---TTGCCACTGGA-CTTCGATGACTCTGGAAGAGAGAGTGAGGCTGA--------TGAC
TTTGTGCAACTCTGCCTCACTTAAATCCAATTCATGCGCAAGTCAAGACA-TCACCCCAT
GA---TGTCATTGGTCCTCTTC---GAAAACG----------------------------
------------------------------------------------------------
------------------------------------------------------------
----AAGGACGAACAACAACAACAA-----------------------------------
-----------------------------
>WSINE1
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------------------------------------------------------------
-------------------------GAGGGGCAGCTAGGTGGTGCAGTGGATAGAGCACC
AGCCCTGGAGTCAGGAGGACCTGAGTTCAAATCCAGCCTCA-------GACACTTACTAG
CTGTGTGACCCTGGGCAAGTCACTTAACCCCAATTGCCTC---AAAAAAAAAAAAAA---
------------------------------------------------------------
-----------------------------
>WSINE1
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------------------------------T
TTTTTTTTTTTTTG-----------------AGGCAATTGGGGTTAAGTGACTTGCCCAG
GGTCACACAGCTA------GTAA-GTGTCTGAGGCTGGATTTGAACTCAGGTCCTCCTGA
CTCCAGGGCTGGTGCTCTATCCACTGCACCACCTAGCTGCCCCTC---------------
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-----------------------------
>Mdo
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ACCCTTCGC-----CGAGC-------TTCCCCATCTCTTCCCGCCTTGGACCTGGGGGGG
GGTTGAGGGTGGGCCACAGGACTGCTGTTTGTTGTGGAGGGGC---AGTGGTCC--GCTC
T---CTCCTTTCC-----------------------------------------------
------------------------------------------------------------
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------------------------------------------------------------
----------------------------GAGGAGGCACCCAC--CTTGCGATTGTGGCAG
AACTCGTAACCTTCCGGCTTACACTCGTG
>Cfu
TTAGAAGCAGAGAATATGGTCAGCAC--CT-ACACAAAAATAGGAGAGAAA--GGATAGG
TA-----------TGGAGC--TTCATTTTCCCATTCATTCT-------------------
-------------CTCGGTGATCATTGTTTGCTGCTGAGGGTA---AGCAATCGAATTCT
TCTCCTCCCTTGCTTTGCTCTACAAGAGTCTTGGGCAA----------------------
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------------------------------------------------------------
-------------------------------CCGGCACCTAC--CTTGCGATTGTGGCAG
AACTCATAGCCTTCTGGCTTGCATTCATG
>Dgl
TTAGAAGCAGAGAAGATGGTTAGCAC--CT-GAACAAAAAGAGGAGAGAAA--GGACGAA
CG----------TTTAGC--TTCATTTTCCC-------TGTTGGCTTCCCACCTTGGACC
C--------TGGTGCTTGTAATTGCTGTTTGTTGTTGAGGGGA---AGCTACTAAACTCC
-CTTCCCCTTTGCTCTGCTCTACAAGACC---TACCTC----------CTAAGTGC----
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---GTACCTAC---------AGAACTCTGGAGGAGAGAGTGAGGCTGA--------TGAC
TTTTCAAAGCTCTGTCTCACTTAAATCCAATTCATTCTCGAGTCAAGACATCCCCCTCCT
GA---CATCACTGGTCTTCTTT---AAGAAGGAAGGACGA--------GGATAGAGCACT
GGCCCTGGAGTCAGGAGTACCTGAGTTCAAATCCAGCCTCAGACACTTAACACTCACTAG
CTGTGTGACCCTGGGCAAGTCACTTAACCCCAATTGCCTCACTAAAAAAAAAAAAAAAAA
A---AAGAAGGAAGGACGAACAAT---AACAAAGGTACCTAC--CTTGCGGTCGTGACAG
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>Pta
TTAGAAGCAGAGAAGATGGTTAGCAC--CT-AAACAAAAACAGGTTAGAGA--GGATGGA
CAC-CTGGATTTTCTTTGCCGTTCACTCTCCCACTCCCTGTTGGGTTCCCACCTTCAAAG
C--------TGGTTTCTCTTGCTGTTATTTGTTGGTGAGGGAA---AGCTACCAAACTCT
-CCTCCCCTTTGCTCTGCTCTACAA-------GAGCTC-----TGGTACCCAAGTC----
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---GTAGGGATGGA-TCTTAAGGACTCTGGAGGAGAGACTAAGGCTGA------------
-------------------CTCAAATCCGATTCACACACAACCCAAGACAT-CCCTCCCT
GA---TGTCACTGGTCCTTCTC--------------------------------------
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----AAGAGCAAAGAATGCAC------AACAGAGGGACCTAC--CTTGCGGTTATGGCAG
```

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AATTCATAGCCTTCCTGCTTGCACTCGTG
>Dgo
TTAGAAGCAGAGAAGATGGTTAGCAC--CT-AAACAAAAACAGGATAGAGA--GAATGGA
CAC-CTGGATTTTCTTTGCTATTCACCCTCCCACTCCCTGTTGGGTTCCCACCTTCAAAG
C--------TGGTTTCTCTTGCTGTTATTTGTTGGTGAGGGAA---AGCTACCAAACTCT
-CCTCCCCTTTGCTCTGCTG----AGAATCTAGAGCTC-----TGGTACCCAACTC----
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---GTAGGGATGGA-TCTTAAGGACTCTGGAGGAAAGACTAAGGCTGA--------CAA-
-----------CTATCTCACTCAAATCCGATTCACACACAACCCAAGACATCCCCTCCCT
GA---TGTCACTGGTCCTTCTC--------------------------------------
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------------------------------------------------------------
----AAGAGCAAAGAATGCAC------AACAAAGGTACCTAC--CTTGCGATTATGGCAG
AATTCATAGCCTTCCTGCTTGCACTCGTG
>Scr
TTAGAAGCAGAGAAGATGGTTGGCAC--CT-AAACAAAAACAGGATAGAGA--AGTTGGA
CAC-CTGGATTTTCTTTGCTATTCACCCTCCCACTCCCTGTTGGGTTCCCACCTTCAAAA
C--------TGGTTTCTCTTGCTGTTATTTGTTGTTGAGGGAATCCAGCTACCAAACTCT
-CTTCCCCTTTGCTCTGCTCTACAAGAGTCTAGGGCTC-----TGGTACCCAAGGT----
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---GTAGGGRTGGA-TCTTAAGGACTCTGGAGGAGAGACTGAGGCTGA--------CAAT
A----------GTACAACTATCAAATCTGATTCACACGCAACCCAAGACATCCCCTTCCT
GA---TGTCACTGGTCCTTCTC--------------------------------------
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AATTCATAGCCTTCCGGCTTGCACTCATK
>Mfa
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CAC-TGAGATTTTCTTTGCTATTCACCCTTCCACTCACTGTTGGGTTCCCATCTTCAAAG
C--------TAGTTTCTTTTGCTGTTGTTTGTTGTTGAGGGAA---AGCTACCAAACTCT
-CCTCCCCTTTGCTCTGCTCTACAAGAGTCTTGGGCTC-----TGGTATCCAAC------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
----TCGGGGT--------GGGGACTCTGGAGGAGAGAGTAAGGCTGA--------CAAC
T--GTAT-ACTCTATCTCACTCAAATCTGCTTCATTTGCAACCTAAGACATTTCCTTCCT
GT---TGTCATTGGTCTTTTTC--------------------------------------
------------------------------------------------------------
------------------------------------------------------------
----AAGGTAT----------------AACAAAGGCACCTAC--CTTACGATTATGGCAG
AATTCATAGCCTTCCTGCTTGCACTCATG
>Bil
TTAGAAGCAGAGAAAATGGTTAGCAC--CT-AAACAAAAACAGAAGAGAAAGAGGATGGA
CACTCAAGCTTTACTTTCCCTTTCACCCTCCCATTCACAGTTAGGTT-CTACCTTGGATG
C---------TGATAGTTCTTGTATTATTTGTTGTTGAGGGAA---AGCTACCACACTCT
-CCTCTCCTTTGCTGTGCTCTACAAGAGTGTTGGGCTC-----TTGCACCCAACAT----
------------------------------------------------------------
------------------------------------------------------------
```

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------------------------------------------------------------
---GTAGGTATATACCCTACAGGACTCTGGAGGAGAGAGTAAGGCTGA--------AGA-
-----------CTGCCTCACTTAAATTCAATTCACACATAAGCCAAGAC-TCACCCTCAT
GG---TGTCATCATTCCTCTTC--------------------------------------
------------------------------------------------------------
------------------------------------------------------------
----AAGAATGAAGGATGAACAAT---AGCAAAAGTCCTTAC--CTTGCGATTGTGGCAG
AACTCATAACCTTCCTGTTTGCACTCATG
>Pgu
TTAGAAGCAGAGAAAATGGTTAGCAC--CT-AAACAAAAACAGAAGAGAAAGAGGATGAA
CACTTAAGCTTTACTTTCCCTTTCACCCTCCCATTCACAATTAGGTT-CTACCTTGGACC
C------------------------TGATTGTTCTTCAGGGAA---TGCTACCATACCCT
-CCTCTCTTTTGCTATGCTCTACAAGAGTCTTGGGCTC-----TTGCACCCACCTT----
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---GTAGGTACATACCCTACAGGACTCTGGAGGAGAGAGTAAGGCTGA--------AGAC
T-AGTGCAACTCTGCCTCACTTAAATGTAGTTCACACCTAAGCCAAGAC-TCACCCTCAG
GG---TGTCATCGTTCCTCTTC--------------------------------------
------------------------------------------------------------
------------------------------------------------------------
----AAGAAGGAAGGATAAACAAC---AGCAAAGGTACTTAC--CTTGCGATTGTGGCAG
AACTCGTAACCTTCCTGCTTGCACTCATG
>Iso
TTAGAAGCAGAGAAAATGGTTAGCAC--CT-AAACAAAAACAGAAGAGAAAGAGGATGAA
CACTTAAGCTTTACTTTCCCTTTCACCCTCCCATTCACAGTTAGGTT-CTACCTTGGACC
C------------------------TGATTGTTCTTCAGGGAA---CGCTACCATACCCT
-CCTCTCCTTTGCTGTGCTCTACAAGAGTCTTGGGCTC-----TTGCACCCACCTT----
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---GTAGGTCCATACCCTACAGGACTCTGGAGGAGAGAGTAAGGCTGA--------AGAC
T-AGTGCAACTCTGCCTCACTTAAATCTAGTTCACACCTAAGCCAAGAC-TCACCCTCAG
GG---TGTCATCGTTCCTCTTC--------------------------------------
------------------------------------------------------------
------------------------------------------------------------
----AAGAAGGAAGGATGAACAAT---AGCAAAGGTACTTAC--CTTGCGATTGTGGCAG
AACTCATAACCTTCCTGCTTGCACTCATK
>Tro
TTAGAAGCAGAGAAGATGGTTAGCAC--CT-AAACAGAAATAGGAGAGAAG--GGATGGG
AGACATGACTTTACTTACCCTTTCTCCCTCCCACTCACTGGTGGGTTCCCACCTTGGACC
C--------------TGGTTATTCTTGTTTGT-GTTGAGGGGA---AGCTTAA-------
----------------------------------GCTC-----TTATCCCTACCTT---T
TTTTCTTTTGCTTTCTGGAGGGGGGAAGGTAGGGCAAGTAGGGTTAAGTGACTTGCCCAA
GATCACACAGCTACTAAATGTTAGGTGTCTGAGGCTGGCTTTGAACTCAGGTCCTCCTGA
CTCCAGGGCTGGTGCTGTATTCACTGTACCTCCTAGCCGCCCCC---TTATCCTCACTTT
---ATAGGTACGTG-CCTACAGGACTC--AAGAAGAGAGTGAGGCTGA------------
------------GGTCTCACTTCAATCCAAATGTCAGGCAAGTGAAGACCTCACTCTCAC
GA---TGTCACTGTTCCTCTTC--------------------------------------
------------------------------------------------------------
------------------------------------------------------------
----CAGCACAAAGGATGAAC------ACCAAGGGGACCTAC--CTTGCGATTGTGGCAG
AACTCGTAACCTTCCGGCTTACACTCGTG
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```
>Tvu
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-CGG-CCCCTTTGCTTGCTCTAT--GAGTCTTGGGCTC-----CTATCCCTACCTC----
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T--GCGCAAACCTCTCTCACTGCCATCCAGTTCATGCGCAAGTCAAGACCTCACCCTCAT
GA---TGTCATCGGTCCTCTTC--------------------------------------
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---GTAGGGACGTG-CCTACAGGACGCTGGAGGAGAGAATGAGGCTGAAGGAAGGACGAC
T--GCGCAACCCTGTCTCATTTCAATCCATTTCACACTCAAGTCAAGACCTTACCCTCAT
GA---TGACATCGGTCCTCCTC--------------------------------------
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T--GGGCAACCCTGTCTCACTTCAATCCAGTTCACACTCAACTCAAGACCTTACCCTCAT
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## MARKER 89

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**MARKER 90**

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**MARKER 93**

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**MARKER 94**

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**MARKER 95**

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CCCCATGATGTCATTGGTCCTCTTCG----AAAACGAA--GGACGAACAACAACAACAA-
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>SINE1a_Mdo
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------------------------TTTTTTTTTTTTTTTTAAACCCTTAC---TTTCTGT
CTTAGTAACAA-------------------CTCTAAGACAGAAG-GGCAAGGGCTAGGCA
ATTGGGGTTAAGTGACTTGCCCAGGGTCACACAGCTAGGAAGTGTCTGAGGCCAGATTTG
AACCCAGGTCCTCCTGACTCCAGGCCTGGTG-CTCTATCCACTGTGCCACCTAG-----C
TGCCCC------------------------------------------------------
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>Plat_RTE1
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---AACACGACAACACAACA------AGGGACA-GCCTTTTTGTGTGCACAATG---TGG
CCGGGACTGTGGGTCCCGCATTGGCCTTTTCAGCCACA-CACGCACTCATAGGTGAACTT
CACCGTCAGTGGCGTCT-TCTTCGAA----TACGAAGGACAACTATATATATATA-----
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--------------------------------------------------TTTTTTTTTT
TTTTTTAAACCCTTACTTTCTGTCTTAGTAAC-------------AACTCTAAGACAGAA
GGGC---AAGGGCTAGGCAATTGGGGTTAAGTGACTTGCCCAGGGTCACACAGCTAGGAA
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>Mdo
TATTGAGGCCTGCTGTCACTAATGGAATTTCGCAG--GTAAGCAAG----TAGGCTACTT
AG----AGACTGACTATAAAC---------------------------------------
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--TATAA---GGGTTTTAAAACAACTATAGAATATAGCCCTT--GTTGAAATAACCCAGT
---------------------TTCATTTTTCTTATCCCAGGACCTACCATTGAGGTTAGA
AAAGGCTTATCTAGAAA-CAGACCTAACAGTTGTTCTAGCACTCCCATAAGGAGCCCTTG
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--TGTTCTTGGTTTGGTTTAG------------TTTTATAAAACTCTTAC---CTTCTGT
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T------GGTGTATGTAATCTTTAAGCTTAGTGATAGGAAAGTGATTCATTTGTT---TG
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A-----------------------------------------------------------
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----------CAAGATTGCTC-TGGCAGGGTCC-AAGCCTTTGTGTGTTCACAG-GATGG
AAAAGTCTCCTGAGCCTCTGTTGGTCTGTTCAGCTACATCTCACAGACAAAACA--GTCA
T------GGTGTGTGTAATCTTTAAGCT-AGTTATAGAAAGG-GA-TCATT-GTT---TA
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>Cfu
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--TATGT-----TTTCTAAAACAACAGTAGAATAGCTCATTGAGGTTAAAATGCTCATGT
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-------AAGAAACAAAACAGATCCCAGAGTTGTTCCAGCTCTCCCACTAGGAGCCAATG
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AG----TAAGGCTTAAAATA-TCCACAGGAATTTATCTGTTTTTACTAAGGTT-GAAGTG
TTAGGCCA-AGTGATATGAAAAGTGGAGGGCATT---CTAAAATTAG-------------
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CTAT-CCATGTCATTGGTCCTCTTTTT-AAAAAACCAAACGGATGAACAA-----GTTA-
--TATGT-----ATTCTCAAGCAATGGTGGAATATA-CTGCTTGTTGAGATTAAGCTCCT
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---------TATGCTCAGTTTTGATTCAG---GG-GAATACTAAA--ACATCTTTGACTT
-----ANAGTCAGGATCACCA-TGTCAGGGTCC-ACATCT--GTGTGTTCACAG-TGTGG
AAAAGACT----AACCTCCATTAGTCTGTCCAGCCATANTGCACAAGCAAA-CATGATC-
-----TGGGGCACAGTTATCTTCAAGCCGGNTGGTATAGA-CTGATTCNTTTGTT---TG
GGATTGTCCCCCTGCAAACTTAATTCCCNAAAATCCTAGNGTAGTCAAAATTAAAAAAAA
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CAGTAGTGAAAGCATAGGAATTGAAAATGCAGGGGGAG--GAGTAGGTAGGTAGAAAGAA
AG----TCAGGTTTGAAGGTGTCTACAGAAATGTTTCTATTTTTACTAAGGTT-GAAGTG
TTCAGGCTGGACGATAT-AAAAATGCAGGGCATT---TTAAAATTAG-------------
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--------------------------------------TCTATAACAAGTATGGTACACA
AGCAAC-TTTTTTT-AGGTATTCTTCTGTATTAGTATGTATAGTTTAT--CTATTTTTCT
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>Nty
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----------GTGCAGCTCTACCTCATTTAAATACAATTCACACAGCAGA-TGAACAG--
-----------------------------------------------CAA-----GTTA-
--TATGT-----GTTCTAAAGCAACTGTAGAATATAGCTGGTTGTTGAGGTTAAACTCCT
TGCATCTG-AGATAACCTAACTTGATCCTCCTCATCCCCAGACCTACCATTGAGCTTAGG
GGACACTCTAGAAA----CAGACCCAAAAGTTGTTCCAACTCATCTACTAGGAGCCAGTG
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---------TGTGCTCAGTTTTGATTCAG---GGGATGTATTAATAAACACTTTTGACTT
-----AGAGTCAAGATTGTTA-TGCCAGGGTCC-AAATCTTTGTATGTTCACAG-TATAG
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A-----TCCTAAAGTTGATTAATTTTATCC-CAAGATCCTGTCAGCATGAAGAATATAGC
TAGTAATGAAAGCATAGGAATTGAAAATTCCAGGGTTCA-GAAGAGTAAGTAAGC-AAAA
AGAAAGTAAAGTATGAAGATGTCCACAGAAATGTTTCTCTTTTTACTAACGTT-GAAGTA
TTGGTCCA-GACAATATGAAAAATGCAGGGCACT---TTAAAATTAG-------------
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--------------------------------------TCTAAAACAATTATGGTATACT
AGCAATAGTTTTT--AAGGTATCTTTTGTGTTACTTTGTGAAATTCAT--CTATTTTTCT
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>Pta
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TGATGACTTTGTATAGCTCTGCCTTACTTAAATCCAGTTCATGAGCAAGTCATGACATCA
CCAT--GATATGATTGGTTCTCT---AAAAAAATCCAAGACAAACAGTAA-----GTTA-
--T--CT-----GTTCTAAAGCAATTTTGGAATATAGGTGTTTGTTGAAGTTCAGCTCCT
CATGTCTGGGGACAACTTAACTTGATTCTTCTTGTCCCCAA-CCTACTATTGAGGTTGTG
AAAGATTTATCTGGAAA-CAGAACC-AAAGTTGTTCTGGCTCATCTGTTAGGAGCCAATG
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---------------------CAAAATCT---TT-CAGT-TTAAA--ACACCTTTGACCT
-----AGGGTCAAGATTGCAA-CGTCAGGGTCC-AAGTCTTTGTGTATTT----------
------------AACTTCCATTAGTCTGTTCAGCCACACTGCACAAGGCAAACACAATC-
-----TGTGGCATCATTATTTTCAAGCTTGGTGATAGGGG-CTGATTCATTTGTT---TG
GTATTGTCATACTATAAACTCTATTCCCAATAATCCTGGTGTGATCAAAGTAAAAAAAAA
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CNATAATAAAAGCATAGAAATTGAAATTGCAGAGGGAA--GAGTAGATAGGTAAAAAGAA
AG----TAAAGCATGAAGTTGTCCACAGAAATAGTTATATTTTTAATAAGGTT-GAAGTA
TTAGAACA-GACAGTATGAAAAGTGAAATGCACT---TTTAAATTAG-------------
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AGCACCACTTTT---AGGTATTCTCTGTTATTCT-----GGAGTTCAT--TTATTTTCCT
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>Dgo
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TTGTCTCAACCTTTGTCCTGTCACTGAACTTTGATGACTTA-GAAAGACAGAGTA-AGGC
TAATGACTTTTTATAGCCCTGCCTTACTTAAATCCAATTCATGAGCAAGTCATAATATCA
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CCAT--AATATCATTGGTTCTCT---AAAAAAATCCAAGACAAACAAGAA-----GTTA-
--TATGT-----T--CTAAAGCAATTTTGGAATATAGGTGTTTGTTGAGGTTAAGCTCCT
CATGTCTGGGGACAACCTAACTTTATTCTTCTTGTCCCCAA-CCTACTATTGAGGTTATG
AAAGATTTATCTGGAAA-CAGACCCAAAAGTTGTTCTGGCTCATCTGCTAGGAGCCAATG
AATGCTTTAGAAATTTTCCAGTG---ACTTCCTAGTTTCTCTTCCTTCATTT--------
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---------------------TAAAATCT---TT-CAGTATTAAA--ACACCTTTGACCT
-----AGAGTCAAGATTGCAA-TGTCAGGGTCC-AAGTCTTTGTGTATTT----------
------------AACTTTAATTAGTCTGTTCAGCCACACTGCACAAGCCAAGCACAATC-
CCATCTGTGGCATCATCATTTTCAAGCTTGGTGATGGGGG-TTGATTCATTTGTT---TG
GTATTGTCATACTATAAACTCTATTCCCNGTAATCCTCATGTAATCAAAGTTAAAAAAAA
AAAA--TCCTGAAGTTGATTAATTTTATTC-TAAGATGCTTTCAGAATGAAGAACACAGC
CAATAATAAAAGCATAGAAATTGAAATTGCAGAGGGAA--GAGTAGGTAGGTAAAAAGAA
AG----TAAAGCATGAAGTTGTCCACAGAAATATTTTTATTTTTAATAAGGTT-CAAGTA
TTAGAACA-AACAGTATGAAAAGTGAAGTGCATT---TTTAAATTAG-------------
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--------------------------------------CCTAAAACAATTAGGGTACACT
AGCACCACTTTT---AGGTATTCTCTGTTATTCT-----GGAGTTCAT--CTATTTTCCT
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>Tro
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AACACTGTAGAAATGTCCCAGTG---ACCTCCTGGTTTCCTTTCCTTCATTA----GTC-
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---------TGTGCTCAGTTTTGATACAG---ATGGAATATTAAA--CTACCTTTGACTT
T----AGAGTCAGGTTTGCCC-TGTTAGAGCCCCAAGTCTTTGTATATTCACTG-TGTGG
AAAACACTATTTAAATTCCATTGGTCTGTTTAGCCGCACTGCACAAGTAAACCACAGTCG
TTGTCTGGGG--TCATTATCTTCAGGCCTGGTGATAGAGA-CTGATTGATTTGTT---TG
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G-----CCTTAAAATTGATTAA-TTTATCC-CAAAAGCCCTTCTGGATAAAGAATACAGC
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AG----TAAGGTATGAAGATGTCCACAGAAATGTTGATGTTTTTACCA-GGTTTGAAGTG
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----------------------------------------------------GGTGCACT
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ACCCATACGTTTTGTAGGTATCCTTCTGTGTTGC----------------CTATTTTTCC
TTCCCAAGTACTTT------AA-GTACAGTTAATGACTATATATTTTTCAG--CTTCCCA
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>Mro
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TCCTCTTGACTTTTGTCCTGCCACTAGACTTTGATGACTTAAGAAAGACAGAGTG-AGGC
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CCTG-GGATGCCACTTGTCCTCTTTAAAAAAAAAAAGAGATGAAGAACAA-----GTTA-
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TTTGTCTG-AGATAACCAGACCTCCCGTT-------------------------------
--------------------------GATGTTGTTCCAGTTCATCTAGTGGGAGCCAATG
AAGGCTTTAGAAATTTCCCAGTG---ACTTCCTGGTTTCCCTTCCTTCATTT----GTC-
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---------TGAT--CAGTGTTGATAGAG---GTAGAATATTAAA--ACACCTTTGATTT
-----CGAGTCAAGATTGCTA-TGTCAGAATCCACAGA----------------------
----GACTATTGAAACTCCATTAGTCCTTTCAGTGATACTGCACAAGCAAAACACGGTCA
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TTAGGCCA-GACA---TG--AAATGCAATGCATT---TTTAAATTAG-------------
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>human
TATTGAGACCTGCCGTCACCAATGGGATGTCACAG--GTAAA----CTGGTGTGTGTGGG
--------------TATAACT---------------------------------------
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-----------------------TGTTGAATTAAATAATGTATGAAATGCCAGTTTACAT
GACAGATTATTCTTCCCAGACCTATTTAGTATGTGAAGCCATTACTAGTTGTATTTTTTT
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**MARKER 96**

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>WALLSI3
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GTCCTTCGTTTTC---GAAGAGGACCAATGACATCAT-GGGGTG---ATGTCTTGACTT-
GCGCATGAATTGGATTT-AAGTGAGGCAGAGTTGCACAAA--GTCATCAGCCTCACTCTC
TCTTCCAGAGTC-ATCGAAGTCCAGTGG--CAAGACAAAAGTCAGGATGACTGGTGATGG
CCCGGGATGCA-------------------------------------------------
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>WALLSI1A
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-----------TGTTTGGGCCCTGAT--TGGCTCAGAGTGAATGTAAATAGCAATTGTTT
-CTGTTT---TGGCCAGAAACCCTGAGGGTCTTCCCCTCCCAGATTGATTTTTTTTTTTT
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>WSINE1
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ACTTACTAG--------CTGTGTGACCCTGGGCAAGTCACTTAACCCCAATTGCCTC---
------------AAAAAAAAAAAAAA----------------------------------
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>Mdo
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T-TTCAGTTATTGCTGGTACAGTGACC----TGGGATTGAGATCCTTTGG----------
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-----------------------------GAAATCTGGTTTAAGCCAA-GCTAA---AAC
TCATCTTAATCCTTTGTCTACTAGTCTCCACCGCAGCCTGGCAGCTTTAGTTGGTTTAAC
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T--AGTCTTTTCTCTCTC----------TACAGATATATGACCTCTCAGTTGATGCATTG
AGC
>Dvi
TGGCTCACAGACAGAGCTGGCCATTGTTACTGCAGACTTTGTCAAGGTACTGACTGTCTC
C-TTCAGTTATTGCTGTTATAGTGACCCTTCTGGGATTGAGATCCTTTGG----------
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T--AGTCTTTTCTCTCTC----------TACAGATATATGACCTCTCAGTTGATGCATTG
AGC
>Mnu
TGGCTCACAGACAGAGCTGGCCATTGTTACTGCAGACTTTGTCAAGGTACTGACTGTCTC
C-TTCAGTTATTGCTGTTACAGTGACCCTTCTGGGATTGAGATCCTTTGG----------
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T--AGTCTTTTCTCTCTC----------TACAGATATATGACCTCTCAGTTGATGCATTG
AGC
>Rra
----------------CTGGCCATTGTTACTGCAGACTTTGTCAAGGTA----CTGTCTC
C----TCCTGGTGTTGCCCCACTGACCCTATGCTGAT-GGGACTCCTTGCTTGTGG-CAT
A---CTTCAGAGGGTCACTCAGCAAAGGCCCCC---------------------------
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**MARKER 107**

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**MARKER 108**

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GGAAAAAAGGGTATAAATTATAATCCAAATTCAGGGATCAGGGTA---------TGTGGA
```

```
AGGACTTTTGGCTTCCTCCC-TCCCCCCC--ACCTTCATCCCCAAA----CACATAGATG
CCTCCAACTCAC--CCGTGACCGCCCCAACTCCTGACAGTTCTTGTCAGTCACACTGATG
CCAT
>Iso
ATGATGATTCGGGAAATGATCACCTGGCAGATGCCAACGACTGCAGCTTT--CTGAGAAC
AGGAAGAATAAAGGTTAAAAA--------CCATCAGAGATCCTAGATTCTAGCCCATTCC
ACATGCATACAGGGA----GCAAGCAACCAGC-ACAATAGCCCTGATA-AACCAATTCAA
AATATGTA---GGAGAGCTTTACCAGAAGACCGCAGCTAAA---TCTTTATTGTT-----
--CAACTTAGTTGTTTTTCAGTC---AGGTCTGACTCTT---------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------------------------GGTGATT
CCACTTGGAA-TTTCTTCACAAAGTAATGGGAGTGCTTTGCCATATTCTCCTCTAGCTTG
TTTTACAGATGAGGAAACTGAGGCAAAC-AGGTTAAGTGATTTGCCCAGGGCTCTTAA-G
AT----------------------------------------GAGTCTTCTTGACTCCA-
------------------------------------------------------------
----AAGGCTAGCTATTTGCCCCCATAAAAGACCCTAT-GGATAGCCAAGCAT-GGGAGC
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CCAT
>Tro
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ACATACATGCAGGGA----GCAAGC-ACCAGCCCAAACTGCCCTGACAGAACCAATCTGA
AATG-TGCAGAGGACCGTTTTA-GAGAAGACCAAAGCTACA---TCTCTGTTGTTGGTCA
GTCACA---------GCTTAATC---ACGTCCAACTCTC---------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------------------------GGTGACT
CCAGCTGGTATTTGTTAGAAAAAGATACTGGAAAGGTTTGCCTTTTCCTTCTCCATCTCA
TTTTACAGAAGAAGAAACTGAGGCAAACAGGATGAAGTGACTTGCCCAGGGTCATACA-G
CTAGCAAGTGTCCAAGGCCAGATTTG-AACTCAGGAAAAT--GACTCCTCTTGAG-TCAG
GCCTGACATTCCATCTACTGTACCACCTAGCTGCCC----ACAGCTAAATCTAATACTA-
CCCAAAGGCCAGCTATAT-CCCCCATAAAAGGTCCTAT-TGATGGCCAAGCAC-GAAAGC
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CCAT
>Ppe
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TCTGAAACT-TGCAGAGGATAGCTTTACTAGAAGACCACAG-TTACATCTTTGTTGCTGT
T-CAG-TCAGGCATATTTTAATC---ATATCCAACTCTT-----TTTTTGTTGTTGTTGC
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GTGCTCTATTCACTGCACCACCTAGCTGCCCCC----ATGTCCAACTCTT---GATGAGT
CTATTTGGGATTTTCTTGGCAAATGTATTGGAGTGGTTTGCCATTTCCTTCTCTAGCTCA
TTTTACAAAAGAGGAAACTGAGGCAAACAGGGTGAAGTGACTTG-------TCACACA-G
CTAGCAAGCATCCAAGGTCAGATCTG-AACTCAGGGAAAC--GAATTTTCTTGAGTTCAG
```

```
GCCTGACATTCTATCTACTGCACCTCCTACCTGACC----ACAGCTAAATCTAACACT--
CCCAAAAAACAGCTATACCCCTCCATAAAAGGTCCTAT-GGATGGCCAAGCAT-GAGAGC
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CCAT
>Mro
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ACGCACATGCAGGGG----TCAGAC-ACCAGC-ACAA------TGACACA----------
-----TGCAGAGGACAGCTCTCCTGGAAGGCCACAGCCACA---TCTTTGCTGTTGGTGT
TGCTGCTTAGTCGTTTTTCAGTC---GTGTCCATCTCTT---------------------
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AGA-----GAGTATAAGTTATCACCCCAATTCAAGGATCAGCACTTGCCTAAAATATGAA
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CCTCCAGCTCAC--CCGTGATCGACCCAGCTCCTGAGAATTCCCGTCAGTCACGCTGATG
CCAT
>Ptr
ATGGTGATTCGGGAAATGACCACCTGGGAGATGCCGATGACTGCAGCTTT--CTGAGAGA
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-----TGCA-GGGACAGCTTTA-TGGAAGGCCACAG--------CCTTCCTTGCTGCTG-
--------------------GTC---ATGTCCATCTCTT---------------------
------------------------------------------------------------
------------------------------------------------------------
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TTTTACAGGAAAGGAAACTGAGGCAAACAGGATGCAGTAACTTGCCCAGGGTCACCCA-G
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AGAAAGAATTAAAGAGAGTAAATCATAAGC--------------------------CCGA
AGA-----GAGTATAAATTATTACCCCAATTCAAGGATCAGCACATGCCTAGAATATGAA
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CCTCCAGCTCAC--CCGTGATCGACCCAGCTCCTGAGAATTCCCATCAGTCACACTGATG
CCAT
>Vur
ATGGTGATTCGGGAAATGACCACCTGGGAGATGCCAATGACTGCAGCTTT--CTGAGAGC
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ACACATGTGAAGGGA----TCAAGC-ACCAGC-ACAACAGCCCTGAGAGAGCCAATCTGA
AATG-TGCAGGGCATAGCTTTACTAGAAGACCACAGCTACA---TCTTCA---TTGGTGT
--TCTGTCA-----------GTC---ACGTCCAACTGTT---------------------
------------------------------------------------------------
------------------------------------------------------------
```

```
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TTTTACAGATGAGGAAACTGAAGCAAACAGGGTGAAGTGACTTACCCAGGGCCACACA-G
CTATTAAGTATCTGAGGCCAGATTTG-AACTCAGGAAAAT--CAGTCTTCTTGAGTCCAG
GCCTGACATTTTATCTACTGTACCACCTAGCTGCCC----ACAGCTAAATCTAACTCTA-
CCCAAAGGCCAGCCATAA-CCCGCATAAAAGGCCCTAT-GGATGGCCAAGCAT-GAAAGC
AGAATGACTTAAAGAGGCTAAGTCATAAGC-AAAGAAAAAA--------------GCAGA
AGAAAAAAGGGTATAAATTA-CAC----ATTCAGTGATCAGCACATGCCTAGAATGTGGA
AGGAATTCTGGCTTCCTCCA-TCCCCC------CTTCATCCCCAAA----CACACAGATG
CCTCCAGCTTAC--CCGTGATCGACCCAGCTCCTGAGAGTTCCTGTCAGTCACGCTGATG
CCAT
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**MARKER 126**

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>Mar1b_Mdo
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TGGCAAACCA------------CTCCAGT-------------------------------
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>WSINE1
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CCTAGCTGCCCCTC----------------------------------------------
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---------------------------------------------------
>Mdo
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--GCTTCACT------------------------CTCCAACTTGACACCTATATTGCTGT
CAAAAT------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
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------------------------------------------------------------
---------------------------------------------------TATGTGTGT
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AGAAGGCTGCCTCAATAGGTGCAGAGGGAACACAAGAGAAACTTCCTGCTT
>Cfu
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CAAAAT---CATCT----------------------------------------------
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```

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------------------------------------------------GTGTATATGTAT
GTTTGCTTGT-AGAGTGAGGTCA--TCTATC-----------AGTCTTGGATAAT-----
----------TTTTATGAGATTATATACAAGAGG-TCCCCAAGCCTACAT--AATGTCTC
T--AGCACTTCAG-GGGCTAAGGTAGAAATGCCA-TTCTTGTACAAGGAGAACAAAAGAA
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>Dgl
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AGAC--CTGAGGG--------GAAAAAAAATTTGGGAGAAGCAATTAAGCCAGATAACA-
--GCCCACCCCCCTA-----------------CCCCCCAGCTTGATACCTGTAATGCTGT
CAAAAT---TGTGCATCACACAC--------------------ATATCTATATCTATATC
TATCTATCTATC-------TATGTCCAGT---ATTTTTTGGTTGTTTTTTGTTTTTTGTG
GGGCAATGGGGGTTAAGTGACTTGCCCAGGGTCACACAGCTAGTAAGTGTCAAGTGTCTG
AGGCTGGATTTGAACTCAGGTACTCCTGAATCCAGGGCTGGTGCTTTATCCACTGCGCCA
CCTAGCTGCCCCC----TATGTCCAGT---GTTTTTGCCAAGAAAAGACCAAATAGGGTT
GTGAAGAGTTGGAGATGACTA-AAACAACTGAAC------AATAT---AAATGTATGTGT
GTATTTTTGT-AGGGAGCTGTCA--TCTATC-AACCTTAAGTGGTCTTGTCTAGAAACCC
TAGAAACCTC-TTGACCAGGCCAGACATGAGAGA-TCCCCAAGCCTCTACAAAATGTCTC
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>Nty
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GGAC--CTGAAGG-----------AAAAAACTTGGGAGAAGCAATTAAGCCAGACAACA-
--ACCTATGACGTTCCCCAAA--------------CCCATATTGACACCTATAATGCTGT
GAATAT---TGTATGTATGTTTA-------------------------------------
-----AATTAT--------GAT---TAGT-------------------------------
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AGGAAGAGTTGGGCAGGACTG-AAGCAATTCAAC------AAG-----AACAGAAAG---
GTAT--------GGGAGAGGTCA--TCTATC-AGTCTTAGATGATCTTGGCTAGAGTCCC
TA-AACCATC-TTGATAAGATGAGGCATGAAAGA--------GTCTATAT-AAATGTCTC
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GGAAGGCTTCTTCCACAGTGGCAGAGGAAATGGAAGAGAAACCTTCTGCTT
>Pta
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AGAC--CTGAAGAAAAAAAAAAAAAAAAAACTTGAGAGGAGCAATTAAACCTGACAACC-
--TGCCACCAGCCCACT----------------CCCCCAAGCTTGAACCTAAAATGCTGT
CAAAAT---TGTGTGTGTGTGTG---------TGTGTGTGTGTGTGTGTGTGTGTGTGTG
TGTGTAAATTG--------TATATCCAGT-------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------ATCTTTGCCAAGAGAACCCTAAATAGGGTC
ATGAAGAGTTGGACGTGATTA-AAACAGCTCGAC------AACAG---AAATGTATGTAT
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TA----------------GACCAGACAT--GAGA-TCCTCAAGCCTACAC-AAATGTCTC
TTCAGCACTGCAG-GGGCCAGGGTGGAGATATCATTTATTG-CACAGGAGAATAAAAGGA
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>Dgo
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AGAC--CTGAAGGGA------AAAAACAAACTTGAGAGGAGCAATTAAGCCCGACAGCC-
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TTATGTTTGT-AGGGAGGGTTTA--TCTATC-AGTCTTAAATGATCTTGGCTAGAG-CCC
TA----------------GACCAGACAT--GAGA-TCCTCAAGCCTATAC-AAATGTCTC
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GGCAGGCTGCCTCTGTGAGGGTAGAGGGAAC-----AGAAACTTCCTGCTT
>Scr
TGTCCTCCAGCTGAACTGCTGCAGCCACTCACAGGTCATGCCTCCTGCCAGAGTGCCCAG
AGAC--CTGAAGGAA-----AAAAAAACAACTTGAGAGGATCAATTAAGCGTGCCA-CC-
--TGCCCACTC----------------------CCTCAAGCTTGCCACCTAGAATGCTGT
CAAAAT---NGTGTGTGTGTGTG-------TGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
TGTGTAAATTG--------TATGTCCAGT-------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------ATCTTTGCCAAGAGAACCCTAAACAGGGTC
ATGAAGAGTTGGATGTGATTA-AAACAACTCAAC------AACAT---AAATGTATGTAT
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-----------------------------------TCCTCAAGCCTACAT-AAATGTCTC
TTTAGCACTGCAG-GGGCCAGGGTAGAAATGTCATTTATTG-CACAGGAGAATA---GAA
GAAAGGCTACCTCTCTGAGGCCAGAGGGAATAGAAAAGAAACTTCCTGCTT
>Pgu
TGTCCTCCAGCTGAACTGCTGCAACCATTCACAGGTCATGCCTCCTGCCAAGGTGCCGAG
AGAC--CTGGGGG----------AAAAAAACTTGGGAGAAGCAATTAAGCCAGACAGCAA
CTTGTCAACTTCTCCCACA--------------CTTCCAGGTTGACACCTGTAATGCTGT
CAAAAC---TGTATGTGTGATTA-------------------------------------
-------AATG--------TCTGTCTAGT-------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------ATTTTTGCCAAGAAAACCCCAA--------
-CAAAGAGCTGGATATGACTG-ACACAACTTCAC------AACA----ATATAAATGTTT
GTATGTTTGT-AGGGAGCAGTCA--TTTATC-AGTCTTAGATGACTTTGGCTAGAATACG
TAGAGATATCTT-GACTAGACCAGATATGAGAGATTCCCCAAGCCTATAT-AAATGTTTC
TTTAGCACTGCAG-GGGCCAGGGTGGAAATGTCATTTATTATATAAAGGGAACAAAAGGA
GGAAGATTGCCTCAACAGAGGCAGAAGGAACAGAAGAGAAACTTCCTGCTT
>Iso
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AGAC--CTGGGGG----------AAAAAAACTTGGGAGAAGCAATTAAGCCAGACAGCAA
CTTGTCAACTTCTCCCACA--------------CTCCCAGATTGACACCTGTAATGCTGT
CAAAAT---TGTATGTGTGATTA-------------------------------------
-------AATG--------TCTGTCTAGT-------------------------------
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------------------------------------------------------------
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>Tro
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CAAAAT---TGTGTGTGTGTCTGTATGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
ATGTGAGTATGTATAA---TATGTCCA---------------------------------
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------------------------------AAATCTGCCAAGAAAATCCCAAATGGGGTC
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ATATGTTTGT-AAGTAGAGGTCA--TCTATC-ANTCTTAGATGATCTTGGCTAGAGTCCC
TAAAGACATCTTTGACTAGACCAGACATGAGAGA-TCCCT-------------ATCTACC
TCTAGCCCGGCAA-GGGTCAGAGTG-------------------------GAACAAAGGA
GG-------CTTCCCCAGGGGCAGAGGGAACAGAAGAGAAGCTTGCTGCTT
>Ppe
TGTCTGCCAACTGAACTGCTGCAGCCACTCACAGGTCATGCCTCCTGCCAGGGTGCCCAG
AAAC--CTGAGGGG----------AAAAAACTTGGGAGAAGCAATTAAGCCAGACAACAG
CTTGCCACCTGCTCCCTA---------------CCCCCAGCTTGAAACCTATAATGCTGT
CAAAAT---TGTGTGTGTGTGTG--------------------------TGTGTGTGTGT
ATGTGTATA-G--------TATGTCCAGT-------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------ATCTTTGCCAAGAAAATCCCAGATGGGGTC
ATGAAGAGTTGGATATGACTG-AAACAACTCAAC---AATGACAT---AAATATATGTAT
ATATGTTTGT-AAGGAGAGGTCA--TCTATCAAGTCTTAGATGATCTTGGCTTGAGTCCC
TAGAGATATCTT-GACTAGACCAGACATGAGAGA-TCCCT-------------ATCTCTC
TTTAGCACTTTGA-GGGTCAGGGTG-------------------------GAACAAAGGA
GGAAGGCTGCTTCAACAAGGGCAGAGGGAACAGAAGAGAAACTTCCTGCTT
>Mro
TGTTTGCCAGCTGAACTGCTGCAGCCACTCACAGGTCATGCCTCCTGCCAGGGTGCCCAG
AGAC--CTGAGGG-----------AAAAAACTTGGGAGAAGCAATTAAAACAGACAACAG
CCTGTCACCTGATCCCTCCCA--------CCCACCCCCAGCTTGACACCTATAATGCTGT
CAAAAT---TGTGTGTGTGTGTG------------------------TGCGCGCGCATAT
GTGTATAAATG--------TACATCCACT-------------------------------
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------------------------------------------------------------
------------------------------ATCTTTGCCAAGAAAATTCCAAATGAGGTC
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TAGAGACATCTT-GAGTAGACCAGACATGAGAGA-TCCCT--ACC-----------TCTC
TTTAGCACTGCAA-GGGTCAGGGTG-------------------------GAATAAAGGA
GGAATGCTGCCTCAACAGGGGCAGAGGGAACACAAGAGAAACTTCCTGTTT
>Vur
TGTCCTCCAGCTGAACTGTTGCAGCCACTCACAGGTCATGCCTCCTGCCAGGGTGCCCAA
AGAC--CTAAGGG----------AAAAAAACTTGGGAGAGGCAATTAAGCCAGACAACAG
CCTGCCACCTACCCCCCCACACACATACCCCAACCCCAAGATTGACACCTATAATGCCGT
CAAAAT---TGTGTGTGTATGTG-------------------------------------
-TGTATAAATG--------TATGTCCAGT-------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------ATCTTCGCCAAGAAAACCCCAAATGGGGTC
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ATATGTTTGT-AGAAAGAGGTCG--TCTATT-AGTCTTAGATGATTTTGGCTAGAGTCCC
TAGAGACATGTT-GACTAGATCATACAT--GAGA-TCCCCAAACCTATAT-AAATGTCTC
TTTAGTACTGCAAGGGGTTAGGGTGGAAATGTCATGCATTGTATAA---GAACAGAAGGA
GGAAGGCTGCCTCAACAGGGG---------CAGAAGAGAAACTCCCTGCTT
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## MARKER 129

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>WSINE1
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CCTCAGACAC---------TTACTAGCTGTGTGACCCTGGGCAAGTCACTTAACCCCAAT
TGCCT--------------CAAAAAAAAAAAAAA--------------------------
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>L1_Opos2_3end
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------------------------------------------------------------
----------CATTTCTTATAGCACAATAGTATTCCATCACAAT-----CATATACCACA
ACTTGTTCAGCCATTCCCCAATTGATGGGCA-TCCCCTCAATTTCCAATTCTTTGCCACC
ACAAAAAGAGCT------------------------------------------------
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------------------------------------------------------------
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>WSINE1
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```

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TCCAGGGCTGGTGCTCTATCCACTGCACCACCTAGCTGCCCCTC----------------
------------------------------------------------------------
------------------------------------------------------------
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----------
>WSINE1
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------------------------------------------------------------
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------------------------------------------------------------
------------------------------------------------------------
-------------------------------------------------------TTTTT
TTTTTTTTTG-AGGCAATTGGGGTTAAGTGACTTGCCC------AGGGTCACACAGCTAG
TAAGTGTC----TGAGG---CTGGATTT--------------------------------
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------------------------------------------------------------
----------------------------------------------GAACTCAGGTCCTC
CTGACTCCAGGGCTGGTGCTCTATC-CACTGCACCACCTAGCTGCCCCTC----------
------------------------------------------------------------
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>WALLSI2
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```

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------------------------------------------------------------
-------------------------------GGGGGCAGCTAGGTGGTGCAGTGGATAGA
GCACCAGTGCAGGAGTCAGGAGGACCTGAGTTCAAATCTCACCTC-AGACACTTGACACT
CACTAGCTGTGTGACCTTGGGCAAGTCACTTAACCCCAATTGCCT---------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
----------
>Mdo
CAGCACATGGTGACGATGG--CTGGAACAGAGGAAGGGTTATTAACA-------------
------------------------------------CCAACTTCAT--------------
------------------------------------------------------------
------------------------------------------------------------
-----CCTCCACCCCCTC-AAATGACCCTGCACTGTGGCTAAACAAGCTACTAAG--TTA
GAAGCCATGACAGAGGAAGAGAG--------CA----TCTGTACAAACACAA---AGGAG
CACTGT------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------------------TCT
CAATAAA-----TGCAAAGAAATCC-----------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------------------------------------ATGCAACCAC
TCTTTT-CT------AACCCATGTGACCAAG-TGGACA-GTGAACGATGTGCT-TGTGAG
AAAGGG--CTCATGTTCTC----ATTCCC---------ACCCCTTGAGGTAGGAACCCCA
AGGCTTTAC--CTGAAGGTCCCCCGTTCAACATCCTGGCCGCTGAGCCGAATGTGGATCC
CTTCTTTCAG
>Dvi
GAGCACATGGTGACGATGG--CTGGAACAGAAGATGGGTTATTAACA-------------
------------------------------------CCAACTTNAT--------------
------------------------------------------------------------
------------------------------------------------------------
-----CCCCCACCTCCTC-AAATGACCCTGCACTATGGCTAAACAAGTTACTAAGTTTTA
GAAGCCAGGACAGAGGAAGAAAG--------CA----TCTGTACAGACACAA---TGGAG
CACTAT------------------------------------------------------
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------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------------------TCT
TAATAAA-----CGCAAAGAAATCC-----------------------------------
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------------------------------------------------------------
--------------------------------------------------ATGCGACCAC
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TCTTTT-CTAACCAAGACCCTTGTGACCGAG-TGGACAGGGCAATGATATGCT-TGTGAG
AAAGGG--CCCCTGCTCTCTCTTATTACC---------ACCCCTTGAGGTAGGAAACCCG
AGGCTTTAC--CTGAAGGTCCCCCGTTCAACATCCTGGCCGCTGAGCCGAATGTGNATCC
CTTCTTTCAG
>Mnu
CAGCACATGGTGACGATGG--CTGGAACAGAAGACGGGTTATTAACA-------------
------------------------------------CCAACTTCAT--------------
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-----CCCCCACCTCCTC-AAATGACCCTGCACTATGGCTAAACAAGTTACTAAGTTTTA
GAAGCCAGGACAGAGGAAGAAAG--------CA----TCTGTACAGACACAA---TGGAG
CACTAT------------------------------------------------------
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------------------------------------------------------------
---------------------------------------------------------TCT
TAATAAA-----CGCAAAGAAATCC-----------------------------------
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------------------------------------------------------------
------------------------------------------------------------
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------------------------------------------------------------
--------------------------------------------------ATGCGACCAC
TCTTTT-CTAACCAAGACCCTTGTGACCGAG-TGGACAGGGCAATGATATGCT-TGTGAG
AAAGGG--CCCCTGCTCTCTCTTATTACC---------ACCCCTTGAGGTAGGAAACCCG
AGGCTTTAC--CTGAAGGTCCCCCGTTCAACATCCTGGCCGCTGAGCCGAATGTGGATCC
CTTCTTTCAG
>Rra
CAGCACATGGTGACGATGG--CTGGAACAGAAGAATGGTTATTAATA-------------
------------------------------------CCAACTTCAC--------------
------------------------------------------------------------
------------------------------------------------------------
-----CCCCTTCCCTCCC-----AATCCTGCGCTGTGGCTAAACAAGCTGCTACG--TAC
AAAGCCATGACAGAGGAAGTGAGCTCCCAAGCA----TCTGTTC-CACACAA---GGGAG
CGCTGT------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------------------TTT
CAATAAAAGCTGTCCAAAGAAATCA-----------------------------------
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------------------------------------------------------------
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------------------------------------------------------------
--------------------------------------------------GTAGGACTGC
TATTTT-CAAACCAGGGCCTATTCCATTGAG-TGGACA-GTTAAGGATCTGCT---TATG
AAAGGC--CTCAGACAGTCTATAATTCCC-------AACCCCACCCAGGTGGGAACCCCT
AGGCTTTAC--CTGAAGGTTCCTCTTTCAACATCCTGACCGCTGAGTCGAATGTGGATCC
CCTCTTTCAG
>Cfu
CAGCACATGGTGACGATGG--CTGGAACAGAAGAATGGTTATTAATA-------------
------------------------------------CCAACTTCAC--------------
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------------------------------------------------------------
------------------------------------------------------------
-----TCCCTCCCCTCCC-----GATCCTGTACTGTGGCTAAACAAGCTGCTACG--TAC
AAAGCCATGACAGAGGAAGCAAGTTCCCAAGCA----TCTGTTC-CACACAA---GGGAG
CACTGT------------------------------------------------------
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------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------------------TTT
CAATAAAAGCTGTCCAAAGAAATCA-----------------------------------
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------------------------------------------------------------
--------------------------------------------------GTAGGACTGC
TCTTTT-CAAACCAGGGCCTATTCCACTGAA-TGGATA-GTTAAGGATCTGCT---TATG
AAAGGA--TTCAGACTATCTGTAATTCCC-------AACCCCACCCAGGTAGGAACCCCT
AGGCTTTAC--CTGAAGGTTCCTCGTTCAACATCCTGACCACTGAGTCGAATGTGGATCC
CCTCTTTCAG
>Dgl
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ACAAAACAAAACCAAACAACAACAACAACAACAAAA-CAACTTCAC--------------
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GAAGCCATTACAGAGGAAGATAGATCCCAAGCA----TCTGTACAAACACAA---CAGAG
TACTGT------------------------------------------------------
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------------------------------------------------------------
---------------------------------------------------------TCT
TCATAAAAGATGTCCAAAGAAATCAGTGCAAGTGT-----TCTTTTCCTTCCTTCCTTCC
TTTCTTTTGGGAGGCAATCAGGGTTAAGTGACTTTCCC------AGGGTCACACAATAAG
TGGC--------TGAAG---CTGGCTTT--------------------------------
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------------------------------------------------------------
----------------------------------------------GAACTCAGGTCCTC
TTGACACCAGGGCTGGTACACTGTG--------CTACCTAGCTGCCTCTT--CAA-TTGC
TCTTTT-TAAACATGTGACT--------GAG-TGGGCA-GTAACATATGCTTG--TTAT-
---GGG---------AATCTCCAATTCCC-------ACTCCCAATGAGGTGGGAATCACT
AGGTTTTAC--CTGAAGGTTCCACGTTCAACATCCTGGCCGCTGAGCCGAATGTGGATCC
CATCTTTCAG
>Nty
TAGCACATGGTGACGATGG--CTGCAACAGAAGAATGGTTATTAATA-------------
------------------------------------CCAACTTCAC--------------
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------------------------------------------------------------
-----TCCCTTCCCCCTC-AAATGATCCTGCACTATGGCTAAACAAGTTANTGAG--TCA
AAAGCCATTACAGAGGGAGAGAGCCCCCAAGCA----TCTGTACAAACACAAC--GGAAG
TACTGC------------------------------------------------------
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------------------------------------------------------------
---------------------------------------------------------TCT
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TTTTTTTGGGGAGGTAATCAGGGTTAAGCACCTGACCA-------GGGTCACACAGTAAA
TATCCAAG-----GCCG------AATTT--------------------------------
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------------------------------------------------------------
----------------------------------------------GAACTCAGGTTCTC
CTGACACTAAGGCTGGTGCTCTATC-CACTATGCCACCTAGCTGCCCTTC------AAGC
TGCCCTAAGCTAAATGTGACAGCTATTTTCCAACCAA-GGCCCCTTCTGACTGAGTAGAC
A---GT-AATGGTA-CACTTGTAATTTCC-------ATCCCCAAAGAGGTTGGAACTACT
AGGCTTTAC--CTGAAGGTTCCTCGTTCAACATCCTGGCCACTGAGTCGAATGTGGATTC
CGTCTTTCAA
>Pta
TAGCACATGGTGACGATGG--CTGAAAAAGAAGAATAGTTATTAATA-------------
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-----CTC-TCCCCCCTC-AAATGACCCTGCACTATAGCTTCACAAGCTACACAG--TAA
GAAACTATGATTGAGGAAGAGAGTTCCCAAAAA----TCTGTACAAACATAAA--AGAGC
ATTGTT------------------------------------------------------
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------------------------------------------------------------
------------------------------------------------------------
----------------------------------------------------------TT
TAACCAAAGCTGCCCAAAGAAATCAGCATGACTG--------CTCTTTTCCTTTCTTTTC
TATGATTTGG-AGACAATTAGGGTTAAATGACTTGCCC------AGGTTCACACAATAAG
CGTCTGAG----ACCAC-------ATCT--------------------------------
------------------------------------------------------------
------------------------------------------------------------
----------------------------------------------GAATTCA-GTTCTC
CTAAAACTAGGGCTAGTGCTCCCCATCATTACACACCTCAGCGGCCTCTG---TGATTAC
TCTTTT-CAAGCCAAGACCCC-ATTGACTAG--AGAG-CAGTAAGGATGTGCTTGTTAAG
A---GT-TCTGA---TCTCTCTAATTCCC------CTGCCCA-------CAGAAACTATT
AGGCTTTAC--CTGAAGGTTCCCCGTTCAACATCCTGGCCACTGAGCCGAATGTGGATTC
CATCTTTCAG
>Scr
TAGCACATGGTGACGATGG--CTGAAAAAGAAGAATGGTTATTAATA-------------
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-----CTCTCCCCCCCTC-AAATGACTCTGCACTGTAGCTTCACAAGCTACACAG--TAA
GAAACCATG--ATTGAGGAAGAGTTCCCAAAAA----TCTGTACAAACATAAA--AGAAC
ATAGTT------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
----------------------------------------------------------TT
TAACCAAAGTTGCTCAAAG-AATCAGTGTGACTG--------CTCTTTTCCTTTCTTTTC
TATGTTTTGG-AGACAATTAGGGTTAAGTGACTTGCCC------AGGTTCACAAAGTAAA
CGTCTGAG----ACCAC-------ATTT--------------------------------
------------------------------------------------------------
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----------------------------------------------GAACTTA-GTTCTC
CTAAAACCAGGGCTAGTGCTCCATC--ATTACACACCTTAGCTGCTTCTG---TGATTTC
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G----C-TCTGA----CTCT--AATTCCC------CTGCCCA-----------AAACGCT
AGGCTTTAC--CTGAAGGTTCCCCGTTCAACATCCTGGCCACTGAGCCGAATGTGGATTC
CATCTTTCAG
>Mfa
TAGTACATGGTGACGATGG--CTGAAAGAGAAGAATGATTATTAATA-------------
------------------------------------TCAAC-TTTC--------------
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-----CCTCTTCCCCCTC-AAATAACCCTGCACTGTGGCTTCACAAGCTTCACAG--TAA
GAAATCATG--ATAGAGAAAGAGTTCCCAAAAA----TCTGTACAAACATAAT--GGAAC
AATATT------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
----------------------------------------------------------TT
TAACTAAAGTTGCCCAAAGAAATCAGCATGACTG--------GTTTTCTCCTTTGTCTTC
TACGTTTTGG-AGACAATTAGAGTTAAGTGACTTGCCC------AGGTTCACAGAGTAAG
CATTTGAG----GCCAC-------ATTT--------------------------------
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CTAAAACCAGGGCTAGTGCTTTATC--ATTACATACCTTAGCTGCCCCCA---TGACTAC
TCTTTT-CAAGCCAAGGTCCTTCAGATTGAG--AAAG-CAGTAAGGATGTGTTTGTTACA
AAGAGG-TCTGA----CTCTCTAATTCCC------ATGTCC-AAGGTGGTGGAAAGTGCT
AAGCTTTAC--CTGAAGGTTCCCCGCTCAACATCCTGGCCACTGAGCCGAATGTGGATTC
CATCTTTCAG
>Bil
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CACTAA----TTTTTTTTTT-ACTGGACTAATTTCCTTTATTATTTTTTCATATACCACA
ACTTGTTGAGTAATT-GTCAAATGATGGGCAATGGTTAAAGAGCACTATTCTTTAAAAAT
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CACACAGCTAGGTAAATTATTAGGTGTTTGAAGCTGGATTTGAACTCAGGTCCTCCTGAC
TCCAGGGCTGGTGGTCTATCTACTGTGCCACCTAGTTGCCCCAA---GGAGCACTCTT--
-AATAGAAATTGTCCAAAGAAATCAGTCAGTCTGC--------TCTTTTCTTTCTCTTTC
ATTTTTTTGG-AGGCAATAAGGGTTAAGTGACTTATC-----------------------
------------TGAGG---CTGGATTT--------------------------------
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CTGACACCAGGGCTGGTGCTCTTTG--------TCATTTAGCTTCTCCTG---CAACTTG
GTTTC--CATACCAAGGTCCTCACAACTGAG-TGGACAGGAAGGGTTCACACT-------
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CGTCCTTCAG
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>Pgu
TAGCACATGATGACGGTGG--CTGGAACATAACAAGGATCATTAATA-------------
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AACTA----TTTTTTTTTTTAACTGAAATAATTTCCTTTATTA-TTTTTTATTTACCACA
ACTTATTTAATAATT-GTCAAATGATGGGCAATAGTTAAGGAGCACTATTCTTTTAAAAA
AA-------------TTTTATCTATTTAAGGCAA-TGGAGTTAAGTGACTTGCCCAAGGT
ATCACAGCTAGCT-AATTATTAAGTGTCTGAGGCTGGATTTGAATTCAGGTTCTCCTGAC
TCCAGGGCCGGCGCTCTATCCACTGTGCC-----------CCAG---GAAGCACTCTTTT
TAATAGAAATTGTCCAAAGAAATCAGTTCAGCTGC--------------TCTTTTCTTTT
TCTTTTTTGG-AGGCAATAAGATTTAAGCAACTTACC-----------------------
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GTCAT--CATACTAAGGCCCCTATGACT-TG-T---GAGGAAGGGTTTATGCT-------
-AAGG-------------TTCCA-TTCAC---------------------------TATC
AGGTTTTAC--CTGAAGGTTCCCCGTTCAACATCCTGGCCACTGAGTCGAATGTGGATTC
CGTCCTTCAG
>Iso
TAGCACATGGTGACGGTGG--CTGGAACATAACAAGGATCATTAATA-------------
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CACTAA---TTTTTTTTTTTAACTGAAATAATTTCCTTTATTA-TTTTTTATTTACCACA
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TCCAGGGCCGGCGCTTTATCCACTGTGCC-----------CCAG---GAAGCACTCTTTT
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------------TGAAG---CTGGATTT--------------------------------
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GTCAT--CATACTAAGGCCCCTATGACT-TG-T---GAGGAAGGGTTTATGCT-------
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AGGTTTTAC--CTGAAGGTTCCCCGTTCAACATCCTGGCCACTGAGTCGAATGTGGATCC
CGTCCTTCAG
>Tro
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------------------------------------------------------------
-----ACCTTTCTCCCTC-AAATGACACTGCACTATAGGTAAACAAGCTCCTAAG--TGG
GAAGCCAGGGCAGAGGAAGAGAGCTCCTCAGCG----TCTGCACAAACACAAC--AGAGT
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GCTGTT------------------------------------------------------
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TT---AAGCGTCTAAGA---CTGGATTC---GGGGATGGTTAGGTGGTGCAGTGAATAGA
GCAC--------------------------------CAATCCTGGAGGT--AAAGGATCT
GAGTTACTAGCCATGTGACCTTGGGCAAGTCACTTAACCCCAATTGCCTGGCCTTAGCCC
CTCCAAAAAG--------TTTAAAAGAAAAGA---CTGGATTT---GAACTTGAGTCCTT
CTAACGCCAGGGTTGGTGCTTTATCC-ACTAAACCACCTAGCTGCACATG---CCATTGC
TCTTTATAAAACCAAGGCCCCCATGACTGAA-TAAACA-ATAATGATACAATT--GTCAG
AAAGGA--CTCAGGCTATCTCCAATTCCC------ATCCT----------------CAGT
AGGCTTTAC--CTGAAGGTTCCCCGTTCAACATCCTGGCCACTGAGCCGAATGTGGATCC
CATCTTTTAG
>Ppe
TAGCACATGATGACGATGG--CTGGAAGAGAAGAATGGTTATTAATA-------------
------------------------------------CCAATTTCAT--------------
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-----CCCCTTCTCCCTC-AAATGACCCTGCACTGTGGCTAAACAAGCTGCTAAG--TAA
GAAGCCATGACAGAGGAAGAGAGCTCCCAAGCA----TTTGTACAAACACAAC--AGAAT
GCTGTT------------------------------------------------------
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------------------------------------------------------------
------------------------------------------------------------
----------------------------------------------------------CT
TAATATAAGTTGTCCAAGGAAATCAGTGCAAACAC-------------------TCTTTT
CTTTTTTTT----------------AAGTGACTTGCCT------AGGGTCACACAGTAAG
TAAGTAAGTGTGTTAGA---CTGGATTT---GGGGGTGGCAAGGTGGTGCAGTGAAGAGA
GCACCAGCCCTGGA----TTCAGGAGGACCTGAGTTCAAATCTGACCTCAGACACTTACT
AC-TTGCTAGCCATGTGACCTTGGGCA-AACACTTAACACCAACTGCCTGGACTC-CCCC
CTCCAAAAAGTTAAAAAAAAAAAAAATGAAAA---CTGG--TT---GAACTGAGGTCCTC
CTAACACCAGGGTTGGTGCTCTATCT-GCTATACCACCTGG-TGTCCATG---TGACTGC
TCTTTT-CAAACCAAGGACCCCATGACTGAATTGGACA-GTAATGATATGACTGTGTGAG
AAAGGG--TTCAGGCTATCTCCAATTCCC------ATCCTCAA-TGAGATGGTAACCAGT
AGGTCTTAC--CTGAACGTTCCCCGTTCAACATCCTGGCCACTGAGCCGAATGTGGATCC
CATCTTTCAG
>Tvu
TAGCACATGATGACGATGG--CTGGAACAGAAGAATGATTGTTAATA-------------
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CCTCAGACACTCGACACACTTACTAGCTCTGTGATCCTGGGCAAGTCACTTAACCCCAAT
TGCCCTGCCTTCCCCCCTCCAAAAAAAACCCCAACCAAAAAAAAATATA---CAAACTTC
AC---CCCCTTCCCCCTC-ATATGACCCTGCACTGTAGCTAAACA-TCTCCTAAG--TGA
GAAGCCATATCAGAGGAAGAGAGCTCCCAAGCA----TCTGTACAAACACAAG--GGAGA
GCTGTT------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
----------------------------------------------------------CT
TAATAAAAGCTGTCCAAAGAAATCAGTGTAATCACTCTTTTATTTCTTTTTTTGTTTGTT
TTTTCTTTTGAAGGCAGTCGGGGTTAAGTGACATGCCC------AGGGTCACACGGTAAA
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TGT--------AAAACA---CTGGATTT--------------------------------
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GAAGGAG-CTCAGGCTATCTCCAATTCCC------ATTCTTGA-TGAGGTGCTAACCACT
ACGCTTTAC--CTGAAGGTTCCCCGTTCAACATCCTGGCCGCTGAGCCTAACGTGGATCC
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>Mro
TAGCACATGATGACGATGG--CTGGAACAGAAGAATGGTTATTAATA-------------
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GAAGCCATG--ATAGGAAGATATCTCCCAAGCATCTACCTATACAAACACAAC--AGAGT
GCTATT------------------------------------------------------
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------------------------------------------------------------
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----------------------------------------------------------CC
TAATAAAAGCTGTCCAAAGAAATCAGAGCAACCAAACATA-----------------CTT
TTTATTTTGG-AGGCAGTTGGAGTTAAGTGACTTGCC-------AGGGTAA----GTAAG
TAAGTATG----TAAGA---CTAGATTT--------------------------------
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----------------------------------------------GAACTGAAGTCCTT
CTAACACCAGGGCTGGTGTTCTATCC-ACTGTGCGATCTGGCTGCCCATG---AGACTAC
TCTATT-TAAACCAAGGCCCCCATGACTGAG-TGAACA-GTAATGATACGACT--CTGAG
AAAGAG--CTCAGGCTATCTCCAATTCCAATTCCTATCCTCAA-TGAGGTGGTAAGCACT
AGGCTTTAC--CTGAAGGTTCCCCGTTCAACATCCTGGCCGCTGAGTCGAATGTGGATGC
CATCTTTCAG
>Vur
TAGCACATGATGACGATGG--CTGAAACAGAAGAATGGTTATGAACT-------------
------------------------------------CCAACTTCAT--------------
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-----CCCCTTCCCCCTC-AAATGACCCTGCACTGTGGCTAAACAAGCTCCTAAG--TGA
GAAGCCATGACAGAGGAAGAGAGCTCCCAAGCA----TCTGTACAAAAACAAT--GAAGC
ACTGTT------------------------------------------------------
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------------------------------------------------------------
------------------------------------------------------------
----------------------------------------------------------CT
TAATAAAAACTGACCAAAGAAATCAGTGCAACTGC----TCTTTTCTTTCTTTCTTTCTT
TTTTTTCTGG-AGGCAGTCAAGGTCAAGTGACTTGCCC------AGGGTCACACAGTAAG
TAAGTGTC----TAAGG---CCGGATTT--------------------------------
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------------------------------------------------------------
----------------------------------------------GAACTCAGGTCCTC
CTGACACCAGGGC--------------------------TAGTGCCCCTT---TAACCCC
TCTTTT-TAAACCAAGGACCCCATGACTGAG-TGGACA-GTAATGATACACTT--GTGAG
AAAGGG--CTCAGGCAATCTCCTATTCCC------ATCCTCAT-TGAGGTGGTAACCACT
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AGGCTTTAC--CTGAAGGTTCCCCTTTCAACATCCTGGCCGCTGAGCCGAATGTGGATCC
CATCTTTCAG

## MARKER 135

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CTCAGTTTCCTCATCTGTAAAA-TGAGCTGG-AGAAGGA---------------------
--AATGGCAAACCACTCCAGTATCTTTG-CCAAGAAAACCCCAAATGGGGTCACGAAGAG
TCAGACACGACTGAAAAATGACTGAACAAC----------------AACAACAA------
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>SINE1_Mdo_partial
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>Mdo
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AAAT-AGTTTATAGAAAAA-----------------------------------------
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GC--TTTGTTTTTATGTAAT----------------------------------------
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AA-T--GATTATTCTTTTA-TGCTT-GTGCCACTTTATATCTTTTAAAAATTCATTTTTA
A-CATTTTCTTTTTAGTT------------------------------------------
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AC--TTTATTTTTATGTAAT----------------------------------------
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GAAT--GATCATTCTTTTA-TACTT-GTGCCACTTCATACCTTTGGTTCCAGATTTGAAA
A-CAATTATTTATTTTTT-------------------AAGCAGAAATTGTATGTAATGGG
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----------------------------------------------TACTAT---ACATG
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TT--------CCATAAGTGGTGGGTATGTGTAGAAGTTTTT----CTAATACAGTTTTAG
GAAT--GATCATTCTTTTA-TACTT-GTGCCACTTCATACCTTTGGTTCCAGATTTGAAA
A-CAATAATTTATTTTTT-------------------AAGCAGAAATTGNATGTAATGGG
GGGTTGCAAAGGGTCTCAGTTGATTTAGAGTCAGGTCTAGAGGTGGTACATCTGGAAATC
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-----------------------AACCAATACACAGTATTGATTTTAAGATGGAAAAAAA
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>Cfu
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TC--CTTATTTTGATGTAGT----------------------------------------
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AATTAACATTATACTTCTA-TATTT-GCGTTGCTATATAGTATTATGTCCAGATTTGAAA
A-CAGTTTTTATATATTA------------------------------------------
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GGAA-GATTTATAGAAAAA-----------------------------------------
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AAAGTGCTATATCT-----GGAGTC----------TTCTTC-CTGAGTTCAAATCCAGCC
TCAGATACTTGTCACTCAGCCACCTGTGTGACCCTGGACAAATCATATAGCCCTATTTGC
CTCAGTTTCCTCATCTGTAAAA-TGAGTTGG-AGAAGGA---------------------
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A-CATTTATTTATTT---------------------------------------------
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GAAA-GGATTTTAGAAAAA-----------------------------------------
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TCAGAAACGT--------ATTACCTGTTTCACCCTGGACAAGTCATGTAACCCTGTTTGC
CTCGGTTTCTTCATTTATAAAAATTAGCTGG-AGAAGGA---------------------
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A-TATTTATGTAAATTTT------------------------------------------
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## MARKER 139

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ATCA--------------------------------------------------------
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**MARKER 142**

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TCTTCCCTAATTCCC-TCTAG--GTTTATTCCAGAGCCAATGAGCAGGAGCCTTGTGGTT
GGTGGCTGGCAAGGGTTC
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**MARKER 144**

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>WSINE1
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-----------------------------------------------------TTTTTTT
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GTGTC-------TGAGGCTGGATTTGAACTCAGGTCCTCCTGACTCCAGGGCTGGTGCTC
TATCCACTGCACCACCTAGCTGCCCCTC--------------------------------
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>MIRc
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------------------------GTT---------TCCTC-------ATCTGTAAAATG
GGGATAATAATA--CCTGCCCTGC--CTACCTCACAGGGTTGTTGTGAGGAT--CAAATG
A-GATAATGTATGTGAAAG-----CGCTTT-GTAAACTGTAAA----GTGCTATACAAAT
--GTAAGGGGTTATTATTATT---------------------------------------
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>MAR1c_Mdo
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-------------------------GGAGGCAGCTAGGTGGCTCAGTGGATAGAGCGCCG
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GCAAACCACTCCAGTATCTTTGCCAAGAAAACCC--CATGGACAGTATTGGCGTGCTATG
GTCCACGGGGTCACGAAGAGTC------------GGACACGACTGAACGACTG-----AA
CAACAACAAA--------------------------------------------------
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>Mdo
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------------------------------------------------------------
---------------------------------------GT--AAAAGAATTTTAAAGTC
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------------------------------------------------------------
----------------ATCTCTC-----ACTTAGTAAGTCTTAGAAGAGAATTGACTTGC
CCAAGG----------------TATTGTCTTTCT-GGTATGAGTCTAGATATTGGGCTCT
TGGGATGT--ATTAAAAGG-----AATATAAGC--ATCTCCTTTTTCTGGGGAAATTTTT
AGCAATTATGTTTTGGCA-AGTCATTCATTGGTAGCTTGTCTTGGATA---TAGTTTAAT
TT-GGTGACTT--ACTTTT-CAGGGATTA-----------------------GTCT-AAA
TATT--GCTTCTTAAGAA-GTAATAGTTTT--TATTTACTCTTTCCCAG--GATTTGGGA
TGAATGGGAAATTTTCAACAACACATTTACTGGCATGTGGAT
>Dvi
TCCAATGTCACACAACATGAACAGACTTTCCGTTGGAATGCCTACAGTGGTATTCTGGG-
-GTGAGCTCACTGAATG------------CTACTTTTCTTTTTCAAACCATCTCCACCAC
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CATCAAAACTCGGTAGATTCTC------------------------------------GT
TCAGGGTAAAGAGGGGCCCCTTCGGCTAGCCTACATGTTAACCTTTGGCAGGGAGGAGTT
GCTCCCCAC-----CC-CTAT----------------CCTCTGCCCCAA-----------
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-----------------------------------------TCTCAAAGATGG---AAAA
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AGGATGGAGCTGAC---------------CTTGAGAAGGTTGTCATGAGCCTG-CTCAAG
T-GAGATAATGTATGTATATAAT-GCATTTTGCAAACTTGATA----CT---AAGCATAT
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--AACTAGGGTA------------------------------------------------
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------------------------------------AATGCCTACAGTGGCATTCTGGG-
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GC-CTCCAC-----CT-TTCCT---------------TCCCTCCCCCAAA----------
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-TTTCCATTGTTATTGAGAGA---AACCAATGG-GA--GCT-AAAAAGGATTTTAAAGAC
--AATTAGGCTA------------------------------------------------
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----------------ATC-CTC---TCTTAAAAAGAGTCTT-CAAGGGAACTGAATTGC
CCGAA-TT---GTGTTCTACCATACTA-CTTT--------------AGATAGAGGGCTCT
TGGGGTAT--GATAAAAA-----TAATTTAAAT--ATCACCTCTT-CTTGG--AATTTTT
AGCTATTATATTTTGATCAACTCGTTCATTGGTAGCTCT--------------CAGACAG
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GC-CTCCAC-----CT-CTCCC---------------TCCCTCCCCCAAA----------
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T-AAGATAATGTATGTAAA-----GCATTTTGTATATTTT-------CTATTATGCATTA
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--AATTAGGCTA------------------------------------------------
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AGCAATTATATTTTGATCAATTTGTTCATTGGTAGCTTT-----------ACTTAGACAA
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----------------TAAGTAA--TAGGTAATATTTATTGTTTCTCAG--GATTT----
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CAGGTGCTGTCTTTCTCCCCTTTCCCCA---------TCTCCAAC-------------TT
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--AATTCTGCTA---TTTCTCT----TGGCGGC-TGGATCGCTCAGTGGATAGAACACTA
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ATA-----TTCCAGTATCTTTGCCAAGAAAACCCCTACACAGCAT--AGTACACAGGGTC
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AGCTACTATGTTTTGACTGAGTCATTCATT--CATCTTT----TGTAAGATATAACTCAT
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>Mfa
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TGTTTTGCC-----ATCCCCTCTCCCCA----------TTCCAACCCA------------
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--TTCCCAGCTA---ATTCTC-----TGGGCAG--------------------AATACTA
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TTTGATGACTC--AGTTTTTCATGGATTATGTGTAGCTTAATAATTA-----ATGC-AAG
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TG--TGATCTTGGG------------CAAATC----------------------------
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------------------ACTTAA--CTTTTGTTGCCTAATCCATTGCAAGAAGAAAATG
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AGCAATTA-----TGGCTGAGTTATTCATTGGTAGATTA----TGTCAGAC--AACTCAT
TTTGGTGACCCCTAGTTTT-CATGGATTA-----------------------GTCT-AAG
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TG--TGATCTTGGG------------CAAATT----------------------------
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GAGAAAGCTG-TG---AGT-CTT--------AGAAGAGAATT-----------GTTTTGC
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T-GAGATAATGTATGTAAA-----GCATTT--CAAACCCTGT-----ATTATGAA-----
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>Ppe
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-TGTCCAGAGTTATTGAGGGA---AACCAATGAAGA--GTT-AAAAAGGATTTTAAAGTC
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>Tvu
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CCTGCTGCC-----TCGTT------------------CCCCCAACCCA------------
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-TGTCCATTGTTATTGAGGGA---AACCAATGA-GA--G---AAAAAGGATTTTAAAGTC
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GCAACCTGTTCCAGTATCTTTGCCAAGAAAATTC--CACAAACAGTACAG--CTCAGAGT
CATT-----------AAGAGTT----GGCATGACTGAACAACTG---------TCGCTTA
GAGAAAGACAGTG---AGT-CTT--------AGAAGAGAATT-----------GATTTGT
CCAAGCCTGCAGTATTCTGTCATATTGTCTTTTT-GATATGAGCCTAGATAGAGA----T
TAAGATAG--GTTAAAA-G----GAATTTAAGC--ATCACCTTTT-CTGGGCAAATTTTT
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AGCAATTATTTTTTGGCTGAGTCGGTCATTGGTAGCTCA----TGTTAGACATAACTCAT
TTTGATAACTCTTGGTTTT-CATGGATTA-----------------------GTGT-AAG
TATT--GTATCTTGAGTA-GTAA--TGGGTTATATTTATTCTTTCCCAG--GATTTGGGA
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>Mro
CACAACGTCACACAGCATGAACAGACTTTCCGTTGGAATGCCTACAGTGGAATTCTGGG-
-GTGAGCTCACTGGCTA-----------TTAGTCTTCTTTTTTGAAAGAACCCCCATCAT
TCCCCAAACTAGGTAGATTCTT------------------------------------GT
TCAAGATAAATGGTAGGGTG-------ATCATACAAAC----TTCTGACAGTAAGAA-GC
TGCCTTCTT-----CCCCACACCTCCAA---------CCCTCAACCCA------------
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TGTCA--------------TTTAACC-TCTCTTTGCCTAATCT-ACTGGAGAAGGAAATG
GCAACCCATTCCACTATCTTTGCCAAGAAAACCC--TATGGAAGATATGGCCCACAGAGT
TGGACATCACTG----------------------AACAACAAGGCTAATCCCCTCACTTA
GAGAAAGACAGTA---AGT-CTT--------AGAAGAAAGAAAATC-------GATTTGT
CCAAGGCTGCAGTGTTCTGCCATACTGTGTTTTT-GGTATGAGCCTAGATATAGGGCCCT
TGAGATAT--GTTAAAAAG----GAATTTAAGC--ATCACCTTTTTTTGGGTAAATTTTT
AGCAATTATGTTTTTGCTGAGTTGTTCATTGGTAGTTCA----TGTTAGACGTAACTCAT
TTTTGTGACTC-----TTT-CATGGATTA-----------------------GTGT-AAG
TA---------------------------TTATATTTATTCTTTCCCAG--GATTTGGGA
TGAATGGGAAATTTTCAACAATACATTTACTGGCATGTGGAT
>Ptr
CACAATGTCACACAGCATGAACAGACTTTCCGTTGGAATGCCTACAGTGGAATTCTGGG-
-GTGAGCTCACTGGCTA-----------TTAGTCTTCTTTTTTGGAAGAACCCCTATCAT
TCCTCAAACTAGGTAGATTCTT------------------------------------GT
TCAAGTTAAATGGTAGGGTG-------ATCCTACAGACAAACTTCTGACAGCAAGAA-GC
TGCCTTCTT-----CTCCGCACCTCCAA---------CCTTCAACTCA------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------------TTTTGTACACAG---GAAA
CTAGA---AA--------------C-----------TTTTTT-----AATCTGTAAAACA
GGGATAATGAGAGCATACTG-----CTTACTTCACAGGGCTGTCATGAGGCTG-CTTAGA
T-GATGTAATGTGTGTAAAAA----CATGTAGCAAACCTTGT-----ATGATACA-----
-TGTCCAGTGTTACCGAGGGA---AACCAATGA-GA--GCT-AAAAGGGATTTTAAAGTC
--AATTCAGCTA---ATTCTC-----TGGGCAGCTAGATGGCTCAGTG----------GA
GGCCTGGAGTCAGGAAGACCTGAGTTAAAATC-----TGGTCTCAGGCATTTATTAGCTG
TGTTACCTTCAGCAAGTCATTTAACC-TCTCTTTCCCTAATCT-GCTGGAGAAGGAAATG
GCAACCCATTCCACTGTCTTTGCCAAGAAAACCC--TATGGACGATATGGCCCACAGAGT
TGGGCATCACTG----------------------AACAACANGGCTAATCCCCTCNCTT-
ANANAAGACAGNG---AGT-CTA---------AAAAAAATTGATTG--------------
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# MARKER 155

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>Mar1b_Mdo
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---------------------------------------TTGTTGTTGTTGTTCAGTCGT
TTTCAGTCATGTCTGACTCTTCGTGACCCCA--TTTGGGGTT------------------
----------------TTCTTGGCAAAGATACTGG---------------------AGTG
GTTTGCCATTTCCTTCTCCAGCTCATTTTA------------CAGATGAGGAAA-CTGAG
GCAAACAG-GGTTAAGTGACTTGCCCA----GGGTCACACAGCTAGTAA-----------
---GTGTCTGAGGCCAGATTTGAACTCAG--------GTCTTCCTGACTCCAG--GCCCG
GC-----GCTCTATCCACTGTGCC-ACCTAGCTGCCCT----------------------
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>Mdo
CTCAGAGAATGCAGCCCTGGTACGGGAACAGAATGGCCATCAGTTACTAGTGGCCCTGGT
TGGGGATAGCCTGCTTGAG--GTGAGTATGAAGAAA------------------------
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------------------------------------------------------------
---------------------------------------------------------AGA
GGGTGTCATTTT-AGAGGGGAGGGATGTATTAATGTTAGAGTATCTGCTA--------CC
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TCCA--------------------------------------------------------
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-----------------------------------------TAGAATGTCATGCTCTTTA
GAGTTCATTTTCCCCCTTTAACTTATTTTGCTCTTTTTCTCTTCTTCTTC--ACATCC--
-----------CCCA-CCCAAA------TTTTTATGTAG--CCTTTTTGGCCAATGGGAA
CTGGAATAGCCCGAGGTTTTCTGGCTGCTATGGACTCCGCCTGGATGGT
>Dvi
CTCAGAGAATGCAGCCATGGTACGGGAACAGAATGGCCATCGGTTACTGGTGGCCCTGGT
TGGGGATAGCCTGCTTGAG--GTGAGTATGAAGGGA------------------------
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---------------------------------------------------------AAA
GGGTATAATTTT-AGAGGAGGGGAGAAATGTAATAAT--GTTATCTGT-----------C
AAATGAGCCATAGCTGGACATTTT-TTAAATATGCCATT---------------------
------------------------------------------------------------
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-----------------------------------------GATAATGTCATGTTCTTTA
--GTTCATTTTCCCCCTTTAACTTAT------CTTTTTCTCTTCTTC-----ACTTCCT-
-----------CCCACCCCAAAAAA---CTATTATGTAG--CCTTTTTGGCCAATGGGAA
CTGGAATAGCCCGAGGCTTTCTAGCTGCTATGGATTCAGCCTGGATGGT
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>Mnu
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TGGGGATAGCCTGCTTGAG--GTGAGTATGAAGGGA------------------------
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------------------------------------------------------------
---------------------------------------------------------AAA
GGGTATAATTTT-AGAGGAGGGGAGAAATGTAATAT--GTTATCTGT------------C
AAATGAGCCATAGCTGGACATTTT-TTAAATATGCCATT---------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------------GATAATGTCATGTTCTTTA
--GTTCATTTT---------------------------CTCTTCTTCTTC--ACTTCCC-
-----------CCCACCCCAAAAAA---CTTTTATGTAG--CCTTTTTGGCCAATGGGAA
CTGGAATAGCCCGAGGCTTTCTAGCTGCTATGGATTCAGCCTGGATGGT
>Rra
ATCAGAGAATGCAGCCCTGGTTCGAGAGCAGAATGGACACCAGCTATTGGTGGCCTTGGT
TGGAGATAGCCTGCTTGAG--GTAAGTGTGAAGGAA------------------------
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------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------------------AAG
GAGTGATATTTTTATAGGGGAGGAATTTCATAC------TATATCTGATATTAT-----G
AAATGAGGCAT-AGGAGAGTTTTTATATTTCATTGTTT----------------------
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--------CTTCCCTTTAAAACTTATTTTACTTTTTTTCTCTCTT-----GCACTCCCTC
CACACCCATACT---CTCCAAAAA----CTTTTATGTAG--CCTTTTTGGCCAATGGGAA
CTGGAATAGCCCGAGGATTTCTGGCTGCCATGGACTCAGCCTGGATGGT
>Cfu
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------------------------------------------------------------
------------------------------------------------------------
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GTT--AGATATGAGGAGAGTTTTTATATTTCATTGTTT----------------------
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---------------------ATTATAACTAAACATCT-AGCAT----------------
--------CTTTCCTTT--AACTTATTTTACTTTTTTTCTCTCTT---GTGC--TCCCTC
CACACCCACACT---CTCCAAAAA----CTTTTATGTAG--CCTTTTTGGCCAATGGGAA
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>Dgl
ATCAGAGAATGCTGCCCTGGTTCGGGAACAGAACGGTCACCAGTTATTGGTGGCTCTGGT
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TGGGGATAGCCTGCTTGAG--GTGAGTATGAAGGAA-----GTTCTTGTT----------
--CAGTCGTGTCCAATACTTAA-----GTGG-----------------------------
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--------TTTCCTTCTCCAGCTCATTTTA------------CAGATGAGAAAA-CTGAG
GCAAACAGAGGTTAAGTGACTTGCCCA----GGGTCACACAGCTAATAA-----------
--GTATCTG-AGGCTGCATTTGAACTCA-----------------TTTTCCTGACTCTAG
GCCTGGTGCTCTATCCACTACACC-ACCTAGCTGCCC-----AATATGAAGGAA---AGG
GAATGATATCTT-ATAGGGGAGTTATGTATCTGATACTACAGAATGAGCCATA-------
GTTAGAGATATGAGTGGAGTTTTTATATATCATTGTTATTT-------------------
------------------------------------------------------------
------------------------------------------------------------
---------------------ACTACAGCTAAACTTCT-AGCAGAATGCCGTGGTTTTTT
--GTTCTTTTTCTCCCTTTAACTGATTTTAC----TTTCTCTCTT---CTGCACTTCCCC
--------TACTG-ACCCCAAAAAA--TCTTCTATGTAG--CCTTTTTGGNCGATGGGAA
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>Nty
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TTGTTTTTTGTTTTTTTTTTTGGCAAAGATTTTGGCAAAGATTTGGCAAAAAATGGCAAA
GTTTGCCATTTCCTTTTCTAGCTCATTTTA------------CAGTTGAAGAAA-CTGAG
GCAAACAG-GGTTAAGTGACTTGCCCA----GGGTCACACAGCTAT--------------
--GTTTCTG-AGTCTGGATTTAAACTCATGAAGATGAATCTCTCTTATTCTTG--GCCTG
GC-----ACTCTATCCACTGTGCC-ATCTAGCTGCCC----GAGTCTGAAGGAA---GAG
GAATGATATTTT-ATAGGATGATAATGTATCTGATACTGTGAG-------ATGGGCCATA
GTTAGAGATATGAGTGGAGTTTTTATATGTCA--TATATTT-------------------
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------------------------------------------------------------
---------------------ACTATAGCTAAACTTCC-AGCAGAATGTAATGCTTTTTT
------GTTTTCCCCTTTTAACTTATTTTAC----TTTCTCTCTTTTTCTCTATTTCCCC
TCACCCCATACTC-ACCCAAAAAA---CCTTCTATACAG--CCTTTTTGGCCAATGGGAA
CTGGAATAGCCCGAGGCTTTCTGGCTGCTATGGACTCAGCTTGGATGGT
>Pta
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----------------TTTCTTTTTTTTTTATG---------------------------
----GCTATTTCCTTCTTCAGCTCATTTTA------------CAGATGA-GAAA-CTGAG
GCAAATAG-GCTTAAGTGATTTGCTCA----GAATTAAAT--------------------
----------------GATTTTACTTGAAG---ATGAATCTTTTTTATTCTAA--GCTTG
GCACTCTGTTCACTTAACTGCATC------------------ATTATGAAGGAA---GGG
GAATAACATTTT-ATAGGGCATACTATAGAATGA-GCCATA-------------------
------------------GTTATTCATAGATACGTATAGCTATATA-GTTAGATC-ATAG
TTAGAGATATGAAGTTTTTATTTATCA---------------------------------
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----------------------TAATAGCTAAATTTGCCAACAAAATGTCATGGGTTTTT
-GGTTCATTTTCCCTTTTTAACTTATTTTCC----TTTCTCTCTTTTTCTGTATTTT-GC
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>Dgo
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----------------TT------------------------------------------
-------------------------TTTTT------------GCTATGA-GAAA-CTGAG
CCAAATAG-ACTTAAGTGAATTGCTCA----GAGTCAAATAGCTATTAA-----------
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GG----TATACTATAGAATGAGCC-ATA--------------GTTATTCATAGA------
-------TATGT-ATAGCTATATAGTTAGA-----TCCATAGTTAGAGATAAGAA-----
------------------GTTTTTATTTATCATAATA-----------------------
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---------------------------GCTAAATTTCTT---------------------
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>Scr
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----------------TTTCTTTTTA----------------------------------
TTTGGCTATTTCCTTCTTCAGCTCATTTTA------------CAGATGA-GAAA-CTAAG
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GA-------ACTCTTAACTGTCTC------------------ACTATGAAGGAA---GGA
GAATTGCATTTT-ATAGCATATACTATAGAATGA--------------------------
----------TATATATAGTTTTTATTTATCATGTATAGCTATATA-GTTAGATCCATAG
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GCTAAAATTTATTTTATTATAATATAATTATAATTATTATTTTAAAATTTATTTTATTGT
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--GTTCATTTTCCTCTTTTAACTTATTTTAC----TTTCTCTCTTTTTCTGTACTTT-GC
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>Mfa
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CGGGGATAGCCTACTTGAG--GTAAGTCTGAAGGAA-----ATTGATGTT----------
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----------------TTATGGCAAAGATAT-GAG--------------------AGCA-
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----------------TGACTTGCTCA----GAGTCAAATAGCTATTAA-----------
--GTGTCTG-AGACTGGATTTGAACTGATGAAAATGAATCTTTT-GATTCTAA--GCCTG
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GAATGACATTTT-ATAGGGTATACTATAGCATGA-GCCATAAGTAGAGATA---------
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TTAGAGATATGAAATTTTTATTTATCACA-------------------------------
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>Bil
ATCAGAAAATGCAGCCCTGGTTCGGGAACAGAATGGTCATCAGTTATTGGTGGCTTTGGT
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AACAACAAGTGTCCATCTCT----------------------------------------
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TTAAACAG-TGTTAAGTGATTTATTTACCTACAGTCATAGAACTAGTGTAA---------
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-------------------------CCCTACTGCCT-----GAGTGTGAAGTAA---GGG
GAATGATATTTT-ATAGGAGAGTAATTTATGTGATACTATAGAATGACATA---------
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--ATTCATTTTCCTCTTTTAACTTATTTTATC-TTTCTCTCTCTCTTTCTGCACTTC-CC
CCATCCGTTACT-TACTCCCCTAAAAA-CTTTTTTGCAG--CCTTTTTGGCCAATGGGAA
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>Pgu
ATCAGAAAATGCAGCCCTTGTTCGGGAACAGCATGGTCATCAGTTANTGGTGGCTTTGGT
TGGGGATAGCTTGCTTGAG--GTGAGTATGAAGGAA-----TTTGTTGTT----------
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----------------------------------G---------------------GGAG
GGTTCCCATTTCCTTTTTCAGCTCATTTTA------------CAGATGA-GAAA-TTGAG
TTAAACAG-GGTTAAGTGT-----------------------------------------
--GTTTCTT-AGGCCAGATTTG-ACCCATGAAGATGAGACCTATCCACTATAC-------
-------------------------CCCCAACTGCCT----GAGTGTGAAGGA-------
---GAATATTTT-ATAGGAGAGTAATTTATCTGATACTATAGAATAAGATA---------
----------TGAGTAA-GTTTTTATATATCATGTATC----------------------
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--------------------------------ACTG---AACAGAATGTCATGCTTTTTC
--ATTCATTTTTCTCCTTTAATTTATTTTATC---TTTCTC--TTTTTCTGCACTTC-CC
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>Iso
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--------------------GGCAAAGATATTGCG-----------------------AG
GTTTCCCATTTCCTTTTTCAGCTCATTTTA------------CAGATGAAGAAA-TTGAG
TTAAACAG-GGTTAAGTGT-----------------------------------------
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-------------------------CCCCAACTGCCT----GAGTGTGAAGGA-------
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--ATTCATTTTTCTCCTTTAATTTATTTTATC---TTTCTC-TTTTTTCTGCACTTC-CC
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>Tro
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---------------ACTACTCGTGACCCCGTTTTTGGGTTCT-----------------
----------------TCTTGGCAGAGGTATCAG----------------------GGTG
GTTTGCCATTTCCTTCTCCAGCTCATTTTA------------CAGATGAAGAAA-TTGAG
ACAAACAG-GGTTAAGTAATTTGCCCA----GCGTCACACAGCTATAAGTAA--------
--GTGTCTG-AGGCCAGATTTGAACTCAGGAAGCTGAACCTTCCTGATTCTAG-GCCAGG
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CATTTTATCCACTGGGCC-------ACCTAGCTGCCC----AAGTATGAAGAAA---GGG
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----AGATAGGAGTGAAATTTTTAATATATCA--TATTCAC-------------------
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--ATTCCTTTTACCTTTTTAACTTATTTTACT-TTTTTCTCTCATTTTCTGCACTTC-CC
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>Ppe
ATCGGAGAATGCAGCCCTGGTTCGGGAACAGAATGGTCACCAGTTATTGGTGGCCCTGGT
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---CAGTCATACCCAATTCTTCGTGACCCCA--TTTG-----------------------
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CCAAACAG-GATTAAGTAACTTGCCCA----GAGTCACACAGCAATAA------------
--GTGTCTG-AGGCCAGATTTGAACTCAGGAAGATGAATCTTCCTGATTCTAG-GTTCAG
TATTCTATCCACTGCACC-------ACCTAGNTGACC----AAGTATGAAGGAA---AGG
GAATGATATTTT-ATAGGGGAGTAATGTATCTGATACTACAGAATGAACCATAGTTAA--
----AGTTATGAGTGGA-GTTTTATTATATCG--TATTTAC-------------------
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------------------------------------------------------------
-----------------------TATAGCTAAA-CTTCCAGCAGAACATCATGCTTTTTT
--GTTTATTTTACCCTCTTAACTTATTTTACTTTTTTTCTCTCTTTTTCTGCACTTC-CC
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>Mro
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GGGGGATAGCCTGCTTGAG--GTGAGTATAAAGGAA-----ATTGTTCAGT---------
---CACG----TCCAACTCTTCGTGACCCCA--TTTGGGGTT------------------
----------------TTCT----TGGTAAAGAGG---------------------TATG
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GCAAACAG-GGTTGAGTGACTTGCCCA---------------------------------
--GTGTTTG-AGGCTAGATTTGAACTCATGAAGATGAATCTTCCTGAATCTAG-GCTCAG
CATTCTATCTACTGTGCC-------ACTTAGCTGCCC----GAGTATGAAGCAA---GGA
GATTGATATTTT-ATAGGGGAGTATTGTATCAG-----------------ATAGTTAG--
------ATATGAGTGGA-GTTTTGATATATCATATATTTAC-------------------
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>Vur
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----------------TTCC----TGGCGAAGAGG---------------------AGTG
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GCAAACAG-GGTTAAGCGACATGCCCA----GGCTCACACAACT---AGTAA--------
--GTGTCTG-AAGCCGGATTTGAACTCATGAAGATGAATCTTCCTGATTCCAG-GCCCAG
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--ATTCATGTTTCCCTTTTAACTTATTTTACTTT----CTTTCTCTTTCTGCACTTC-CC
CCACCCCCTCTTC-ACCCTCAAAAAA--CTTTTACGCAG--CCCTTTTGGCCGATGGGAA
CTGGAATAGCCCGCGGCTTTCTGGCTGCTATGGACTCAGCCTGGATGGT
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**MARKER 102**

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>WSINE1
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G-GTCCTCCTGACTCCAGGGCTGGTGCTCTATCCACTGCACCACCTAGCTGCCCCTC---
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>Mdo
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CCATTAAG--GTAGACCATGGGCCACAGGGTTGT------------CCTGGACCTTGGGA
TGGAAA----GCAGAAATGGCAGCT-----ATTGGCGGGGAGAGGTAGACGACAGACGAC
AGGAGGGACGTCCTAAAAGTAGCCAGTGTAAGCACTGGA-AAAGGCAGCCTACTTCAGCA
GAGAGACTGAGTCCTGGTTTCTCAGTGGAAGGATGAACCCTGAAGCTCACAGTGGCAGGG
AGGAA-----CCTGATGACTTCTGAAGAGAGCTCGGCTTGGGGTCAGGGTGGGCAGAGAC
AGGGGA-GTACTCCCTGGGGCCATTATGTGGGCAATGAGGAGAAGA---GATTGTAGGCC
T---CCTAGACATGATTT------------------------------------------
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--------------------------------------------------------TAAA
GGTTCAACCAGG-----------------------GTGAGAGTGGAA--TCATTAACCAG
TTCCTGAGTCATATTCTCCCCATTACTTAGGATATGGGAGATGCTCATACCCTGTTCCCA
CC-CCCGTCCCCATTTCTCTTTTCCCCAATCCCCTGTCTCCCACCC-CCATTTCCCCACT
GATCTTCCAATTAC-TTCC-----------CTGTTCCTTATGGCATTCCTGTC-------
-----------ACTCTCCATTTCCCTCCCATTCCTC----CCCTCCTCTATCTGCCCC--
--------ACCTAG--GAGACAGGAAGATATCCAGCCTACAAGGAGATGGTGTCCGAATA
CTGCT
>Dvi
ACCACATCAGTCACAGCCAGGCTGTGGAAGTGCTGAAGGGGCAGACGCACATCATGCTGA
CCATTAAG--GTAAGCCAGGGACCACAGGGTCGTCG----GGAGCCCCAAGACCCAGGGA
TGGAAA----GCAGAAATGGAAGG------------------------AAGACAGACTAC
AGGAAAAGCTTCCTAAAAG-------------CACTATA-AAAGGCAGCCCACTTCATCA
GAGAGCCTGAGCCCTGGTCTCTCAGGGAAAGAATGAACCCTGAAGCTCATAGTGGCAGGG
AGGAA-----CAGGATGACTTCTGGAGGGAGCTAGGCTTGGGATCAAAGTGGGCAGAGAC
-CAGGA-TCACTCCCTGGGGCCATCATGTGGGCAATGAGAACAAGAAGAGACTGTAGGCC
T---CCTGGGCGTGATTT------------------------------------------
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--------------------------------------------------------CAAA
GGTTCAACGAGG-----------------------GAGAGAGTGGAA--TCATTAACCAG
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TTCTTGAGTCAAATTCTCCCCATTACTTAGGCTATGGGAGATACTCATACCCTG------
-------------TTTCTCTTTTCCCCAATCCCCTGTCTCCCACCC-CCACTTCCACACT
GACCTTCCAATCACCTTCCCCACTACATCCCTGTTCCTTATTGCATTCCTGTC-------
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--------ACCTAG--GAGACGGGAAGGTATCCAGCCTACAAGGAGATGGTGTCTGAATA
CTGCT
>Mnu
ACCACATCAGTCACAGCCAGGCTGTGGAAGTGCTGAAGGGGCAGACGCACATCATGCTGA
CCATTAAG--GTAAGCCAGGGACCACAGGGTCGTCGT---GGAGCCCCAGGACCCAGGGA
TGGAAA----GCAGAAATGGAAGG------------------------AAGACAGACTAC
AGGGAAAGCTTCCTAAAAGT------AGCAAGCACTATA-AAAGGCAGCCCACTTCATCA
GAGAGCCTGAGCCCTGGTCTCTCAGGGAAAGGATGAACCCTGAAGCTCATAGTGGCAGGG
AGGAA-----CAGGATGACTTCTGGAGGGAGCTAGGCTTGGGATCAAGGTGGGCAGAGAC
-CAGGA-TCACTCCCTGGGGCCATCATGTGGGCAATGAGAACAAGAAGAGACTGTAGGCC
T---CCTGGGCGTGATTT------------------------------------------
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------------------------------------------------------------
--------------------------------------------------------CAAA
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TTCTTGAGTCAAATTCTCCCCATTACTTAGGCTATGGGAGATACTCATACCCTG------
-------------TTTCTCTTTTCCCCAATTCCCTGTCTCCCACCC-CCACTTCCACACT
T---CCACACTGACCTTCCAATCACCTTCCCC-------ACTACATCCCTGTTCCTTATT
GCATTCCTGTCCCTCTCCACTTCCCTCCTGTTCCTTCTCTCTCTCCTCTCTGTGCCCC--
--------ACCTAG--GAGACGGGAAGGTATCCAGCCTACAAGGAGATGGTGTCTGAATA
CTGCT
>Cfu
ACCACATCAGTCATAGCCAGGCTGTGGAGGTGCTGAAGGGCCAGACCCACATCATGCTGA
CCATCAAG--GTAGATCCCTGAACACAGGCTTATTATCATAGACCCAGAGGACCCTGGGA
TGGAAG----GCAGAAATGGTAGCTA---CTATGTTGGGAGGGATAGAAGTCAGACTTGC
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## MARKER 168

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>Vur
TGACAAGCGCAGTCTTCG--GTGAGCTCAGCGTGGCTGCCCTGCCCTTAT----------
---TCTGATGAA---TAACTGGGGAGGGGGATGGAGACC-AGGCAGGTAGGGC-CATCCT
AATAATTGGGG-----TTGTGG------CTGTGATAGGGTCAGTTAAC------------
----ATAGCTGGCGTTCAGATAGTGCTTTAAGGTTGACAAAGTG------CGTCCCTTAT
ATCATTCGATCCTCACGACC---ACCCTGTCAGAGTGTGTGCAGGGGATGT---------
------GTAGGGC----TGTGTGTTAGTGTGTATAAGAAAGTGGAGCAGCAGTATGTGTG
TGCAT----ATGTGCGTA------------------------------TG-GCCCCTGCA
TGGCCCTGGGGGCCCTGTCTCCTTCCTCCCCAC--TAG--GGTCCCCAAACGTCCTGTCA
TCAACACACCG
>Human
TGACAAGCGCAGCTTGAG--GTCAGC----------------------------------
--------------------AGCTAGGGAC----------AGGTGTGGG-----------
-----TAGGGG-----TATGGG-----------TCGGGCGGTGAGTGC------------
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------------------------------------------------------------
------TGA-GGC-------------------ATG-GAGGGGGTCGGGGGCGT-------
-----------CTCCCCA---------------------------------GTCATGTGA
CTGCCGTGGTGACTGTGCACCTGACTGCCCCACATCAG--AGTCCCCAAACGCCCGATCA
TCAACACACCC
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**MARKER 169**

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>MIR3_MarsA
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------------------------GGGAAGCAGCGTGGTACAGTGGAAAGAGCGCTGGAT
TTGGAGTCAGAGGACCTGGGTTCAAATCC---------------------------CGG-
-------CTC-TGCCACTTACTACCTG-TG--TGACCTTGGGC-AAGTCAC-TTAACCTC
TCTGGGCCTCAG-TTTCCTCATCTGTAAAATGAGGGGGTTGGACTAGATGACCTCTAAGG
TCCCTTCCAGCTCTAAATCTA-TGATCCTAT---GATCCTATGA----------------
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>L1-4_ME_3end
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----TTTTTATTTAAAATTTTGAGTTCCAAATTTTTCTCCCTCCCTCCCCTCCCCCCTCC
CTAAGAT---------GGTAAGCAATTTGATATAGGTTATACATGTGCAATCATGTAAAA
CATATTTCCATATTAGTCATGTTGTAAAAGAAGACACAGAATAAAAAAAAAA--------
--------------------------------------------GTCTGCTTCATCTGCA
TTCMGATTCCACAGTTTTTCTCTGGATGTGGATAGCATTTTGCATCATGAGTCCTTTGG-
----------AAATGTTTTGGATCMTTGCATTGCTGAGAAGAGCTAAGTCTATCAAAAAY
AGTCMTCACACACTGTKGCTGTTACTGTGTACAATGTTCTCCTGGTTCTGCTCACTTCAC
TCAGCATCAGTTCATGTAAGTCTTTCCAGGTTTTTCTGAAGTCTACCTGTTCATCATTTC
TTATAGCACAATAATATTCCATTACATTCATATACCACAATTTGTTCAGCCATTCCCCAA
TTGATGGACATCCCCTCAATTTCCAGTTCTTTGCCACCACAAAAAGAGCTGCTATAAATA
TTTTTGTACATGT-----------------------------------------------
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>Mdo
TTACCAAACAGAAGTTTGATAACCTCTACTGTTGCCGAGAGTCAATCTTGGATGG--GTA
AGTAGAGACTGCAAGTATCAGACCC----------------GTGAGAAA-GGGGAGAGAG
GGGTAGCTTAAAGCTTTCAGC---------------------------------------
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----------------C-TTTGATCCTATTGGCACCAGCAGCCTTGCCTCACCTGGACTA
A-TAACTATTGCTTTCCTTTACTTTAAAT-GGGTGCCTGTGAAACCCCTTTCAAGAGACC
CTAGTTCAGTATCCTTTCCCTG----------------------AGGCACCTACCTCTGT
GAAA----------------TCCTCACA---CTAGGATTGCATTTGAATGGCACCTTCAT
CT-TT--TCCCACAG--CCTCAAGAGGACCACAGATG
>Dvi
TTACCAAACAGAAGTTTGATAACCTGTACTGCTGCCGAGAGTCAATCTTGGATGG--GTA
AGTAGAGACTGCAAGTGTCAGACCC----------------GTGAGAAAAAGGGGAGGAG
GGGTAGCTTAAAGGTTTCAGC---------------------------------------
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----------------TTTGTGATCCTATTGGCACCAGCAGCCTTGCCTCACCTGGTCTA
A--CTCTATTGCTTTCCTTTACTTTGGAC-GGGTGCCTATGAAACCCCTTTCAAGAGACC
CTAGCTTGGTGTCCTTTCCCTG----------------------AGACACCTACCTCTGT
GAAA----------------TCCGCACA---CCAGGATTGCATTTGAATGGCACCTTCAT
CT-TT--TCCCACAG--CCTCAAGAGGACCACAGATG
>Mnu
TTACCAAACAGAAGTTTGATAACCTGTACTGCTGCCGAGAGTCAATCTTGGATGG--GTA
AGTAGAGACTGCAAGTGTCAGACCC----------------GTGAGAAAAAGGGGAGGAG
GGGTAGCTTAAAGGTTTCAGC---------------------------------------
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----------------TTTGTGATCCTATTGGCACCAGCAGCCTTGCCTCACCTGGTGTA
A--CTCTATTGCTTTCCTTTACTTTGGAC-GGGTGCCTATGAAACCCCTTTCAAGAGACT
CTAGCTTGGTGTCCTTTCCCTG----------------------AGACACCTATCTCTGT
GAAA----------------TCCGCACA---CCAGGATTGCATTTGAATGGCACCTTCAT
CT-TT--TCCCACAG--CCTCAAGAGGACCACAGATG
>Rra
TCACCAAGCAGAAGTTTGATAATCTCTACTGCTGCCGGGAGTCCATTTTGGATGG--GTG
AGTAGAGACTGCAAGTCTCAGACCT----------------GTGAGGGA--GGGGAAGAG
AGAAAGTTTTTAGCCACGGAA-----------------------GCAAAGGAGGTGGATT
TGGGGGTCAGAGAATCAAG-GCC-------------------------------------
-TAAAG-CTA----------CCACCTACTCTCTG--------------------------
------CCTCGG-TTTCCTCACCTATAAAATGAATCATTGTA-CTAGATAGTGTCTGGT-
--CTCTTCTCCC--------------CCCTC-----------------------------
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------------------------------------------------------------
----------------TCAGT----CT-TAGGCAACAATGACCTCTCCTCTCCCAGTTTC
ACTCTTCATTGCCTTCCTTTCCATTGGGC-TGGTGCCTGTGAATTCC-------------
-----------------AGTTCAGGATCCT--GAGCCTGTG---ACCT----CCCTGTAT
GAAA---TCTACATA-----CCAGCATG---AACTCACAGGTTTTTAATGCAACCTTACT
CT-TT--TCCCTCAG--CCTCAAGAGGACCACAGATG
>Cfu
TCACCAAGCAGAAGTTTGATAATCTCTACTGCTGTCGGGAGTCCATTTTGGATGG--GTG
AGTAGTGACTGCAAGTCTCAGACCT----------------GTGAGGGA--GGGGAGGAG
AGAAAGTTTTTAGCCACCGCA-----------------------GCAAAGGAGGTGGG-T
TTGGGGTCAGAGAATCAAG-GCC-------------------------------------
-TAAAG-CTA----------CCACCTACTCTCTG--------------------------
------CCTCGG-TTTCCTCACTTATAAAATGAATCGTTGTA-CTAGATAGTGTTTGGTC
TCCTCTTCTCCC--------------CTCTC-----------------------------
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----------------TCAGT----CT-TAGGCAACAAGGACTTCTCCTCTCCCAGTCTC
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ACTCTTCATTGCCTTCCTTTCCATTGGGC-TTGTGCCTGTGAATTCC-------------
-----------------AGTTCAGGATCCTCTGAACCTGTG---AGCT----CCCTGTAT
GAAA---TATACATA-----CCAGCACG---AATTCACAGGTTTTTAATGCAACCTTACT
CT-TT--TCCCTCAG--CCTCAAGAGGACCACAGATG
>Dgl
TTACCAAACAGAAGTTTGATAATCTGTACTGCTGCCGAGAGTCCATTTTGGATGG--GTG
AGTAGAGGCTGGAAGTATCAAACTT----------------GTGAGGAA--GGAGAGGAG
AGAGGGCTCGAAGCTGTCATG-----------------------GGAAAGGCTGTGGGCT
TGGG-GT--AGGGATCAGG-CCCAGGTC---------------------------TAGGT
ATGAAGCCTCATGC----CGCCACCTGCTCTGTGAC--------------TTGT-ACCTC
ACTTGACCTCAG-TTTC-TCATCTGTAAAATGGAAGGGTTGGACTAGATAGTGGCCAGTC
TCTTCT--AGCTCACATTCTTGTGATCCTCT-----------------------------
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----------------TCACTGGTGCAGGAAGCAACAGCAGCCCTGTGTCTCCCAGTCTG
ACTCTTTTTTGCCTTCCTTTACTTTGGGC-AGGTGTCTGTA--------------AGATA
GCAGTTTGGTGTCTTCTACCTGAGGCACCCCGAGCCTATAAAAAGGGTCTGTCCCCACCA
TCCCCCCTGCACACAAGGATTGTACTTG---AATGAGCAGTGTTTGAAAGGAACCTTCAT
CT-TT--TTCCACAG--CCTCAAGAGGACCACAGATG
>Nty
TTACCAAACAGAAGTTTGATAACCTGTACTGCTGCCGAGAGTCCATTTTGGATGG--GTA
AGTAGAGACTGTAAGGAA--------------------------GGGGA--GGAGAGAAG
AGATTTCTGGAAGCTGTCATG-----------------------GGAAAGGTCATGGA-T
TTGG-GTCAAAGCATGATG-CCCAGGTC-------------------------TCTAGGT
ATGAGGCCTCATGC----TGTCCTCGGCT-------------------CATTTT-ACCTC
ACTTGACCTGAG-CTTCCTTATCTGTAAAATGAAAGGGCTGGACTAGCTGGTGTTTAGTC
TCTTTTCCAAGTCACAGTCTTGTGATCCCAT-----------------------------
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----------------TACTTGGTACAAGTGGAAACGGCATACTTTCTTCACCCTGCCTC
ACTCTGTTT--CCTTCCTTTTCTTTGGGC-AGGCATCCATG--ACTTATTTCCAGAGACA
CCAGTTTGGGGTCCTCAATCTGAGGCCCTCCAGGCCTCTAA---GGCT-CCCCACTATGT
GAAA---AACACACAGGGATTGCATTTG---AATGGACAGTATTTGAATGGAACCCTCAT
CT-CTTTTTCCACAG--CCTCAAGAGGACCACAGATG
>Pta
TTACCAAACAGAAGTTTGATAACCTGTACTGCTGCCGAGAGTCCATTTTGGATGG--GTG
AGTAGACACTGCTGGTGTCAAACCT----------------GTGAGAAA--GGGGAGGAG
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AGAGAGCTTGAAGTTGTTGTA-----------------------GAAAAAGCCATGAG-T
TTGAGGCCAGAGGATCAGG-CCCAGGTC---------------------------TAGAT
ATGAAGCCTTATGC----TGTCACCTGCTTTGGGACCCACAAGAAAGTCATTTT-ACCTA
ACTTGAGCTCAG-TTTCCTCATCTATAAACTGAAAAGATTGGGCTAGATAGTGTCAAGTC
CCTTTTTCAGCTTACAGTCTTGTGATACTAT-----------------------------
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----------------TACTTGGTACCCTAACTGACTAAAGA------------------
-------ATAGCCACTCTTTACTTTGGGC-ATGTGTATGCC-------------------
-------------CTTTACCTGAGGCACCCTA------------GGCC-TTCTCTCATGT
GAAAA-CTGTACACTGGGATTGTATTTG---AATTAGCAGTATTTGGATGGAACCTTCAT
CT-TTT-TTTCACAG--CCTCAAGAGGACCACAGATG
>Dgo
TTACCAAACAGAAGTTTGATAACCTGTACTGCTGTCGAGAGTCCATTTTAGATGG--GTG
AGTAGACACTGCTAGTGTCAAACCT----------------ATGAGGAA--GGGGAGGAG
AGAGAGCTTGAAGTTGTTGTA-----------------------GAAAAAGCCATGAG-T
TTAAGGCCAGAGGATCAGG-CCCAGGTCTAGATATGAAGCCTTATGGCCCAGGTCTAGAT
ATGAAGCCTTATGC----TGCCACCTGCTTTGGGACCCACAAGAAAGTCATTTT-ACCTA
ACTTGACCTCAG-TTTCCTCATCTGTAAACTGAAAAGATTGGGCTAGATAGTGTCAAGTC
CCTTTTTCAGCTTACAGTCTTGTGATACTAT-----------------------------
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----------------TACTTGGTACCCTAACTGACTAAAGA------------------
-------ATAGCCACTCTTTACTTTGGGC-ATTTGTGTGTC-------------------
-------------CTCTACCTGAGGCACCCTG------------GGCC-TTCCCTCATGT
GAAAG-CTGTACACTGGGATTGCATTTG---AATTAGCAGTATTTGGATGGAACCTTCAT
CT-TTT-TTTCACAG--CCTCAAGAGGACCACAGATG
>Scr
TTACCAAACAGAAGTTTGATAACCTATACTGCTGCCGAGAGTCCATTTTGGATGG--GTG
AGTAGACACTACTGGTATCAAACCT----------------ATGAGGAA--GGGGAGGAG
AGAGAGCTTGAAGTTGTTGTA-----------------------GAAAAAGCCATGAG-T
TTGAGGCCAGAGGATCAGG-CCCAGGTC----------------------------TGAT
A--AAGCCTTATGC----TGCCACCTGCTTTGGGACCCACAAAAAAGTCATTTT-ACCTA
ACTTGACCTCAG-TTTCCACATCTGTAAACTGAAAAGATTGGGCTAGATAGTGTCAAGTC
CCTTTTTCAGCTCACAATCTTGTAATACTGT-----------------------------
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----------------TACTTGGTACCCTAACTGACTAAAGA------------------
-------ATAGCCACTCTTTACTTTGGGC-ATGTGCGTGTG-------------------
-----------TCCTCTAATTGAGGCACCCTG------------GGCC-TTCCCTCATGT
GAAAG-CTGTACACTGGGATTGCATTTG---AACTAGCAGTATTTGGATGGAACCTTCAT
CT-TTT-TTTCACAG--CCTCAAGAGGACCACAGATG
>Bil
TTACCAAACAGAAGTTTGATAATCTGTATTGCTGCCGAGAGTCCATTCTAGATGG--GTG
AGTGGAGACTGCAAGTGTCAAATCCATGAGGAGATGAAAATGTGAGGAA--TGGGAGGAA
AGATAACTTGAAGCTGTCATG-----------------------GGAAAGGCCATGGA-T
TTGAGATAAGGGGATCAGG-CCCAGGA---------------------------------
------------------------CTGCTCTGTGACCCACAAGAAAGTCATTTT-ACTCC
ATTTGGCCTCAG-TTTCCTCCTCTTTAAAATGAAAGGGTTGGACTAGATGGTATCTAGCC
TCTTTTCCAGCTCAATCTTA------TTCTC----------------TTTTTTTAATTTA
TTTTTATTAACAATATTATTTGAGTTTTACAATTCCCCCCCCATCTTGCTTCCCTCCCCC
CACCCCACCCCCACGGAAAGCACTCTATCAGTCTTTACTTTGTTTCCATGTTGTACCTTG
ATCCAAATTG--GGTGTGATGAGCTAAATCATATCTTTAAAGAAGAAAAGAGAAGTCCTA
AGAGGTAACAAGATCAGACAATAAGCTATCTGTTTTTTTCTAAATTAAAGGGAATAGTCC
TTGCACTTTGTTCAAACTCCACAGCTCCTTATCTGGATACAGATGGCACTCTCCTTTGCA
GACAGCCCCAAACTGTTCCCGATTGTTGCACTGATGGAATGAGCGAGTCCTTCAAGGTTG
ATCATCACTCCCATGTTGCTGTTAGGGTGTACAG-TGTTTTCTGGTTCTGCTCATCTCAC
TCAGCATCAGTTCATGCAAATCCCTCCAGACTTCTCTGAAATCCTGTCCCTCCTGGTTTC
TAATANAGCAATAGTGTTCCATGACATACATATACCACAGTTTGCTAAGCCATTTCCCAA
TTGAAGGACATTTACTTGATTTCTGATTCTTTACCACCACAAACAGTGCTGCTATAAATC
AATCTTATTCTCT---TACTTGGGACAAATGACAACAGCAGCCTTTTCTCACTCTGTCTG
ACTCTTTATTGCCTTCTTTTACTCTGGCCCAGGTGGATGTGAATCCCATTTCAAGAGATG
CCAGTTTGGAGTCCTTTATTTGAGGCACCCCAAGCCTGGAA---GGC--T-CCCCTATGT
GAAAA-CTGCATACAGGGATTGTCTTTA---AATTAGCAGTATTTGAATAGAACCTTCAT
CTTTTTTT-CCACAG--CCTCAAGAGGACCACAGATG
>Pgu
TTACCAAACAGAAGTTTGATAACCTGTACTGCTGCCGAGAGTCCATTCTGGATGG--GTG
AGTGGAGACTG-------CAAATCCGTGAGGAGATG-AAGTGTGAGGAA--CAGGAGGAG
AGTTAACTTGAAGCTTTCGTG-----------------------GGAAAGGCCATGGT-T
TTGGGATTAGAGGATCAGA-CCCAGG----------------------------------
-----------------------ACTGCTCTGTGACCCACAAGAA-GTCATTTT-ACTTC
ATTTGGCCTCAG-TTTCCTCCGCTGTAAAATGAAAGGGTTGG-CTAGATGGTATCTGGTC
TCTTTTCCAGCTCA--GTCTTATC---CTTT-----------------------------
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----------------TACTTGGTATAAATGACAACAGCAGCCTTTTCTCACTCTGTCTG
ACTCTTTATTGCCTTCTTTTACTCTGGCC-AGGTGGATGTGAATCCCATTTCAAGAGATG
CCNGTTTGGAGTCCTTTATTTGAGGCACCCCAAGGCTGGAA---GGC--TCCCTTTACGT
GACAA-CTGCACACAGGGATTGTCTTTG---AATTAGCAGTATTTGAATAGAACCTTCAT
CT-TTTTTTCCACAG--CCTCAAGAGGACCACAGATG
>Iso
TTACCAAACAGAAGTTTGATAACCTGTACTGCTGCCGAGAGTCCATTCTGGATGG--GTG
AGTGGAGACTG-------CAAATCTGTGAGGAGATG-AAGTGTGAGGAA--CAGGAGGAG
AGATAACTTGAAGCTGTCGTG-----------------------GGAAAGGCCATGGT-T
TTGGGATTAGAGGATCAGA-CCCAGGA---------------------------------
------------------------CTGCTCTGTGACCCACAAGAAAGTCATTTT-ACTTC
ATTCGGCCTCAG-TTTCCTCCGCTGTAAAATGAAAGGGTTGGACTAGATGGTATCTGGTC
TCTTTTCCAGCTCA--GTCTTATGATCCTTT-----------------------------
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----------------TACTTGGTATAAATGACCTCAGCAGCCTTTTCTCACTCTGTCTG
ACTCTTTATTGCCTTCTTTTACTCTGGCC-AGGTGGATGTGAATCCCATTTCAAGAGATG
CCAGTTTGGAGTCCTTTATTTGAGGCACCCCAAGGCTGGAA---GGC--TCCTTTTACGT
GAAAA-CTGCACACAGGGATTGTCTTTG---AATTAGCAGTATTTGAATAGAACCTTCAT
CT-TTTTTTCCACAG--CCTCAAGAGGACCACAGATG
>Tro
TTACCAAACAGAAGTTTGATAACTTGTACTGCTGCCGAGAGTCCATTTTGGATGG--GTG
AGTATTAGACCTCTGCGAAA-------------------------------GGGGAGGAG
AGAGAACTTGGAGCTGTCATG-----------------------GGGAA-ACCATAGG-T
TTGGGGTCTGAGAGTCAGG-CCCAGGCCC---------------------------AGG-
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--------------------------------------------TCTAGAGTCTCACTTC
CCTCTTCCAGCTCACAATCTTTGGATCCTCC-----------------------------
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----------------TCCTTGGCACAAG-GGAAAGAGCAG-CTTTCCTCACCCTTTCT-
---CTTTATTGCTTTCTTTTATTTTGGGC-AGGTGTCTGTGAATCCCATTTCAAGGGACG
CCATTTTGGGGTCCTCTACCTAAGACACCCCGAGCCTGTAA---GGC--TCCCCCAGTGT
GAATG-CTGCACGGG-GCATTACATTTG---AATTG---GCATTTGAATGGAGCCTTCAT
CT-TTT-TTCTACAG--CCTCAAGAGGACCACAGATG
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>Ppe
TCACCAAGCAGAAGTTTGATAACTTGTACTGCTGCCGAGAGTCCATTCTAGATGG--GTG
AGTAAAGTCTGGCAGTATCAAACCT----------------CTGAGGAA--GGGGAGGAG
AGAA--CTCGAAGCTATCATG-----------------------GGAAAGACCATGGG-C
TTGGGGTCCAGGTATGGAG-TCTCATGC--------------------------------
------------------TGCCACCTGCTCTGTGACCCACAAGAAAGTCATTTT-ACCT-
ACTTGGCCTCAG-TTTCCTCATCTGTAAAATGAAAAGGCTGGACTAGATGGTGTCCAGTC
TCTTTTCCAGCTCACAGTCTTGCGATCTTAT-----------------------------
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----------------CACTTGGTACAAGTGACAACAGCAGCCTTTTCTCATCGTATCT-
---CTTTATTGCTTTCCTTTACTTTGAGC-AGATGTCTGTGAATCCTATTTCAAGGGACA
CCAGTTTGGGGTCCTCTACCTGAGGCACCCTGAGCCTGTAA---GGC--TCCCCCAATGC
GAAAG-CTGCATGCAGGGATTACACTTG---AATTAGCAGCATTTGAATGGAGCCTTCAT
CT-TTT-TTCCACAG--CCTCAAGAGGACCACAGATG
>Tvu
TTACCAAACAGAAGTTTGATAACTTGTACTGCTGCCGAGAGTCCATTTTGGATGG--GTG
AGTAGAGACTGCAGGTGTCAAACCT----------------GTGAGGAA--GGGGAGGAG
AGAGAACTTGAAGGTGTCATG-----------------------GGAAAGACCATGGA-T
TTGGGGTCAGAGGATCAGG-TCCAAGTCC---------------------------AGGT
ATGAAGTCTTGTGC----TGCCACCTGCTTGATGACCTC----------------ACTTG
ACCTCAG------TTTCCTTATCTGTAAAATGAAAGGGCCGGACTATATGGTACCCAGTC
CCTTTTCCAGGTCACAGTCTTGTCATCCTGT-----------------------------
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----------------TACTTGGCATAAGTGATGATAGCAGCCTTTCCTCACACTGTCTG
ATTCTCTATTGCTTTCCTTCACTTTGGGC-AGGTGTCTGTGAATCCCATTTCAAGAGACA
CCAGTTTGGGGTCTTCTACCTGAGGCACC-TGAGCCTATAA---GGC--TCCCCCAATGG
GAAAG-CTGCACGCAGGGATTGCATTTG---AATTAGCAGTATTTGAATGGAGTCTTCGT
CT-TTT-TTCCACAG--CCTCAAGAGGACCACAGATG
>Mro
TTACCAAGCAGAAGTTTGATAACTTGTACTGCTGCCGAGAATCCATTTTGGATGG--GTA
AGTAGAGACTGCAAGTATCCAACCT----------------GTGAGGAA--GGGGAAGAG
AGAGAACTTGAAGCTGTCATG-----------------------GGAAAGACCATAAA-T
TTGGGGTCAGAGGATCAGG-TTCAGGTCC---------------------------AGGT
ATGAAGTCTCATGC----TGCCACCTGCTC--TGACCCACAAGAAAGTCATTTTTACTTC
ACTTGACCTCTTATTTCCTTATCTGTAAAGTGAAAGGACTGGACTAGATGGTGTCCACTC
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TCTTTTCCAGCTCA--GTCTTGTGATCCTGT-----------------------------
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----------------CACTTCNTACAAATGACAGCAGCAACCTTTCCTCACCATCT--G
ACCCTTTA-----TTACTTTACTTTGGGC-AG--GTTTCTGAATCCCATTTCAGGAGACA
CCAGTTTGGGGTCCCCTACCTAAGGCACCCTGATCCTATAA---GGC--TCCCCCAGTAT
GAAAG-CCGCACACAGG-ATTGCC-TTG---AATTAGCAGTATTTGAATGGAGCCTTCAT
CT-TTT-TTCCACAG--CCTCAAGAGGACCACAGATG
>Vur
TTACCAAACAGAAGTTTGATAACTTGTACTGCTGCCGAGAGTCCATTTTGGATGG--GTG
AGTAGAGACTGCAAGTATCAAACCT----------------ATGAGGAA--GGGGAGGAG
AGAGAGCTTGAAGCTGTCATT-----------------------GGAAAGGCCCTGGG-T
TTGGGGTCAGAGGATCAGG-CCCAGGTCC---------------------------AGGT
GTGAAGCCTTATGC----TGCCACCTGCTCTGTGACCCACAAGAAAGTCATTTT-ACCTC
ACTTGACTTCAC-TTTGCTCATCTGGAGGCTA-AAGGGTTGGACTGCATGGTGTCCAGTC
TCTTTTCCAGCTCA-AGTCTTGTGATCCTGT-----------------------------
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----------------CACTTGGTACAAGTGACAAGAGCAACCTTTGTTTACCTTGTCTG
ACTCTTTATTGCTTTTCTTTACTTTGGGC-AGGTGTCTGTGAATCCCATTTAAAGAGACA
GCAGTTTGGGGTCCTCTAGCTGAGGCACCCCGAGCCTGTAA---GAC--TCACCCTATGT
GACAG-GTGCACAGAGTGATTGCATTTG---AATTAGCAGTGTTTGAATGGAGCCTTCAT
CT-TTT-TTCCATAG--CCTCAAGAGGACCACAGATG
>human
TTACCAAACAGAAGTTTGATAACTTGTACTGCTGCCGAGAATCCATTTTGGATGG--GTA
GGTTGAATGTATATATATTCAAACT----------------TCTAGGGG-----------
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----------------------------------------------------------CT
CTGGTCTT-----CCTTTGGCTTTAAAAG-TTT-ATTAGAGGGA-CCATT---TCATACT
GAGCTCAACCAGCTTCCAATTGATATTCTCATGGGCATT-----GGC----CCACACTTT
TAACT-TTGTGAAGAGGGACTGAGTTTGAGCTATTAACG---TTTGAGTTGAGCCCTTGT
CTGTTT---CCACAG--CCTGAAGAGGACCACAGATG
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**MARKER 172**

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>MIR3_MarsB
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-------GAGAAGCAGCATGG-TGTAG---------------------------------
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------------------------TGGATAGAGCAC------TGGACTTGGAGTCAGGAA
GACCTGGGTTCAAATCCCGC-CTCAGACACTTACTAGCTGTGTGAC-CCTGGGCAAGTC-
AC----------------------------------------------------------
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----------------------------------------------------TTA---AC
C-----------------------------------------------------------
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-------------------------------------------------TCTCTGGGCCT
CAGTTTCCTCATCTGTAAAA-------TGAGGGGGTTG----------------------
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---------------GACTAGAT---GGCCTCTAAGGTCCC---TTCCAGCTCTAAAT--
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>WSINE1
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------------------------------TTTTT--------TTTTTTTTTGAGGCAAT
TGGGGTTAAGTGACTTGCCCAGGGTCACACAGCTAGT-------AAGTGTCTGAGGCTGG
ATTTGAACTCAGGTCCTCCTGACTCCAGGGCTGGTGCTCT-ATCCACTGCACCACCTAGC
TGCCCCTC----------------------------------------------------
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>MAR1b_Mdo
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------------------------------------TTGTTGTTGTTGTTCAGTCGTTTT
CAGTCATGTCTGACTCTTCGTGACCCCATTT-----------GGGGTTTTCTTGG-----
-------CAAAGATACTGGAGTGGTTT-GCCATTTCCTTCTCCA------------GCTC
ATTTTACAGATGAGGAAACTGAGGCAAACAGGGT-------------TAAGTGACTTGCC
CAGGGTCACACAGCTAGTAAGTGTCTGAGGCCAGATTTGAACTCAGGTCTTCCTGACT-C
CAGGCCCGGCGCTCTATCCACTGTGCCACCTA-GCTGCCCTC------------------
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--------------------------------------------TTTTTTTTTTTTT---
AAACCCTTA-CCTTCCATCTTGGAATCAATACTGTGTATTGGTTCCAAGGCAGAAGAGTG
GTAAGGGCTAGGCAATGGGGGTCAAGTGAC-TTGCCCAGGGTCACACAGCTGGGAAGTGT
CTGAGGCCAGATTTGAACCTAGGACCTCCCATCTCTAGGCCTGGCTCTCAATCCACTGAG
CTACCCAGCTGCCCCC--------------------------------------------
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-------------GGAAAGAGCACGGGCCTGGGAGTCAGAGGACCTGGGTTCTAATCCCG
GCTCTGCCACTTGCCTGCTGTGTGACCTTGGGCAAGTCACTTAACTTCTCT---GTGCCT
CAGTTTCCTCANCTGTAAAA-------TG-------------------------------
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>RTE-2_MD
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----------TTGGTTGGTTGTTGTC----CTTCGTACTCGAAGAGGACCAAAATGACAT
CACTATGTCGGGGTCAATGTACAGTGTGTCCGACTGTGGCTGATCAGACCAATATGAGCT
CGGAAGGCTCTACCACAGGTTGGGCACAAATAGCCCGTATGAACATTTGGGA-TGGAGAT
GTCTCTAAATTTGCGCATCTCACGTTTCTTTTG--AGCT---------------------
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>DNAT_ME
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----------------------------------------------------CAGGGGTG
GGGAACCTGCAGCCTCGAGGCCACATGTGGCCCTCTAGGTCCTCAAGTGCGGCCCTTTGA
CTGAATCCAAACTTCACAGAACAAATCCCCTTAATAAAAGGATTTGTTCTGTAAAACTTG
GACTCAGTCAAAAGGCCACACCCAAGGACCTAGAAGGCCACATGTGGCCTTGAGGCTGCA
GGTTCCCCACCCCTG---------------------------------------------
------------------------------------------------------------
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>Mdo
GGCCATG---GAAACAGCAGTTCTCAGGCAACAATATCAAAGGAATCAGCTTGCCCTTTA
AAC-CAGTCATCTCATCAGCCCTTCTCTTTTCAAAGAGATTAGTGGCAGCAGTCTCAACC
-TACAGGCATTTGGTTGGCCT--AAGGAAAGTCAATTCTTTGATGTGT------------
-------GAG--GCTGCATGGGCATAG---------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------TTGACAGAATTC------AAGATTGAGAGTCAGGAA
GACCTGGGTTTAAATCCCC-ATTCTGACACTTACAGACTGTGCGACTACTCATCCTCTCT
GC----------------------------------------------------------
------------------------------------------------------------
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------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------CA-AGACTC----AT
CTACTCCATTATAGACAGATTACAT----------------------CTGTGTTGGTAAA
GGGAAT---TCCAGGACCAATGAA----TTTGCATTTTGG------TTTTTTTTTTT---
AAACTCTTA-CCTTCCGTCTTAGAATCAATACTACACGTCAGTTCCAAGGCAGAAGAGCA
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TTAAGGGCTAAGCAATAGGGGTTAAATGATTTTGCCCAGTGTCACAAAGCTAGGAAGTGT
CTGAGGCCACATTTGAATCCAGGACCTCC-------AGGCCTGGCCCTCTGT-CACTGTG
CTACCTAGCTGC-------TCCTAAATTCTTGAT---TGTCTCTA---------------
----------------------AATGTCTTATCTTTTCAGTTGTA---AGACCA--TTTC
CCTC-T------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--GATTTTTCACAGG-AAGAGCCCTAGGCTAGAATTCAAAAGATCTGAGTTCTAATTCCA
GTTTAGCTGCTCATAGACTTGAT-------------CTTTGTC--TTTGATTTTGCTTCT
CAGTTTCCTTCACTATAAAA-------TGATGAGTTTG----------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------GACTAGGG---TAGCCTTAAAATCCT---TCAAAACCCCAGCA--
-----------TTCTTGGCATGGTTCTTTGTATGTGACATT-GCTTAAGTGTACATGTTT
GTTCTTAG--GGTTATGAGATACGTATGTATGACAGC
>Dvi
GGCCATG---GAAGCAGCAGTTCTCAAGCAACAATATCAAAGGAATCAGCATGCCCTATA
AAC-CAGTCATCTCATCAGCCCTTCTATTTCCAAAGAGATTAGTGGCAGCAGTCTCAACC
-TACAGGCATTTGGTCAGCCT--AAGGAAAGTCAATTCTTTGATGTGATAACCTTAAAAT
GTGT---GAG--GCTGCATGGGTATAG---------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------GGGACAGAATTC------AAGATTGGGAATCAGGAA
GATCTGGGTTTAAATTCC-CATTCTGACACTTACAGGCTGTGCAACTACTCGGCCTCTCT
GC----------------------------------------------------------
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------------------------------------------------------------
-----------CAAGAC----TCA----TTTGCATTTTCTTTC-TTTTTTTTTTTTTAAC
AAACTCTTACCCTTCCATCTTAGAATCAATACTATGCATCAGTTCCAAGACAGAAGAGTA
TTAAGGGCTA-GCAATAGGGGTTAAATGACTTTATGCAGTGTCGCACAGCTAGGAAGTGT
CTGAGGCCACATTTGAACCCAGGATCTTC-TATCTTCAGGCCTGGCCCTCTGTCACTGAG
CCACCTAGCTGC-------TCCTAA------------ATTATATATTCTTGGAATACTGT
TGGAATCCTGTATT-GTATCTTAATGTCTTATCTTTCCAGTTATA---AGACCA--TTTT
CCTCTGA-----------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--CACTTTTCACAGG-AAGAGCCCTAGGCTAAAAGTCAAAAGATCTGAGTTCTAATTTGA
GCTTAACTGGTCATAGACTTGAT-------------CTTTGTT--TTTGACTTTGCTTCT
CAGTTTCCTTCACTATAAAA-------TGATGGGTTTG----------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------GACTAGGG---CATCCTTAAAATCCT---TGAAAATCCCAGCA--
-----------TTCTTGGCATAGTTCTTTGTATGTGACATT-GCTTAAGTGTACATGTTT
ATTGGTAG--GGTTATGAGATACGTATGTATGACAGC
>Mnu
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GGCCATG---GAAGCAGCAGTTCTCAAGCAACAATATCAAAGGAATCAGCATGCCCTATA
AAC-CAGTCATCTCATCAGCCCTTCTATTTCCAAAGAGATTAGTGGCAGCAGTCTCAACC
-TACAGGCATTTGGTCAGCCT--AAGGAAAGTCAATTCTTTGATGTGATAACCTTAAAAT
GTGT---GAG--ACTGCATGGGTATAG---------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------GGGACAGAATTC------AAGATTGGGAATCAGGAA
GATCTGGGTTTAAATTCC-CATTCTGACACTTACAGGCTGTGCAACTACTCGGCCTCTCT
GC----------------------------------------------------------
------------------------------------------------------------
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------------------------------------------------------------
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------------------------------------------------------------
-----------CAAGAC----TCA----TTTGAATTTTCTTTCTTTTTTTTTTTTTTAAC
AAACTCTTACCCTTCCATCTTAGAATCAATACTATGCATCAGTTCCAAGGCAGAAGAGTA
TTAAGGGCTA-GCAATAGGGGTTAAATGACTTTATGCAGTGTCACACAGCTAGGAAGTGT
CTGAGGCCACATTTAAACCCAGGATCTTC-TATTTTCAGGCCTGGCCCTCTGTCACTGAG
CCACCTAGCTGC-------TCCTAA------------ATTATATATTCTTGGAGTGCTGT
TGGAATCCTGTATT-GTATCTTAATGTCTTATCTTTCCAGTTATA---AGACCA--TTTT
CCTCTGA-----------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--CACTTTTCACAGG-AAGAGCCCTAGGATAAAAGTCAAAAGATCTGAGTTCTGATTTGG
GCTTAACTGGTCATAGACTTGAT-------------CTTTGTT--TTTGACTTTGCTTCT
CAGTTTCCTTCACTATAAAA-------TGATGGGTTTG----------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------GACTAGGG---CATCCTTAAAATCCT---TGAAAACCCCAGCA--
-----------TTCTTGGCATAGTTCTTTGTATGTGACATT-GCTTAAGTGTACATGTTT
ATTGGTAG--GGTTATGAGATACGTATGTATGACAGC
>Rra
AGTCATG---GAAGCTGCTGTCCTTGAGCAGCAATAGCAG-----TCAGCTTGCCTGCTA
CAC-TCATCATCTCAAAGGCCCTTCTCTTCCC-TCAAAATCACTAGCAGTTGTGTGAACT
-GAAAGGCTTTTCCTTGGCCT--GTGGAAAGTCAGTTTTTGGATGTGTTAGCCTTAAAAA
GTAT---GAG--AC-ACTATAGCATAG---------------------------------
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------------------------------------------------------------
------------------------TTGATAGAGTTC------AAGATTTGTAGTCAAAAG
GAC-----------TCTTT-ACTTTAACATTTAGAAGCTATGTGACCATACATCCTCTCT
GAACCTGAGGCAACTAATTCC---CCAAGACCT----TGTTGTT---GTTCAGTCATTTT
-AGAGACATCTGACTCTTTGTGGCCCCTATAGCCTTTTATCTGTGTGTTG------TTTT
TTTTTAACAAGGACATTGGAGTGGTTTTTCTATTTCTTTGTCCTGGGATTCATGAAAGGC
ACTT-ACAGTCATTACTGTATTTGCATTTCAAATACAAGTCCCCTCATAAGTGACTTCTC
CAGGGTCACATAGCTAGTATGTGTCTGAAGCTGGATTTAAACTCAGGTTCTCCTGGCTAA
TAAACCCAGTGATCTGCCCATTGTACCACCTAAGCTGCCCAC---CTGAGACTT----AC
CTTCTGAGTTGTAGACAGATTTTAC----------------------CTGCCACCATAAA
GAGAAT---TCCAGTAAC------------------------------------------
------------------------------------------------------------
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------------------------------------------------------------
-------------------------------------ACTACATATACTTGACATACCAT
TGTAACCCTATATT-GTATCCTAATGTCTCATCTTTCCAATTATG---AGACCA--ATTT
CCCTAT------------------------------------------------------
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------------------------------------------------------------
------------------------------------------------------------
--GACTTTTCA-TGGAAAAACCAAA-GGCTAGAAATTAAGAG-------TTCTAATGCCT
ACTTAGCTGGCTTTGGACTTGGT-------------CTCTGACCAGATAACTGTGCTTCT
TAGTGTCTTTCTCTAT-AAA-------TGATGAGTTTG----------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------GACGTGTG---TATCTTTAAGGTCCC---TTAAAACTCCCACA--
-----------TTCTTGGTCTGGTCCTTTATGTGTGATATTTCCTTATGTGCACCTTCTT
GCTCTTAG--GGTTATGAGATACGCATGTATGACAGT
>Cfu
AGCCATG---GAAGCTGCTGTCCTTGAGCAGCAGTATCAGAGCAATTAGCTTGCCCACTA
CAC-TCATCGTCTCATCAGCCCTTCTCTTCCC-TCAAAATCACTAGCAGCTGTGTGAACT
-GAAAGGCTTTTCCTTGGCCT--GGGGAAAGTCAGTTCTTGGATGTGTTAGCCTTAAAAA
GTGT---GAG--AC-ATTATAGCATAG---------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------TTGATAGAGTTC------AAGATTTGTAGTCAAAAG
GAC-----------TCCCT-ACTCTAACATTTAGAAGCTGTGTGACCGTACATCCTCTCT
GAAACTCAAGCAACTAACTCC---CCAAGACTT----TGTTGTT---ATTCACTTGTTTT
-AGAGACATCTGACTCTTTGTGGCCCCCATAGCCTTTTGTCTGTGGTTTTTTTTGTTTTT
TTTTTAACAAGGACATTGGAGNGTTTTTGCCATTTCTTTGTCCTGGGATTCATGAAGGGC
ATTT-ACAGTCATTACTGTATTTGCATTTCAAATACAAGTCCCCTC-TAAGTGACTTCTC
CAGGGTCACATAACTAGTATGTGTCTGAAGCTGAATTTAAACTCAGGTTCTCCTGGCTAA
TAAACCCAGTGCTCTGCCCACTGTACCACCTAAGCTGCCCAC---CTGAGACTT----AC
CTTCTGAGTTGTAGACAGATTTTAC----------------------CTGCCACCATAAA
GAGAAT---TCCAGTGAC------------------------------------------
------------------------------------------------------------
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------------------------------------------------------------
-------------------------------------ACTGCATATACTTGACATACCAT
TGTAAACCTATATT-GTATCCTAATGTCTCATCTTGCCAATTATG---AGACCA--ATTT
CCCTAT------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--GACTTTTCA-TGGAAAAACCAAA-GACTAGAAATT--GAG-------TTCTAATGCTT
ACTTAGCTGGCTGTGGACTTGGT-------------CTCTGACCAGATAACTTTGCTTCT
AAGTGTCCTTCCCTAT-AAA-------TGATGAGTTTG----------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------GACGTGTG---TATCTTTAAGGTCCC---TTAAAACTCCCACA--
-----------TTCTTGGTCTGGTCCTTTGGGTGTGATATTTCCTTATGTGCACCTTCTT
GCTCTTAG--GGTTATGAGATACGCATGTATGACAGC
>Dgl
GGCCATG---GAAGCAGCTGTCCTCCAGCAATAGCATCAAAGGAATCAGCTCGCCCTATA
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AAC-CAGTCATCTCATCAGCCTTTCTCTTTCCAAAGAGATAAGTGGCAGCAATTTGAACT
-TAAAGGCATTTGGTTGGCCT--CAGGAAAATCATCTCTTTGGTGTGGTAACCTTAAAAT
GCTT---GAG--GCAATATGG-CATAG---------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------TTGATAGACTTT------AAGACATGGAGTCGAAAA
GAA---------AATCCCC-ACTCTAACTCTTAGGGGCTGTGTGACTTCTCACTCTCTTT
-C----------------------------------------------------------
------------------------------------------------------------
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------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------TAAC-ACTTA---AC
CTGTTCAGT----GATAGATTAGAT----------------------TTGTGTTGGCAAA
GGGAAT---TCCCACACCAGTGAA------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------------------------ATTGCATGTTCTTGATGTGTTAT
TGTAA--CTATATT-ATATCCTAATGTCTCCATTTTCTAATCACG---AGACCA--TTTT
CTCTAC-----TGGTTGGTTGTTGTC----CTTTGTTCTCAAAGGGGATCAAAATGACAT
CACTATGTTGGGGTCAAAGG-CAGTGTGTCCCATTGTGTTTGATCAGACCAAGATGAGCT
CCAAAGGCTCTGGCACAGGTGGGACACAAGTAATCCATGTGAACATTTAGAG-TGGAGAT
GTCTCTAAATTGACACATCTCCTGTTTCTTTTG--AGCT---ACT-GTTTTTTCCTTAA-
--TACTTTTCA-TGGAAAGAGTACTAGGCTAGAAGTCAAGAGATCTGAGTTCAA-TCCCA
GCTTAGCTTACCATGCACTTGAT-------CTCTGTCTTTGACCAGATCACTTTGCGCCT
CAGTTTCCTTCACTATAAAA-------TGATGGGTTTG----------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------GACCAGAA---CATCTTTGAGGTCCC---TTAAAACTTTAACA--
-----------TTCTTGGTATGGTTCTTTGTTCGTGATATTTCCTCAAGTCTACATGTTT
GCTCTTAG--GGCTACGAGATACGCATGTATGACAGT
>Nty
AGTCACA---TAAGCAGCTGGCCTCAAGCAACAATATCAAAGGAATCAGCTTGCCCTATA
AAC-CAGTCATCTCATTAGCCCTTTTCTTTCCATAGAGATAAATGGCAGCAATTTGAACT
-TAAAGGCATTTGGTTGGCCT--AAGAAAAGTCAGTTATTTGAGGTGGTAACCTCAAAAT
CTTT---GAG--GC-AATAGGGCATAG---TTTTTTTTAAAAATTATTTTACAAGGCAAT
AATGGTTAAGTAATTTGCCCAAGGTCACACACCTTGTAAGTATCAAGTGTCAGAGGCTGA
ATTTGAACTCAGGTCCTCCTGACTCCAGGGCTGGTGTTCTTATTTCCTGTTCCATCTAGC
TACCCC---GGTATGACATAG---TTGATAGAGTTC------AAGACTTAGAGTCCAAAA
GGA-TATGTTTAAATTGCC-ACTCTGATACGCAGGGGCTTTGTGACTCCTCAACTATTCT
GC----------------------------------------------------------
------------------------------------------------------------
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------------------------------------------------------------
---------------------------------------------TTAG-ACGT----AC
CTGATCAGTTATAGACAGATTACAT----------------------TTGCATTGGTAAA
GGGAAT---TCCCACGCTAGTTAA------------------------------------
------------------------------------------------------------
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-------------------------------------ATTGCATGTTCTTGATATATTTT
TATAACTTTGTATT-GTTTTCCAATGTCTGCACTTTCTAATTATG---AGACCA--TTTT
TCCTAT-----TGGTTGGTTGTTGTC----CTTTGTTCTTGAAGAGGACCAAAA-----C
CATTAGGTGGGGGTCGAGGTACAGTATGTCTGACTGTGTCTGATCCGACCAATAGGACCT
CGGACATCTCTGCAGAA-TTTGGGCACAAATAGTCCATATAATTATTTAGG--TGGAAAT
GTCTCTAAATTTGGGCGTCTCATGTTTATTTTG--AGCT---ACTACATTTTTCCT-AC-
--TGCTTTTCA-TGGAAAAAGCACTAGGCTAGATATGAAGAGATCTGCGATCTAATCCCA
GTTTTGCTAGCCATGGACTCAAT-------ATGTGTCTTTGACCAGATCACTTTGTTTCT
CAGTTTCCTTCACTATAAAG-------TGATGGGTTTG----------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------GACCAGGA---TAACTTTGAGGTCCC---TTAAAACTCCAAACA-
-----------TTCTTGCTATGGCTCTTTGTATATGATATTTGCTC--ATCTACATGTTT
GCTCTTAG--GGTTATGAGATACGCATGTATGACAGT
>Pta
A-----------------------------------------------------------
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--ACTGGATTTAAATCC---------------TAGGCCTGTGTGAGAACTAAACCTTCCT
GC----------------------------------------------------------
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------------------------------------------------------------
---------------------------------------------TAAA-ACTT----AC
CTGTCCAGTTACAGACAGGTTACAT----------------------TTGCATCGGAAAA
GGAAAT---TCTCATGTCAGTTAA------------------------------------
------------------------------------------------------------
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------------------------------------------------------------
-------------------------------------ACTGCACTTAT-TGATGTGTTAT
TGGTACTCTATATT-GTATTCTCATGTCCCTACTTTCCCGTTATG---AGGTCA--CTCT
CCCTAG-----GGGTTGGGTATTG-C----CATCTTGATTCTCTGAGATCC-AAGGACAT
CACCACGTCGGGGTCTCGGTGCAGTGTGCCCAACTGTGGCTCATCAGACCATTATGAGTT
CCGAGATCTGTACCACAGATTGGGCACAAATAGTCCATATGAATATT-AGG--TGGAAAT
GCCTCTAA-TTTGCATGTTTCATGTTTCTTTTG--AGCT---ATTGCA-TTTCCCCTAA-
--GTCTTTTCA-TGGAAAGAGCACAAGGCTAGAAGA-------TCTGAGTTCTAATCTCA
GCTTAGTTAGCCATAGACTCGAT-------CTATGTCTTTGCCTAGATCATTTTGCTCCT
CA-TTTACTTCACTATAAAA-------TGATGGGTTCG----------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------CATCAGGA---CATTTTTGAGGTTCC---TTAAAACTCCAACC--
------------TCTTGCTATGGTTCTTTCTTTGTGATATATCCTC--ATCTACATGTTT
GCTCTTAG--GGTTACGAGATCCGTATGTATGACAGT
>Dgo
A-----------------------------------------------------------
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------------------------------------------------------------
--ACTGGATTTAAATCC---------------TAGGCCTGTGTGAGAACTAAACCTTTCT
GC----------------------------------------------------------
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------------------------------------------------------------
---------------------------------------------TAAA-ACTT----AC
CT-TCCAGTTACAGACAGGTCATAT----------------------TTGTATCGGAAAA
GGAAAT---TCTCACATCAGTGAA------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------------------------ATTGTACTTACTTGATGTGTTAT
TGGCACTCTGTATT-GTATCCTCATGTCCCTACTTTCCAGTTATG---AGGTCA--TTCT
CCCTAC-----GGGTTGGTTATTGTC-----ATCTTGATCCTCTGAGATC-AAAGGACAT
CCCCATGTCGGGGTCTCGGTGCATTGTGCCCAACTGGGGTTCATCAGACCATTGTGAGCT
CTGAGATCTCTACCATAGTTTGGGTACAAATAGTCCATATGAATATT-ATG--TGGAAAT
GTCTCTAA-TTTTCATGTTTCATGTTTCTTTTG--AGCT---ATTACA-TTTTCCTTAA-
--GTCCTTTCA-TGGAAGGAGCACAAGGCTAGAAGA-------TCTGAGTTTTAATCTTA
GCTTAGCTAGCCATAGACTTGAT-------CTATGTCTTTGCCTAGATCGTTTTGCTCCT
CATTTTCCTTCACTATAAAA-------TGATGGGTTTG----------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------GATCAGGA---CATTTTTGAGGTTCC---TTAAAACTCCAAC---
-----------TTCTTGATGTGGTTCTTTGTTTGTGATATGTCCTT--GTCTACATGTTT
GCTCTTAG--GGTTACGAGATACGTATGTATGACAGT
>Bil
AGCCGCCATGTAAGCAGCTGTCCTCAAGCAGCTGTGTCAAAGGAATCATTTTGCCCTATA
AA-TTAGTCATCTCATCAACCCTTCTCTTTCCAAAGAGATAATTGGCAGCAATTTGAACT
-TAAAGGTATTTGGTTAGCCTA-AAGGAAAGTCAGTTATTGGATGTGGTAACCTTAAAAT
ATTT---ATG--GAAATATAG-CATAG---------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------TTAAACTGATAG-AGTTCACAACTTGGAGTCCAAAA
GTCCTGGGTTTGAATCCCTACTCTTGACACTTTGGA-GT---------------CTCTCC
AC----------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
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------------------------------------------------------------
---------------------------------------------TAGG-AGTT----AC
CTGTTCAGTTATAAAGAGATTACATTTGCAGTG-----------------------TAAA
GGGAGG---TCCCACACAAAGGAA------------------------------------
------------------------------------------------------------
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------------------------------------------------------------
-------------------------------------ATTGCATTTTCTTGATTTTGTTA
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TAACTCTTTATT---GTATCCTAACATCTCCACTTTCTAATTACT---TAACCATTTTTT
TCCTAC-----TAGTTGG-TGTTGTC-----TTTGTTCTCAAGGAGGATCAAACTGACAT
CACTATATT-GGGTC-AGGTGTGTCGA---------TTGATCAGACCAATGCAA-GCTCA
GAGG--TCTCTACTACAGATCGGACACAAATAGTCCAAATCTATCTATAGA--TGGATAT
GTCTCTAGATTTGCACTTCTCATTTTTTTTA----AGCT---ACTGCATTTTTCCTTAC-
--TACTTTTCA-TGGAAAGAGCTCTAGGTTAGAAGTCAAGAGATCCGACTTGA-------
-------------------------------TTTCTGTCTGATCAGATCATTTTGTTCTT
CAGTTTTCTTCACTGTAAAA-------TGATGGGTTTG----------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------GACCAAAA---CATATTTGAGATCCC---TTAAAACTCCAAAAT-
----------TGTCTTGGTATGGGTCTTTGTATGCGATATTTGCTCAGGTCTACATGTTT
GCCCTTAG--GGTTACGAGATACGCATGTATGACAGC
>Pgu
AGCCGCCGTGTAAGCAGCTGTCTTCAAACAGCTGTGTCAAAGGAATCATTTTGCCCTATA
AA-TTAGTCATCTCACCAATCCTTATCTTTCC--------------AGATAATTTGAACT
-TAAAGGTATTTGATAGGCCT--AAGGAAAGTCAGTTATTGGATGTGGTAATCTTAAAAT
ATTT---GTG--GAAATATAA-TACAG----------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------TTAAAC------------------TGGAGTCTAAAA
GACTTGGGTTTGAATCCCCATCCTT-ACATTTTGGAGGT----------------TCTCT
AC----------------------------------------------------------
------------------------------------------------------------
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------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------TAGG-ACTT----AC
CTATTCAGTTATAAAGAGATTACATTTGCAGTGGATACTGGTTA----ATATCTAGTAAA
GGAAGG---TCCCACACAAGTGA--------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------------------------ATTGCATTTTCTTGATATTATTA
TAACTCTATATT-------------GTATCCACTTTCCAATTACT---TAACCA--TTTT
TCCTAC-----TAGTTGG-TGTTGTCTTTGTTTTGTTTTCAAAAAGGACCAAACTGACAG
CACCATATTGGGGTC-AGGTGTATCGG---------TTGATCAGCCCAATACAA-GCTCA
GAGGTCTCTCTACCACAC-GTGGACACAAATTATCCGAACCTACCT-TAGA--TGGAGAT
GTCTCTAGATTTGCACATCTCATTTTTTTAAAC--TACT------GC-TTTTTCCTTAC-
--TACTTTTCA-TGGTAAGAGCTCTAGGTTAGAAGTCAATCAGACTCAA-----------
-------------------------------TCTCTGTCTGATCAGATCATTTTGTTCCC
CAGTTTTCTTCACTGTAAAA-------TGATGGGTTTG----------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------GACAAGGA---CGTATTTGAGATCCC---TTAAAATGCCAACA--
-----------TTCTTGGTATGGTTCTTTGTATGTGATATTTGCTC--ATCTACATGTTT
GCTCTTAG--GGTTACGAGATACGCATGTATGACAGT
>Iso
AGCCGCCGTGTAAGCAGCTGTCCTCAAGCAGCTGTGTCAAAGGAATCATTTTGCCCTATA
AA-TTAGTCATCTCACCAATCCTTATCTTTCC--------------AGGTAATTTGAACT
-TAAAGGTATTTGTTTGGCCT--AAGGAAAGTCAGTTATTGGATGTGGTAATCTTAAAAT
```

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ATTT---GTG--GAAATATAA-TACAG---------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------TTAAACTGATAG---TCACAACTTGGGAGTCTAAAA
GACTTGGGTTTGAATCCCCATCCTT-ACATTTTGGAGGT----------------TCTCT
AC----------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------TAGG-ACTT----AC
CTATTCAGTTATAAAGAGATTATATTTGCAGTGGATACTGGTTATTATATATCTAGCAAA
GGGAGG---TCCCACACAAGTAAA------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------------------------ATTGCATTTTCTTGATATTATTA
TAACTTTATATT-------------GTATCTACTTTCCAATTACT---TAACCA--TTTT
CCCTAC-----TAGTTGG-TGTTGTCTTTGTTTTGTTTTCAAAAAGGACCAAACTGACAG
CACCATATTGGGGTC-AGGTGTATCGG---------TTGATCAGCCCAATACAA-GCACA
GAGGTCTCTCTACCACACGTTGGACACAAATTATCCAAACCTACCT-TAGA--TGGAGAT
GTCTCTAGATTTGCACATCTCATTTTTTTTTTTTAAGCT---ACTGC-TTTTTCCTTAC-
--TACTTTTCA-TGGTAAGAGCTTTAGGTTAGAAGTCAATCAGACTCAA-----------
-----------------------------------TCTCTGATCAGATCATTTTGTTCCC
CAGTTTTCTTCACTGTAAAA-------TGATGGGTTTG----------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------GACAAGGA---AATATTTGAGATCCC---TTAAAATACCAACA--
-----------TTCTTGATATGGTTCTTTTTATGTGATATTTGCGC--GTCTACATGTTT
GCTCTTAG--GGTTACGAGATACGCATGTATGACAGT
>Tro
AGCCATG---TAAGCAACTGTCCTCAAGCAGCAGCATCGACGGGATCAGCTTGCCCTATA
AA------CCTCCCAT--CCACCCCTCTTTCC--AGAGAGAAGTGGCAGCGGGTTGAACT
CTAAAGGCATTTGGCCAGCAT--ACGGAAAGTCAGTTATCTGATGTGGTAACCTCGAAAC
GCTT---GAG--GCAGTATTG-CAGAG---------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------TTGATGGACTTCAGGACTTGGT-GTCCACAT
GACCTGGGTTTAAACTCCT-GCTCTGACCCTTAGGGGCTGTGTGACTCCCCGCCTTGT--
GC----------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------CGAG-GCTT----AT
CTGCTCCATT----ACAGATTACAT----------------------CTGCATCAGTAAA
GGGAAC---TCCCACACCTGTGAAG-----------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------------------------ATACCCTATTTTTCATGTGCTAC
TGTTACTTG--TGCTGAAGCCTAATGTCTTTAGTTTCCATTTACA---AGACCA--TTTT
```

```
CCCTG------CTGATCAGGGGCGTC----CTTTGTCTTG-AAGAGGACCAAAATGACAG
CACTATGTTGGGGTC-AAGTACAGTGTGCCCAAAGGTGGCTGGTCAGAGCAGTATGAGCT
-GGGAGGGCCTATCACAGATTGAGCACAAACAGTCTGTGTGAACATTTGGGCTTCTAGAG
GTCTCTAAATTTGCACATCTTATTTTTCTTTTG--AGCT-----------CCCCCC-AC-
------TTTAA-TCAAAAGACCACTAGGGGAGAAGTCAAGGGACTTGAATTTTAATCCTA
GCTTAGCTGGCCCTGGACTTCAT-------CTCTATGTCTGATCAGATCACTTTGCTGCC
CAGTGTCCTTTACTACGAAATACTATATGATCAGTTTA---GACCACGA---CAGGGGTA
AGGAACCTGCAGCCTCAAGGCCACACGTGGCCCTCTAGGCGGCCCTTTTTTAAGGGTCAA
------------------------ATCTCCTTAATAAAAGGATTTGTTCTGTAAAACTTG
G-------ACTCAGTCCACACCTGATTACCTACAAGGCCACATGGGGCCTCAAGACCCTG
---------------AACCAGGA---CATGTTTGAGGGCCC---CCAACACTCCAGCA--
-----------TTCTTGGTATGGT-CTGCGTATCTGATATTTGCTCAAGTCTACGTGTTT
GCTCCTAG--GGTTATGAGATACGTATGTATGACAGC
>Ppe
AGCCACA---GAAGCAGCTGTCCTCAAGCAGCAATATCAGCGGAATCAGCTTGCCCTATA
A-GCCAGTCATCTCATCCACCCTTCTCTTTCC--AGAGATAAGTGGCAGCAAACTGAGCT
TTAAAGGCATTTGGTTGGCCT--AAGGAAAGTCAGTTATCTGATGTGGTTACCTTGAAGT
ATTT---GAG--GCAGTGTGG-CATAG---------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------TTGATAGAGTCCAAGACCTGGC-GTCCAAAT
GACCTGGGCTTAAACCCCCTACTCTGACCATTAGGGGCTGTGTGAATCCCCACCTTCT--
GC----------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------CAAG-GCTT----AC
CTGCTCAGTT----ACAGATTATGT----------------------TTGCATCGGTAAA
GGGAAT---TCTCACACCAGTGAA------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------------------------ACTGC------------CATGAC
TATAACTCTTATGTTTTATCCTCATGTCTCTGCTTTCCAGTTATG---AGGACA--TTTT
CCCTAC-----TCATCCGTTGTTGTC----CTTTCTCTT-AAAGAGGACCAAACTGACAT
CGTTATGTTGGGGTCCAGGTACAGCGTGCCCTACGGTGGCTGGTCAGATCAGCATGAGCT
TAGCAGTCCCTGTCACAGACCGAGCACAGATCATCCGGGTGAACATTTGGAG-TGCAGAT
GTCTCTGAATTTGCACATCTCATATTTCTTTTG--AGTT---ACTGC-ATTTCCCT-AC-
------TTTA--TGGAAAGAACACTAGGGTAGAAGTCAAGAGATCTGAATTCTAATCCCA
GCTTAGCTGGCCCTGGACTTCAT-------CCCTGTGTTTGACTAGATCACTTTGCTCCT
CAGTTTACTTCACTATAAAG-------TGATCGGTTTG---GACCAGGC---CAGGGGTG
AGGAACTGGTGGCCTCAAGGCGGCACATGGCCCTCTAGTTCTTCAAGTGCAGTCCTTTGA
CTGAATCAAGATTTCACAGATCAGATCTCCTTAATAAAAGGATCTGTTCTGTAATGCTTG
GACTCAGTCAGAAGGCCACACCTGAGGACCTAAGAGGCCCCATGTGGCCTCGAGGTCCTG
---------------AACCAGGA---CATCTTTGAGGCCCC---CTAACACTCCAGCA--
-----------TTCTTGGCATGGCACTTTG----TGATATTTGCTCAAGTCTACATGTTT
GCTCTTAG--GGTTACGAGATACGCATGTATGACAGC
>Mro
AGCTACG---TAAA--TAGCTCCTCAAGAAGCACTATCAACGGAATCAACTTGCCCTATA
AAC-CAGTCATCTCATCAGCTCTTCTCTTTCC--AGAGATAAGTGGCAGCAAATTGAACT
TTGAAGGCATTTTTTTT---------GGAAGTCAGTTATTTGATGTAGTAACCTTAAAAT
GTTT---GAG--GA-ACATGG-CACAG---------------------------------
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-----------------------------TTGATAGAAGTCAAGACTTGGG-GTCCAAAA
GATCTGAGTTTAAATCCCT-GCTCTGACCCTTAGGGGCTGTGTGACTACTCAACTTCT--
GC----------------------------------------------------------
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------------------------------------------------------------
---------------------------------------------TAAG-GTTT----AC
CTGCCCAGTT----ACATATTACAT----------------------TTGCATGGGTAAA
GGGAAT---TCCCCTGCCAGTGAT------------------------------------
------------------------------------------------------------
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------------------------------------------------------------
-------------------------------------ACTGCATATTCTTGATGTATTAC
TGTAACTCTATATT-GTATCCTAATGTCTCCACTCTCCAATTATG---AGGCTA------
--TTAC------AATCAGTTGTTGTC----CTTTGTTTTGGAAGAGGACCAAAATGGCAT
CACTATGTTGGGGTC--------AACTGTGTCTGACTGGCTGATCAGACCAATATGAGCT
TGGAACATTCTACCCCAGAACGGGAGCAAATAATCCATGTGAACATCTAGGG-TAGAGAT
GTCTCTCAATGTGCCCATCTCATATT------------------------TCCCCT-AC-
------TTTCA-TGGAAAGAGCACTAGG---------------CTAGAATTCTAATCCCA
GCTTAGCTGGCCACGGACTTAAT-------CTCTGTCTTTGACCGGATCACTTTGCTCCT
CAGTTTCCTTCACTATGGAA-------TGATCAGTTGG---GATCAGGA---CAGGGGTA
GGGAACCTGTAGCCTTGAGACCAC---GTGGCCTCTAGGTCTTCAAGTGCGACCCTTTGA
CTGAATCCAAATTTCACAGTCCAAACCCCCTTCATAAAAGGATTTGTTCTGTATAACTTG
GACTCAGTCAAAAAGCCGCACCCAAGGACCCAGAAGGCCACATGTGACCTCAGGATCACA
GGTTCCCCACCCCTGAACTAAGA---CATCTTTGAGGTCCC---TTAACACTCCAGTA--
-----------TTCTTGGTAGGGTTCTTTGTATGTGATATTTGCTCAAGAGTACACGTTT
GCTCTTAG--GGTTACGAGATACGCATGTATGACAGT
>human
TCGCTG----AGGGTGGGACTGTGGCTTCAGTACC----------AGGAGTTGAGCTGCA
CTCTCAGCCTGGCATCTCAGCACTCTCTTCCCAGATAAATTACAGGGAGCAGGAGGCACT
TGAAGATACTGTGCTAACTTATGAAGAACACCTTGATTTTGTTTGGTTTTGCTATTGGTA
GGC---------------------------------------------------------
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-----------------------------------------------------------C
AATATGGTATTCACAGCAAAAGACAGGGGAAGAGGAGTGAGACCTGGGAGTAGATTGTTT
GTTTTCAG--GGCTATGAGATACACATGTTTGATAGT
```

**MARKER 182**

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>WALLSI1A
------------------------------------------------------------
---------------------TGCATCCTGGGCCATCTCCAGTCATCCTGATCTATATCT
TGCCACTGGACCCAGATGGCTCTGGAGGAGAAAGTGAGGCTGGTGACTTTGCACAGCCCT
CCCTCACTTAAATCCAATTCACTTGCAAGTCATGKCATCACCTCCCTGATGTCATGGTCC
TCTTTGAGAACAAAGGACAAACAA---CAA------------------------------
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>SPIN_NA_6_Et
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------------------------------------------------------------
-----------------------------------------CAGTGGTTCTCAACCTTCC
TAATGCCGCGACCCTTTAATACAGTTCCTCATGTTGTGGTGACCCCCCAACCATAAAATT
ATTTTCGTTGCTACTTCATAACTGTAATTTTGCTACTGTTATGAATCGTAATGTAAATAT
CTGATATGCAG-ATGTATTTTCATTGTTACAAA----------TTGAACATAA-------
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>MdoRep1
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------------------------------------------------------------
------------------------------ACCCTAAGGACCATGGGACCTTTCCATCTG
ACTTGCAGCTGAAA--CCTTCCATATGTGTTGTCTCCCCCATTAGAATGTGAGCTCCTTG
AGAGCAGGGACTGTCTTACTTTTCTATTTGTA-TCCCCAGCGCTTAGCACAG-------T
GCTTTGCACATAGTAAGTGCTTAATAAATGCTTTATTCATTCATTCATT-----------
------------------------------------------------------------
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------------------------------------------------------------
----------------------------
>Mdo
-TATTG-CTCGCCCAG--GTAAGTTGGCCATGGCTGAGGGCGGAATGAGGA-AGGACTTA
AGAGCCATAGTCAAAGC----ATGACTTCCGTGCCATTCCATTTCTCTGTACCAGCTGGC
ACT---------------------------------------------------------
------------------------------------------------------------
---------------------------CAT-CACCCC---CCAGGCAAATCCT--TTCTT
CTTCCTCTCTTTTCTTTCCCATCCCATCTCTTT---------------------------
--TCTTCCTTTCTCCTTCTCACT---TTCCTCAATCCTC---------------------
CCATTGCCCTTCCCTTCCTTC---------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------TTCCTC-----TCCTTGCATATTGTCC-TCCATTAGAATGTATTCTCCTTG
AGGTCAAAGACTGTTTTGTCTTTGTCTTAGCA-TCAACTGAT------GGAAAA-----T
GGCTCTGAATAA-TTGTTGATTAATTCCTCC--------------CTTTTCTCCTTTCTT
TTCTGCTGATCCTTAATAAGGAATTGGGCAGTGAGTGCCCTCTACAGCTCTCTCTTCCCT
GGGAGTCTGTAAGGTGT-TCTGGATGG-GGCTGGGGATCAGGTGTCTGCTTCTGGAATGG
CCTTTACCTCTTATGGGCAGAGGTGGGG-TCAATAACTCACAATTGGATCCCCTTCTAG-
-GATGAAGATGGGAAGCAGCTGTCAGAT
>Dvi
-TATTG-CTGGCCCAG--GTAAGCCGGCCATAGCTGAGGGCCAGATGAGGA-AGGGCTGA
AGAGTCATGGGCAAAGC----ATGACTTTGTTGTCATTCCCTTTCTCTGTACCAACTGGC
ACT---------------------------------------------------------
------------------------------------------------------------
---------------------------CAT-CA-CCT---CCAGGCAAATCCT--TTCTT
CTTCCACTCTTTCCTTTCCTAACCCATATCTTT-------------TCTCTCCTTCTCTC
TTCTCTCTCCCTTTCTCCTCACTCTCCTCCTCAATCCTCTTCCCTTCCTTTTTCAGTTTC
CTTCTGCCCATTGTCC------TTTCTCTCCTTT---CTCTCCTTGCATGT---------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------------------TGTCC-TCCATTAGAATGTATGCTCCTTG
AGGTCAAAGATTGTTTTGTCTTTGCCTTAACA-TCAGTTCATTGCCTAG----------T
GG-ATGGCATAA-TTATTGATTGATTTCTCC--------------CTTTCCTCCTTTCTT
TNCTGCTGATCCTCAACTGGAAATTGGGTAGTGAGTGACCTCTACAGCTCTTCCTTCCCT
GGGGGTCTGGAAAGTAT-TCTGGA-GGGGGCTGGGGATCAGGTGTCCGATTCTGGAATGG
CCTTTGCCTGTTATGGGCAGAGGTGGGAGTCAACAACTCACAACTAGATCCCCTTCTAG-
-GATGAAGATGGGAAGCAGCTGTCAGAT
>Mnu
GTATTGCGTGGCCCAG--GTAAGCTGGCCATAGCTGAGGGCCAGATGAGGA-AGGGCTGA
AGAGTCATGGGCAAAGC----ATGACTTTGTTGTCATTCCCTTTCTCTGTACCAACTGGC
ACT---------------------------------------------------------
```

```
------------------------------------------------------------
---------------------------CAT-CG-CCT---CCAGGCAAATCCT--TTCTT
CTTCCACTCTTTCCTTTCCTAACCCATATCTTT-------------TCTTTCCTTCTCTC
TTCTCTCTCCCTTTCTCCTCACTCTCCTCCTCAATCCTCTTCCCTTCCTTTTTCAGTTTC
CTTCTGCCCATTGTCC------TTTCTCTCCTTTTTCCTCTCCTTGCATGT---------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------------------TGTCC-TCCATTAGAATGTATGCTCCTTG
AGGTCAAAGACTGTTTTGTCTTTGCCTTAACA-TCAGTTCATTGCCTAG----------T
GG-ATGGCATAA-TTATTGATTGATTTCTCC--------------CTTTCCTCCTTTCTT
TTCTGCTGATCCTCAACTGGAAATTGGGTAGTGAGTGACCTCTACAGCTCTTCCTTCCCT
GGGGGTCTGGAAGGTGT-TCTGGA-GGGGGCTGGGGATCAGGTGTCCGATTCTGGAATGG
CCTTTGCCTGTTATGGGCAGAGGTGGGGGTCAACAACTCACAACTAGATCCCCTTCTAG-
-GATGAAGATGGGAAGCAGCTGTCAGAT
>Dgo
-TGNTG-CTGGCCAAG--GTGAGCAAAAGGAGGACGAGGGTGGGGTGAGGA-AGGGC-T-
GGAGTCATGGCCAAAGC----CTGACGTTGACTTTATGCCAGTTCTCTGAACCACCCCTC
ACT---------------------------------------------------------
------------------------------------------------------------
---------------------------CAT-CA-CCC---CCTAGCAAATCCT--TTCTC
TTTCTCCT--CATCTCCCTCCGTGCCTCTCTT---------CCCTTTCCCTTCCTCTCGG
TTTTCTTTCCCTTCCCTTTTTCTTTTCTTCCAAATTCCTCTTCTCTTCTCTT-CCCCC--
----TTTTTCCTCTTC------TTCTCCCTCTTCTTGCTGTCCTTCCATGC---------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
TACTTCTC-------CCTTCCTTGTGTACTATGTCC-TCCATTAAACTCTAATCTGCTTG
AAGTCAGGGGCTGCTTTGCCTTTGTTTTCACA-TCAGCTCACAGCCTGAAACAC-----A
GTGACTGAACAA-TTGCTTGGTGATCTATTC----------CTACTTCTCTTCCTTCC-T
CTCTGCTGTTCCTCAACGTGGCACGGGGCAGCATGTGCCATCTACAACCTTCCCTTCCCT
GGGAGTCTGGAGGGTGA-------------------GCCAGGTGTCTTCTCCTG-----G
CCTTTACCTCTTATAGGTAGAGGTAAGG-TCCATCATTCCCAACTGCAATCCCTTTCAG-
-GATGAAGACGGGAAGCAGCTATCAGAT
>Scr
-TGTTG-CTGGCCAAG--GTGAGCAAGGGA-GGCTGAGGGTGGAGTGAGGA-AGGGC-T-
GGAGTCATGGTCAAAGC----CTGACTTGGACTTTATGCCAGTTCTCTGAACTATCCCTC
TCT---------------------------------------------------------
------------------------------------------------------------
---------------------------CAG-GA-CCC---CCTGGCAAATCCT--TTCTT
TCTCCTCA----TCTCCCTTCTTGCCTCTCTT---------CCCTTTTCCTTTCTTTCTG
TTTTCTTTCCCTTCCCTTTTTCTTTTCTTCCAAATTCCTCTTCTCTTCTCCTTCCCCC--
-TTCTCTTTCCTCTTC------TTCTCCCTTTTCTTGCTCTCCTTCCATGCTACTTCTCC
TTTGTGCCCTT-------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------------------TGTGC-TCCATTAGAATCTAATCTGCTT-
-AGTCAGAGACTGTTTTGCCTTTGTTTTTGCA-TGAGCTCACAGCCTGAAACAG----CA
GTGACTGAACAA-TTGCTTGGTGATTGATTC----------CTACTTCTCTTCCTTCC-T
CTCTGCTGATCCTCCACATGGCACTGGGTAGCGAGTGCCATCTACCACCTTCCCTTCCCT
```

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GGGAGTCTGGAGGGTGA-------------------GCCAGATGTCTTGTCCTG-----G
CCTTTACCTCTTATGGGTAGAGGTAAGC-TCCATCATTCCCAACTGTAATCCCTTCTAG-
-GATGAAGATGGGAGGCAGCTGTCAGAT
>Pgu
-TGTTG-CTGGCCAAG--GTGAGCAAGGGA-GAATGAGGGCAGGGTGAAGG-AGGGCCT-
AGAGTCATGGTCGAAGG----CTGACTAGGACTTAATGCCATTTCTCTGAAGCATTCCTT
GCA---------------------------------------------------------
------------------------------------------------------------
---------------------------CAT-CA-CTC---CCTGGCAAGTCTTCTTTCTT
CTTCCTC-------CCCTCCAT----------------------TTCCCTTCCTTTCTCT
TTTCTTTTTCTTTCCTTCT-CCCTTTCTTCTTTATTCCTCTTCTCTTCT----CCCCC--
-TTCTTCCTCTTCTTC----TCATTCTTCTTTCCCTGCT-GCCTCTCATC----------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------------------TTT
TATTTCTGTC-----CTATATATGTGCACATTGCCCCCTCATTAGAATCTAATCTGCTTG
AAGTCAGGGGCTGTTTTGCCTTTGCCTTTGC--TCAGCCCATGGATTGGCACAG-----T
GGCTCTGAACAAATTGCTTGTTGTTTGATTC----------CTACTCCCCTTT----GTT
CTCTGCTCTTCTTCAACTAGACTCTGGGTAGAGGGTTCCCTCTATAGTCTTTCCTTCCCT
GGGAATCTGGAAGGTAATTCTGGA------GAGTGGGACAGGTGTCTCCTCCTGGAATGA
TCTTTGTTTATTATGGGCAGAGGTGGGGGTCAATCACTCACAACTGGAACCCCTTCTAG-
-GATGAAGATGGGAAGCAGCTTTCAGAT
>Iso
-TGTTG-CTGGCCAAG--GTGAGCAAGGGA-GAATGAGGGCAGGGTGAAGG-AGGGCCT-
AGAGTCATGGTCAAAGG----CTGACTTGGACTTAATGCCATTTCTCTGAAGCATTCCTT
GCA---------------------------------------------------------
------------------------------------------------------------
---------------------------CAT-CA-CTC---CCAGGCAGGTCTTCTTTCTT
CTTCCTC-------CCCTCCAT----------------------TTCCCTTCCTTTCTCT
TTTCTTTCTCTTTCCTTCT-CCCTTTCTTCTTTATTCGTCTTCTCTTCT----CCCCC--
-TTCTTCCTCTTCTTC----TCATTCTTCTTTCCCTGCT-GCCTCTCATC----------
------------------------------------------------------------
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------------------------------------------------------------
---------------------------------------------------------TTT
TATTTCTGTC-----CTATATATGTGCACATTGCCCCCTCATTAGAATCTAATCTGTTTG
AAGTCAGGGGCTGTTTTGCCTTTGCCTTTGC--TCAGCTCATGGATTGGCACAG-----T
GGCTCTGAACAAATTGCTTGTTGTTTGATTC----------CTACTCCCCTTT----GTT
CTCTGCTCTTCTTCAACTAGACTCTGGGTAGAGGGTTCCCTCTACAGTCTTTCCTTCCCT
GGGAATCTGGAAGGTAATTCTGGA------GAGTGGGTCAGGTGTCTCCTCCTGGAATGA
TCTTTGTTTATTATGGGCAGAGGTGGGGGTCAATCACTCATAACTGGAACCCCTTCTAG-
-GATGAAGATGGGAAGCAGCTTTCAGAT
>Tro
-TGCTG-CTGGCCAAG--GTTGGTGGCCAA-GGGC------AGGGTGAGGA-AGGGCCT-
AGAGCCATGGGCAAAGCCTGCCTGGC-TTTACTTGAAGTCATTTCTCTGAACCACCTTTC
CCT---------------------------------------------------------
------------------------------------------------------------
---------------------------CAT-CA-TCC---CCTCGCAAGTCCTCTTTCTT
CTTCCTC---TCCTCTCTGCACGCCTCTTCCCATGT---------TCCCTTCCTGTCTCT
CTTCTTTCCTTTCTTCCCCATTCCTCTTTCTCTTCCCTT--------------CCCCC--
-TTCCTCTGCTCTCTCTTC---TTGCTCTCCTTCCAGTTTACTTCTTCCCTTTT------
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------------------------------------------------------------
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------------------------------------------------------------
-ATTTTTGTT-----TGCTGTATGTGGACTTTGTTTCC-CATTAGAATCTAATCTGCTTG
AAGTCAAGGGCTGCTTGGACTTTGTCTTTGCCCGTAGCC--TGG---CACACAG-----A
GGCTCTGAACAA-TTGCTTGTGGAGTGATGC----------CTACCTTTCTTTCCTTCTT
CTCTGCTGTTACTTAACTACACTTTGGGTAGCGAGTGTCCTCTAGAGTCCTCCCTTCCCA
GGGAGTCTGGAGGGTGGTTCTGGA------GGGCAGATCAGGTGTCTCTTCCTCCCGTGG
CCTTTGCCTCTACTGGGCAGAGGTGGGG-TCAATCACTCACACCTGGTACCTCTTCTAG-
-GATGAAGAGGGGAAGCAGCTGTCAGAT
>Ppe
-TGTTG-CTGGCCAAG--GTGAGCAAAGGA-GGCC-----AATGGTGAGAA-AGGGCCT-
AGAGCTGTGGTCAAAGC----CTGGCTTTGACTTGATGCCATTTCTCTGAACCATCCCTC
ACT---------------------------------------------------------
------------------------------------------------------------
---------------------------CAT-CA-TGC---CCT-----GTTCTCTTTCTT
CCTCTTC---TCCTCCCTGCATGCCTCTTCCCCCTT---------TCCCTTCCTTTCTCT
T---CTTCCTTTCCTCCTCATTTCTCTT-CTCTTCTCTT--------------CCCCG--
-TTCCTCTTCTCCTCCCTCTCCTTGCTCTTCTTCCATGCTACTTCTCCTTCCCTTTTTTT
TTGGTCCTATGTATGTGTACTTTATTTTCCCATTAGAA---CAGTGGTTCTCAATCTTCC
TAATGCCGTGACCCTTTAATACAGTTCCTCATGTTGTGGTAACCCCCCAGCCATAAAATT
ATTTTTGTTGCTACTTCATAACTGTAATTTTGTTACTGTTATGAATCATAATGTAAATAT
CTGATACGCAGGATGTATTTAAATTGAAAATAACCTACAGGTTGAGAACTGCTG------
---------------------------------------CATTAGAATCTAATCTGCTTT
AAATCAAGGGCTATTT-GCCTTTGTCTTTGCTCA-------------CACAGAG------
-GTTCTGAACCA-TTGCTTGTGGACTGATTC----------CTACCTTTCCTTCCTTCTT
CTCTGC----------------ATTGGGTAGCAAGTGCCCTCCAGAGTCCTCC-TTCCCT
GGGAGTCTGGAGGGTGGTTCTGGA------AGGCAGACGAGGTGTCTGCTCCTGGAATGG
CCTTTGCCTCTACTGGGC--AGGTGGGGGGCAATCACTCACAACTGGTACCCCTTCTAG-
-GATGAAGATGGGAAGCAGCTGTCAGAT
>Tvu
-TGTTG-CTGGCC----------------------------AGGGTGAGCCGAGGGCCT-
AAAGTCATGGTCAAAGC----CTGACTTTGACTTTATGCCATTTCTCTGAACCATTCCTC
ACT---------------------------------------------------------
------------------------------------------------------------
---------------------------CAT-CA-TCC---CCAAGCAAATCCTCTTTCTT
CTTCCTC---TCCTCCCTCCATGCCTCTTCC-CTTT---------TCCCTTCCTTTATCC
TTTCTTTCCCTTCTCTTCTTCCTTTCCTCCTCATTCCTCTTCTCTTCCT----CCCTTC-
-------------TTCTTCTTCTTGCTCTCCTTCCATGCTACTTCTT--CCCCTTTATTT
TTG---------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------T-----CCTATATATGTGCACATTGTCCCCTATTAGAATCTAATCTGCTTG
AAGTCAAGGGCTATTTTGCCCTTATCTTTGCTCATGGCC-----TGACACACAG-----T
GGCTCTGAACAA-TTACTTGTGGATTGATTC----------CTACCTTCCCTTCCTTCTT
CTCTGCTGTTCCTTAACTAGGCATTGGGTAGCAAGTGCCTTCTATAG-------------
-------------CTGGTTCTAGA------GGGCGGGCCAGGCATCTGCTCCTGGGATTG
TCTTTGCTTCTACTAGGCAGAGGTGGGG-CCAATTGCTCACAACTGGTACTCCTTCTAG-
-GATGAAGATGGGAAGCAGCTGTCAGAT
>Mro
-TGTTG-CTGGCCAAG--GTGAGCAAGAAA-GGCCCAGGGTAGGGTGAAGA-AGGGCCT-
AGAGTCATGGTCAAAGC----CTGACTTTGACTTTATGGCATTTCTCTGAACCATCTCTC
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ACT---CAATATCT---GGCTCAGGAGAAGAAGGTGAGATTGGTGACCTTGCACAGCCCT
CTCTCACTCAAATCAAAGTCAGCTGCAAGTCACGTCATCATCT---TGATGTCATGGTCC
TCTTCGAGAACAAAGGACAGACA----CAAACAATCC---CCTAGCAAGTCCTCTTCCTT
CTTCCTC---TCCTCCCTTCATGCCTCTTCTCCCCTT-------TTCTTCCTCTCCTCCT
CTGTCTTCCCCTCCCCTCCCCTCCTCTCTCTCTTCTGTT--------------CCCCTTT
CTTC---CTTTTCTCCCACTTCTTGCTCTCCTTTCACACTACTTCCCTTTTATTTTTGT-
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------CCTATGTATGTACATGTTGTCCCCCATTAGAATCTGATCTGCTTG
AAGTCAAGGGCTATTTTGCCTTTGTTTTTGCTCATGGCC-----TGATACATGG-----T
GGCTCTGAACAA-TTGCTTGTGGGTTGATTC----------CTACCTTCCCTTCCTTCTT
CTCTGCTGTTCCTTGACTAGC-ATTGGGTAGTGAGTGCTCCCTACAGTTCTCCCTTCCC-
TGGGAGTTGGAGGGTGGTTCTGGA-------GGGTGGCCAGGTGTCTGCTCCTGGAATGG
CCTTTGCCTCTCTTGGGTAGAGGTGGGG-CCAATCAGTCACAACTGGTACCCCTTCTAG-
-GATGAAGATGGGAAGCAGCTGTCAGAT
>Ptr
-TGTTG-CTGGCCAAG--GTGAGCAAGAGA-GGCCCAGGGAAGGGTGGAGA-AGA-CCT-
AGAGTGATGGTCAAAGC----CTGATTTTGACTT-ATGCCATTTCTCTGAACCATCTCTC
ACT---CAATATCC---AGCTCAGGAGAAGAAGGTGAGGTTGGTGACCTTGCACAGCCCT
CTCTCACTCAAATCAAAGTCAGCAGCAAGTCATGTCATCATCT---TGATGTCACGGTCT
TCTTTGAGAATGAAGGACAAACA----CAAATAATCC---CCTAGCAAGTCCTCTTTCTT
CTTCCTT---TTCTCCCTTCATGCCTCTTCTCCCCCT-------TTCTTTCTCTACTCCT
TTGTCCTCTCCTTCCTTTCCCTCTTCTCTCTCTTTTCTCTTCCTCTTCCTT---CCTTTT
CTTC------------CACTTCTTGCTCTCCTTTCATGATACTTCTCCTTCCCTTTT---
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--ATTTTTAT-----CCTATGTATGTGCATATTGTCCCCCATTAGAATCTGATCTGCTTG
AAGTCAAGGGCTATTCTGCCTTTGTTTTTGCTCATGGCC-----TGACACGCAG-----T
GGCTTTGAACAA-TTGCTTGTGGATTAATTC----------CTACCTTCCCTTCCTTC-T
CTCTGCTGTTCCTTAACTAGC-ATTGGGTAGCGAGTACCTTCTACGGTCCTCCCTTCCC-
TGGGAGTTGGAGGGTGGTTCTGGA-------GGGTGGCCAAGTGTCTGCTCCTGGAATGG
CCTTTGCCTCTC------AGAAGTGGG--CCAATCAGTCACAACTGGTACTCCTTCTAG-
-GATGAAGATGGGAAGCAGCTGTCAGAT
>Vur
-TGTTG-CTGGCCAAG--GCGAGCAAGGGA-GGCC-AAGGAGGGGTGAGGA-AGGGCCT-
AGAGTCATGGTCGAAGT----CGCT------------------TCTCTGAACCATCTCTC
ACT---------------------------------------------------------
------------------------------------------------------------
---------------------------CAT-CA-TTG---GCTAGCAAATCCTCTTTCTT
CCTCCCC---CTCTCCATNCCTCTCCCCCCTTTCCCTTTGTCTTTTCTTTCCCTTTGTCT
TTTCTTTCCCTTCTCTTCTTCCTTTCTTCCTCATTCCTCTTCTCTTCCCTT--CCCCCCT
CTTCTTCCCCTTCNTCCTTTTCTAGCTATCCNTCGATGCCACTTCTCTTTCCTTTTT---
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--ATTTTTGT-----CCTATGTATATGTATGTTGTCCCCCATTAAAATCTAATCTGCTTG
AAGTCAAGGGATGTTTTGCCTTTGTCTTTGCTCGCAGCC-----TGACACACACACTGAC
AGCTCTGAACAA-TTGCTTGTTGATAGATTC----------CTACCTCCCCTTCCTTCT-
```

```
--CTGCGGTTCCTCAACAAGGCACTGGGTAGGG--------------TCCTCCCTTCCC-
TGGGGTTTGGAGGGTGGTTCTAGA------GGGCAGGCCAGGTGTCTGCTCCTGGAATGG
CCTTTGCCTCTACTGGGCGGAGGTGGGG-CTAATCACTCACAACTGGAACCCTTTCTAG-
-GATGAAGATGGGAAGCAGCTGTCAGAT
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**MARKER 194**

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>WSINE1
------------------------------------------------------------
------------------------------------------------------------
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---------------------------GAGGGGCAGCTAGGTGGTGCAGTGGATAGAGCA
CCAGCCCTGGAGTCAGGAGGACCTGAGTTCAAATCCAGCCTCAGACACTTA-------CT
AGCTGTGTGACCCTGGGCAAGTCACTTAACCCCAATTGCCTC------------------
---AAAAAAAAAAAAAA-------------------------------------------
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
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>Mdo
AGTCAGCATTTGAACCCCTCGTGGCAAATGGAGCCCCAGCATCTCTTGTTCCCAA--GTA
AGTG---TTTCCCT-AATAGGATGTTTAGCAAGGAGGCACTTGAGTCCAAGTTATTCTTC
CCAAA--CCTGTACTTATTAAGAACAGA--------------------------------
---CTTCATTAC------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------CCAGTAACTG---TTTCTCTTTGCC------TGTTATGTT
AGTTCAAGATAGTATCTGTCACCTTCAGAGACTTAGGCAGGATTAAAATTCAAA-TGTGC
T----------------------------------------TAGCTAAA-TTGTTACCAG
---TAAAATTAGCCTAATTCCTTC-CCCCTCAACCACATGAAGAAAGGAGTTATGGCCAA
GTTAGATGTAGCCTTAAAAAATGTCACTTTTCATGAGATCTCTGACTCCTTTTTTT----
-----CCTTCCATTAG--GCCTGGAT
>Dvi
AGTCAGCATTTGAACCCCTTGTGGCAAATGGAGCCCCAGCATCTCTTGTTCCCAA--GTA
AG-----TTTCCCT-AATAGGATGTTTAGCAAGGAAGCAAACAGA---------------
-------GC---------------CAGA--------------------------------
---CTTCATTAC------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------CCAATAACTG---TTTTTCTTTGCTTATT-ATATTACGTT
GGTTCAAAATAGTATCTGTCACCTTCAG-GATTTAGGCAGGATTAAAATTCAAA-TGTGT
AGATCTTTCTCATAGCCCTACTCTCTTTTCATAATCCTTCTTAGCTAAA-TTGTTAACAG
---TAAAATTAGCCTAATTCCTTT-CCCTTCAACCATATGAAGAAAGGAGCTACAACCAA
GTTAAGTGTAGTCTTAAAAAATGTCACTTTTCCTGAGATCTCTGACACCTTTTTTTTTTT
TTTCTCCTTCCATTAG--GCCTGGAT
>Dgo
ACTCGGCATTTGAACCCTTGGTGGCAAATGGGGCCCCAGCGTCTCTTGTTCCCAA--GTA
AGTAATGGCTCCCTAAAT---AAGTTT-ACAAGGAGGTAAACA-----------------
-------GCCTGAATTTAAGTGATTCTGCCCAA-CCTGTACT--GAACATCAGAATCATA
AAAATTAATGAT------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------CCGATAATTG--------TTTCTCTATAC-CTGTCATGCT
GGTTCCAGATACAATCTGTTGGCTTCAGAGCTTTTAACAGGATTAAATTTCAAA-TACCT
TGATCTTCATATT---CCCAGCATGTTA--------------------------------
---CTACATTAATATAATT-CTTCTCCTGGGTT--ACATAAAGAAAGAGGCCATGGCTAA
GT--------CGCA-----CACGTCACATCCCAAGAGGTTTCTGACTC---------CTT
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TTGTTCCTTCCATTAG--GCCTGGGT
>Scr
ACTCGGCATTTGAACCCTTGGTGGCAAATGGGGCCCCAGCGTCTCTTGTTCCCAA--GTA
AGTAATGG------------AAAGTTT-AATAGAAACTTAATAGAAAGTTTAACAAGGAG
GTAAACAGCCTGAGTCTAAGTGACTCTGCCCAA-CCTGTACTTGGAACATCAGAACCATA
AAAATTAATGAT------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------CCGATAATGG--------TTTCTCTCTGC-CTATCATGCT
-GTTCCAGATACAATCTGTTAGCTGCAGAGCCTTGAGCAGGATTAAATTTCAAA-TACCT
TGATCTTTATATT---CCCACTGTGTTG--------------------------------
---CTACATTAACATAATTCCTTCTCCTGGGTT--ACATAAAGA----GGCCATGGCCAA
GT----------------------CACATCCCAAGATG-------------------CTT
TTGTTCCTTCCATTAG--GCCTGGAT
>Bil
ACTCGGCATTTGAACCCCTGGTGGCAAATGGAGCCCCAGCATCACTTGTTCCCAA--GTA
AGTCAGAGTTCCCTTTATAGAATGTTTAGCAAGGATGGAA--GGA---------------
-------ACCTAAATCTAAGAGATTCTGCCTAGACCTGCTT---GTAAAGAATATCATAT
CAAATTATTTAC------------------------------------------------
------------------------------------------------------------
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--------------------CCAATAACTC-------TTTTCTCTTTGC-ATGTCATGTT
GGTTCAGGATAGATT----CACTGTCAGAGCCTTATGCAGGGTTAGTTTTTAAA-TACTT
AGATCTTCTTCCTATTCCCACTTGGTTTTCATAAC--TGTCTCACCAAA-TCGTTACCAA
---TAATATTAATATAATTCCTCT-CACGAATT--GGATCAAGAAAGAAGCCTTGTTCAA
GTTAGATGTAGCCTTGAGAAATGACACTTCTCAAGAGATCCCCAATTG---------CCT
TTATTTCTTCCATTAG--ACCTGGAT
>Ppe
ATTCAGCATTTGAACCTCTGGTCGCAAATGGAGCCCCAGCATCTCTTGTTCCGAA--GTA
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>Tvu
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A----TGTGACCTTCGGCAAGGCACTTAACCCTGATTGCCTCATCTCCCCCCCAAAGAAA
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**MARKER 205**

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----TGGGG---------------------------------------------------
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GAGGAGGTTG---------GCGGG------------------------------------
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G----CGCTTGGTGTGG-GGCCGTTGAGGCGACACCGAGTCCC-AGCCCCGCTTTCCCAT
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AGATCCC----------------------------------------ATCATTGCTGCTT
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CATCTTCTC
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CATCTTCTC
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GT-TCACAGCCA-CCCGAGGCT---GGCCTCAAGAGGACCCCC-TGCAGCCCTTGCCCCT
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**MARKER 206**

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CTGCCCCTC---------------------------------------------------
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CGGAGCCTCC---TCCCTGTCTAG------------------------------------
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>Dvi
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>Tro
CCTTAGGAAAACA--CTGCAGA-GAAAGAACAGAAAATGCATTAACTGCTCTAGGTTGGC
ACCACTTAGCCAACAGAAC-----TGC-----TTTTCAGTTCAAATTCCTTAATACC-AG
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GGATTTTAACTCAGGTCTTCACC--TCCACAGCCAGTACTCTTTCTACTG-CCCCCT-CA
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CACCTTCTGTTAC--CTTCTTCTCCTT
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-----CTTCC---TGCCCCTCTAG------TTTTTTTGGGGGGTAGGGGGGTGGG--GAG
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CACCCACTGTTAC--CTTCTTCTCCTT
>Mro
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>Vur
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CACCTTTTGTTAC--CTTTTTTTCCTT
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