

The images below show alignments of lncRNA1-7 against RNA-seq and the corresponding genomic sequences.

### Alignments of lncRNA1-7 against RNA-seq sequences.

#### lncRNA1 against TCONS\_00179561

TCONS_00179561	<u>GTCCATTGATCACAACATTTTACTAATTACATTTGATTCCTCCTCAATGATTCGACAAACTAAACCCGAAAATGTGGACCACTCATATCCCTGGCGATCCACCCGGCAGTCCG</u>	120
lncRNA1	<u>GTCCATTGATCACAACATTTTACTAATTACATTTGATTCCTCCTCAATGATTCGACAAACTAAACCCGAAAATGTGGACCACTCATATCCCTGGCGATCCACCCGGCAGTCCG</u>	115
TCONS_00179561	<u>GCAGCAGCAACAGCAGCTCTGACAGCGCGGGCCGAGAGCAGCAGCAAC.....AACAGAGCAGCGAANCTGAAGACATGGCCATATACGA</u>	207
lncRNA1	<u>GCAGCAGCAACAGCAGCTCTGACAGCGCGGGCCGAGAGCAGCAGCAAC.....AACAGAGCAGCGAANCTGAAGACATGGCCATATACGA</u>	235
TCONS_00179561	<u>CTAAGATGACCACAAAACCCACATGATCACTAGGAACAAAACAGGTACATGCACATGTGGAAATGGGAATAGCTTGCAGCAGCAGCAGCAGAGAGATTGTTATTGTGATCAAAGAT</u>	327
lncRNA1	<u>CTAAGATGACCACAAAACCCACATGATCACTAGGAACAAAACAGGTACATGCACATGTGGAAATGGGAATAGCTTGCAGCAGCAGCAGCAGAGAGATTGTTATTGTGATCAAAGAT</u>	349
TCONS_00179561	<u>TATTGATTTATTGGTTAATTGTAATTCGTTAATTATTATTGTTCGTTTCGTTCTTATTGGTCTATCTGTTAATTGGTAGCTTTTGACC</u>	420
lncRNA1	<u>TATTGATTTATTGGTTAATTGTAATTCGTTAATTATTATTGTTCGTTTCGTTCTTATTGGTCTATCTGTTAATTGGTAGCTTTTGACC</u>	438

#### lncRNA2 against TCONS\_00109592

TCONS_00109592.seq	<u>TCTTCTACCACTTCCACCGTCTCCTTTTGTCTGAGATGTCACAACCTCTGTACATTGTTCTGTGAGATTCTATTGAAACGGCAAAATCCAAAGGATTAGAAGCAATCTGATGT</u>	120
lncRNA2	<u>TCTTCTACCACTTCCACCGTCTCCTTTTGTCTGAGATGTCACAACCTCTGTACATTGTTCTGTGAGATTCTATTGAAACGGCAAAATCCAAAGGATTAGAAGCAATCTGATGT</u>	120
TCONS_00109592.seq	<u>TGGAGCCATTCACAACCTTCCAAATCAGTCTCTTTTCAACAACCTTTGGCCCTCCAAAGCTCTCCATCTCCAAGAGTGTCTGAAACGATGTCGGAACCTCTTATGTTGCTT</u>	240
lncRNA2	<u>TGGAGCCATTCACAACCTTCCAAATCAGTCTCTTTTCAACAACCTTTGGCCCTCCAAAGCTCTCCATCTCCAAGAGTGTCTGAAACGATGTCGGAACCTCTTATGTTGCTT</u>	240
TCONS_00109592.seq	<u>TCTTGGTTGGTTGTGTCGACGGCAGGTTAGGAAGGGCATTCACTGCTCCCAATGATGAAATTTTTTACCAGATGATCAAGCATTTGTTCCACTTCTCTAAGTTGTTGTT</u>	360
lncRNA2	<u>TCTTGGTTGGTTGTGTCGACGGCAGGTTAGGAAGGGCATTCACTGCTCCCAATGATGAAATTTTTTACCAGATGATCAAGCATTTGTTCCACTTCTCTAAGTTGTTGTT</u>	360
TCONS_00109592.seq	<u>GTCTGCAATGAAAATCAATATTGATACAAATGATGTTTAGATAATTTGTTATTAGCAATAAATTTGAAATCTCACTTAATCCCAATCATTGTTTTGCGCTTTGGTTGAGTA</u>	480
lncRNA2	<u>GTCTGCAATGAAAATCAATATTGATACAAATGATGTTTAGATAATTTGTTATTAGCAATAAATTTGAAATCTCACTTAATCCCAATCATTGTTTTGCGCTTTGGTTGAGTA</u>	471
TCONS_00109592.seq	<u>CTCCATGAATTTTATACATATACACAACAATCAAATTTATGTAATGGAACAAATGGGCTGTATTAGGAGAACCGGTATACATCTCAATTGAACCTTACTAATTAAAGTATTGTTAGGTT</u>	600
lncRNA2	<u>CTCCATGAATTTTATACATATACACAACAATCAAATTTATGTAATGGAACAAATGGGCTGTATTAGGAGAACCGGTATACATCTCAATTGAACCTTACTAATTAAAGTATTGTTAGGTT</u>	591
TCONS_00109592.seq	<u>TTGAGGGGATT</u>	612
lncRNA2	<u>TTGAGGGGATT</u>	603

#### lncRNA3 against TCONS\_00133884

TCONS_00133884	<u>TCTTCTCTCCAGTGTGTGTGGAGAAATTCGGCTTCAGATCAGCAAGAGGGATTAGAAATGTCITTCGAAATGGATCTTATTGTCATGATGTCGATGAGATAGATTCTCGTTTT</u>	120
lncRNA3	<u>TCTTCTCTCCAGTGTGTGTGGAGAAATTCGGCTTCAGATCAGCAAGAGGGATTAGAAATGTCITTCGAAATGGATCTTATTGTCATGATGTCGATGAGATAGATTCTCGTTTT</u>	120
TCONS_00133884	<u>GTCTGAGTCAATGATTTCGGATCAAGTCAAAAGAATTTATCTCCTGTCTAAAGAGGTTGAATCTTTTTGACCTAATTGAGATCATCACTCCGACAAAATTAAGTCTATATCGACCT</u>	240
lncRNA3	<u>GTCTGAGTCAATGATTTCGGATCAAGTCAAAAGAATTTATCTCCTGTCTAAAGAGGTTGAATCTTTTTGACCTAATTGAGATCATCACTCCGACAAAATTAAGTCTATATCGACCT</u>	240
TCONS_00133884	<u>CAACTTCATGAGAGCAAGGAAAGAAACAATTAAGTGGTTAGAAACCTAAATGTTTCCAAATTTGTAGTAATGGAAGGAATAGACAACTGCATGACA</u>	348
lncRNA3	<u>CAACTTCATGAGAGCAAGGAAAGAAACAATTAAGTGGTTAGAAACCTAAATGTTTCCAAATTTGTAGTAATGGAAGGAATAGACAACTGCATGACA</u>	348

#### lncRNA4 against TCONS\_00009270

TCONS_00009270	<u>TCCCACATGCAAGCTGAGACATTAATTGAGCACCAGAGTCTTAAACTCTTACTACCAGTTGTTGAATCTGAAGCCAAATGGCRAAGAAACCAATTACCATAGACATCAATACAATTGCC</u>	120
lncRNA4	<u>TCCCACATGCAAGCTGAGACATTAATTGAGCACCAGAGTCTTAAACTCTTACTACCAGTTGTTGAATCTGAAGCCAAATGGCRAAGAAACCAATTACCATAGACATCAATACAATTGCC</u>	120
TCONS_00009270	<u>TAGAAAAGCAAGCTCCAAAGTAAAAAAGGATCCTGCTCATTAGATATGACCAACTGGGTAGTAGAGGATCCCATTAAGAAAACCTTAATGGAAGAACTCCATATTTGGTAA</u>	240
lncRNA4	<u>TAGAAAAGCAAGCTCCAAAGTAAAAAAGGATCCTGCTCATTAGATATGACCAACTGGGTAGTAGAGGATCCCATTAAGAAAACCTTAATGGAAGAACTCCATATTTGGTAA</u>	240
TCONS_00009270	<u>TTTGTGTTGCACAGCTATGACTCGAAACCTTCCATTTTCCAGGGGAAAGCGGATCTTAGGGCAGTGCCTTAGAATCAGGAAATAGAACCTTTGCCAAAAATTTGGACATTCAAATA</u>	360
lncRNA4	<u>TTTGTGTTGCACAGCTATGACTCGAAACCTTCCATTTTCCAGGGGAAAGCGGATCTTAGGGCAGTGCCTTAGAATCAGGAAATAGAACCTTTGCCAAAAATTTGGACATTCAAATA</u>	360
TCONS_00009270	<u>ACAGAAAATCAAAACAACTTTGGAGTATAGAAATTTATCTCAACCGGATTCAGAAACAATGGATTGTA AAAACACATAATAAACGATTTGAGAAATCCCTCAGATTATTTTTTCTCAAT</u>	480
lncRNA4	<u>ACAGAAAATCAAAACAACTTTGGAGTATAGAAATTTATCTCAACCGGATTCAGAAACAATGGATTGTA AAAACACATAATAAACGATTTGAGAAATCCCTCAGATTATTTTTTCTCAAT</u>	480
TCONS_00009270	<u>GGAAATTCGGTCCACTCTTTAAATATTATAAATGTCCAGGGAAAGCATTATATGTCAATAATCTGCATTAGAAATCAACAAAACCTCACCTAATCTTGAATACCAGCCAAAATAACAA</u>	600
lncRNA4	<u>GGAAATTCGGTCCACTCTTTAAATATTATAAATGTCCAGGGAAAGCATTATATGTCAATAATCTGCATTAGAAATCAACAAAACCTCACCTAATCTTGAATACCAGCCAAAATAACAA</u>	600
TCONS_00009270	<u>TTTTTAAAAAATAATAATAAAGATAAAGAAAGAAATTTAATAAAAAGCATCCAATGAGATGAAGAAATACTGAACAACTCTCTCTTTAAGAAATCTCCGAAACCAACCGCG</u>	717
lncRNA4	<u>TTTTTAAAAAATAATAATAAAGATAAAGAAAGAAATTTAATAAAAAGCATCCAATGAGATGAAGAAATACTGAACAACTCTCTCTTTAAGAAATCTCCGAAACCAACCGCG</u>	717

# lncRNA5 against TCONS\_00262811

TCONS\_00262811  
lncRNA5  
TCATCACCTCCCAACTGACCTCTATTCTACTCTTAATCTTTACCTCATTGTGCACCTTACCCCACTAAATCAAATAAACTGAGAGTTAATTAATTTTGATTTTTCATTTTG 120  
TCATCACCTCCCAACTGACCTCTATTCTACTCTTAATCTTTACCTCATTGTGCACCTTACCCCACTAAATCAAATAAACTGAGAGTTAATTAATTTTGATTTTTCATTTTG 120

TCONS\_00262811  
lncRNA5  
TCTCTAATAAATTTCTGCTTCTCAGTTCTATTTTTTTTTAAATATTATATAAATGAAAAAATACTAAATCTAATTAATTAATAATTTAGCTAATCTGTGTCTTTTTATGTAATTTT 240  
TCTCTAATAAATTTCTGCTTCTCAGTTCTATTTTTTTTTAAATATTATATAAATGAAAAAATACTAAATCTAATTAATTAATAATTTAGCTAATCTGTGTCTTTTTATGTAATTTT 240

TCONS\_00262811  
lncRNA5  
CCTAATTACACCAATTAATAGTATTCTGAGCCACACAGCAAAATCTCAATATATTATTATTTCATGAAATGAGGAGAGTAATAGGCTTTCCTCAAGTACCAAGTGTCTGC 360  
CCTAATTACACCAATTAATAGTATTCTGAGCCACACAGCAAAATCTCAATATATTATTATTTCATGAAATGAGGAGAGTAATAGGCTTTCCTCAAGTACCAAGTGTCTGC 360

TCONS\_00262811  
lncRNA5  
TAGTTTCACAAATCAGAATTGGATTGGCTTGAATGTTTGTGATAGCCCTAGAGCCACAGCAATAGTGGGATAACCAATGAATATTATAAATGAAACCTCATTGCAATCATGCATGGTT 480  
TAGTTTCACAAATCAGAATTGGATTGGCTTGAATGTTTGTGATAGCCCTAGAGCCACAGCAATAGTGGGATAACCAATGAATATTATAAATGAAACCTCATTGCAATCATGCATGGTT 480

TCONS\_00262811  
lncRNA5  
GTCACTTGTCAATGCAACATTGACGTGGTGGCTGAGCTAATACAGCTCTCCGGAACTGAGGACCTACATTATCTTAGTGATGAATGCATCACTTGAATACCCCTTCATCAT 600  
GTCACTTGTCAATGCAACATTGACGTGGTGGCTGAGCTAATACAGCTCTCCGGAACTGAGGACCTACATTATCTTAGTGATGAATGCATCACTTGAATACCCCTTCATCAT 600

TCONS\_00262811  
lncRNA5  
CAATTCACACCCCTCAACTCGTGAATAAAGTTACAAATCCTAAATGCTCCATATTATTTATTTAATTTCATTTTTCTTTATTAGATCTTAGCTTTTAAATTTACAAACT 720  
CAATTCACACCCCTCAACTCGTGAATAAAGTTACAAATCCTAAATGCTCCATATTATTTATTTAATTTCATTTTTCTTTATTAGATCTTAGCTTTTAAATTTACAAACT 720

TCONS\_00262811  
lncRNA5  
GTGAGATAGTCAATTTTTGTCTTAACTGTAAGATGAATATAAGGACTACATATGCTCTTTGTAATTTAGAAAATAATCTAGATCAATTTATAAATTTGGAACCTAATTAG 840  
GTGAGATAGTCAATTTTTGTCTTAACTGTAAGATGAATATAAGGACTACATATGCTCTTTGTAATTTAGAAAATAATCTAGATCAATTTATAAATTTGGAACCTAATTAG 840

TCONS\_00262811  
lncRNA5  
GGATAAATAAGACTTAACTGAATTTGTCCTCAACCAAAAATAAAGTCTGAGGACCAATTTGAAATTTTCTCAAGAGTATTCTCAATTTATAAATTTAGTACCGAATAAT 960  
GGATAAATAAGACTTAACTGAATTTGTCCTCAACCAAAAATAAAGTCTGAGGACCAATTTGAAATTTTCTCAAGAGTATTCTCAATTTATAAATTTAGTACCGAATAAT 960

TCONS\_00262811  
lncRNA5  
TCAACTGC 968  
TCAACTGC 968

# lncRNA6 against TCONS\_00236479

TCONS\_00236479  
lncRNA6  
ATTCTCACCAATGATAGTACATCATAGTTAATTAACTAAGTTTCABAATAATCCAGAATGGCATCAATTTTGAAGAAAAGATTCCATTCTACTCACCTTGAAGTGAACAAGA 120  
ATTCTCACCAATGATAGTACATCATAGTTAATTAACTAAGTTTCABAATAATCCAGAATGGCATCAATTTTGAAGAAAAGATTCCATTCTACTCACCTTGAAGTGAACAAGA 120

TCONS\_00236479  
lncRNA6  
TGCATCCACACTGCTGCTTTTTTTTTTCCCAATTGATTCACACATTACAGATTCACCTTGTCTCTCCCTCAGTTCATCAAACTACACATCAGCTTCATCATTTTGAATCAAAATGTC 240  
TGCATCCACACTGCTGCTTTTTTTTTTCCCAATTGATTCACACATTACAGATTCACCTTGTCTCTCCCTCAGTTCATCAAACTACACATCAGCTTCATCATTTTGAATCAAAATGTC 240

TCONS\_00236479  
lncRNA6  
AGCAACGGTAATCTTTTGTGATCCAAATTTATAGCACTTTCAACGTTTGGGCCATTTTACCTGGACTGACTACCAAAATCAACCACAACTTGTGATGCTGTGAACTCTGAACAATTA 360  
AGCAACGGTAATCTTTTGTGATCCAAATTTATAGCACTTTCAACGTTTGGGCCATTTTACCTGGACTGACTACCAAAATCAACCACAACTTGTGATGCTGTGAACTCTGAACAATTA 360

TCONS\_00236479  
lncRNA6  
TGCACACACATCCTCTCCTCTGATATCCAGGAAATGCACTGACACTTGC 417  
TGCACACACATCCTCTCCTCTGATATCCAGGAAATGCACTGACACTTGC 417

# lncRNA7 against TCONS\_00286692

TCONS\_00286692  
lncRNA7  
AACTACGAGAAACCGAACCATACCATGGTCGATTCCTCCCAATGTCAAGACAGCTTCATCAAGCTTCCAGACTCCAAATCAATCCAAACAGCTCTAATTTGCCAATTCAGAACCC 120  
AACTACGAGAAACCGAACCATACCATGGTCGATTCCTCCCAATGTCAAGACAGCTTCATCAAGCTTCCAGACTCCAAATCAATCCAAACAGCTCTAATTTGCCAATTCAGAACCC 118

TCONS\_00286692  
lncRNA7  
AATTCAACCAATTCATCTATTTCATGAAATTCACCAATTAAGTAGGCTCACATAATTAATTAACCGGATAGGTTTAGAGTTTCCCTTACCTTACCCGAGATTAATAGCAAAAGC 240  
AATTCAACCAATTCATCTATTTCATGAAATTCACCAATTAAGTAGGCTCACATAATTAATTAACCGGATAGGTTTAGAGTTTCCCTTACCTTACCCGAGATTAATAGCAAAAGC 238

TCONS\_00286692  
lncRNA7  
CTTATACTTATCCACCACAGTAGATACCTTAACCCTCAAAATTACAAAATCTCAATACCAAGAAATCAATCAGAACTGAAAGGAAAGAAATGGACAAAATCAGAAATTTCTT 360  
CTTATACTTATCCACCACAGTAGATACCTTAACCCTCAAAATTACAAAATCTCAATACCAAGAAATCAATCAGAACTGAAAGGAAAGAAATGGACAAAATCAGAAATTTCTT 358

TCONS\_00286692  
lncRNA7  
TACCAAATTTGTGAGTGTTTTTATAGAAATCCGAGACAAACAGTGTACTGTGACGGCTCTCAATGGAGGCTATAAGGATGATTGGACTTGAACCTGGGTGATCTGTAGATT 480  
TACCAAATTTGTGAGTGTTTTTATAGAAATCCGAGACAAACAGTGTACTGTGACGGCTCTCAATGGAGGCTATAAGGATGATTGGACTTGAACCTGGGTGATCTGTAGATT 478

TCONS\_00286692  
lncRNA7  
GTTGAGGCTCCAAATCTAGATCCAGAACATATATATCCATAATTTTAGCGAAGACTGAAATCACACTTGTCTGAAAGCTGTCTTGTATCACCACCTTAAACACAAATGCCAAGA 600  
GTTGAGGCTCCAAATCTAGATCCAGAACATATATATCCATAATTTTAGCGAAGACTGAAATCACACTTGTCTGAAAGCTGTCTTGTATCACCACCTTAAACACAAATGCCAAGA 598

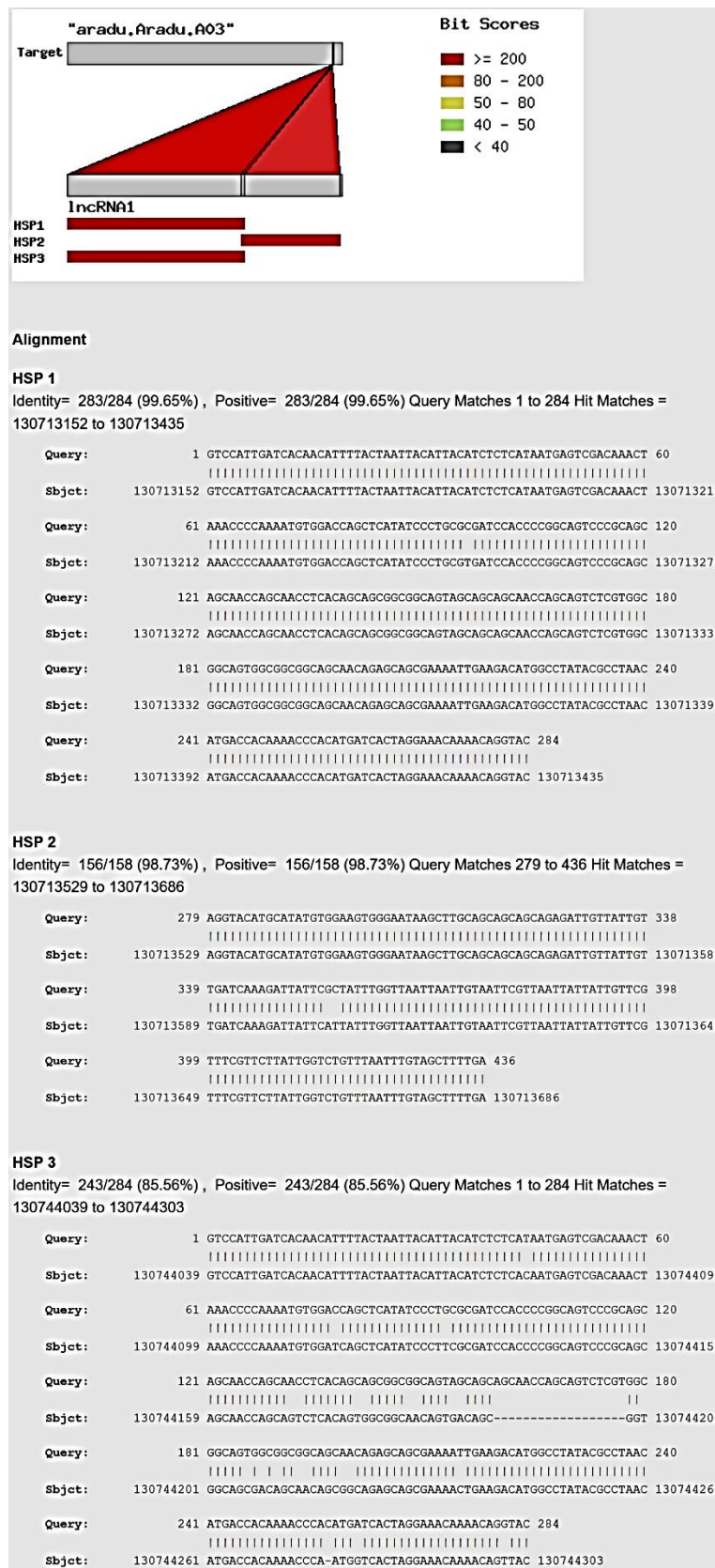
TCONS\_00286692  
lncRNA7  
AGTAACATGTTGCAGTAGTAGTATGAAAGCTTACCAAAATGATTAATAACAGTGGTTAGCCCAACATATATATAACAGTTCAACAAATGATGCACATAATTTCCATTTTGCRAAGC 720  
AGTAACATGTTGCAGTAGTAGTATGAAAGCTTACCAAAATGATTAATAACAGTGGTTAGCCCAACATATATATAACAGTTCAACAAATGATGCACATAATTTCCATTTTGCRAAGC 718

TCONS\_00286692  
lncRNA7  
CCTAATTAAATCAGTAATTCATGCACTACAGCAATTTAAATATATAAAGTATCCCTTTGGCAATCAATTAACCAAAATACITTTTTGGCTGTGTTGCTTATGGCAAGAGC 840  
CCTAATTAAATCAGTAATTCATGCACTACAGCAATTTAAATATATAAAGTATCCCTTTGGCAATCAATTAACCAAAATACITTTTTGGCTGTGTTGCTTATGGCAAGAGC 838

TCONS\_00286692  
lncRNA7  
TAGTAGATCCCACTCCACCCCTCTTCATGATCTTCCTCTCTCGTTGATGATAAG 900  
TAGTAGATCCCACTCCACCCCTCTTCATGATCTTCCTCTCTCGTTGATGATAAG 898

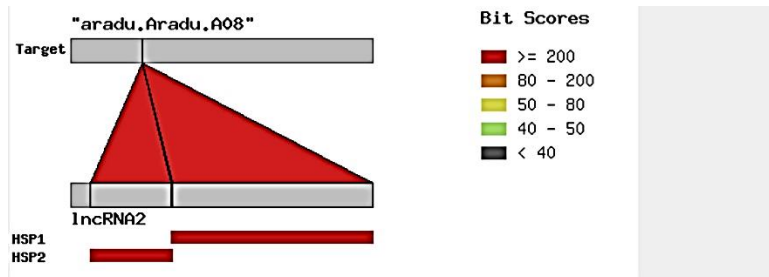
Alignments of lncRNA1-7 against the corresponding genomic sequences.

lncRNA1 against Aradu.A03: 130713152 – 130713435.





# lncRNA2 against Aradu.A08: 11755848-11759272



## Alignment

### HSP 1

Identity= 398/411 (96.84%) , Positive= 398/411 (96.84%) Query Matches 202 to 603 Hit Matches = 11758842 to 11759252

```

Query:      202 AGGTGCTGTGAACGATGCCGAACCTCCTTATGTTCTTGGTTGGTTGTGTGCGCAC 261
           |||
Sbjct:     11758842 AGGTGCTGTGAACGATGCCGAACCTCCTTATGTTCTTGGTTGGTTGTGTGCGCAC 11758901

Query:      262 GGCAGGGTAAGGAAAGGGCATTCASTGCTCTCCAATGACTGAATTTTTTACCAGAAT 321
           |||
Sbjct:     11758902 GGCAGGGTAAGGAAAGGGCATTCASTGCTCTCCAATGACTGAATTTTTTACCAGAAT 11758961

Query:      322 GATATCAACATTGTTCCATCTTGTCTAACTTGTGGTGTCTGCGCATGTGAAAATAAAT 381
           |||
Sbjct:     11758962 GATATCAACATTGTTCCATCTTGTCTAACTTGTGGTGTCTGCGCATGTGAAAATAAAT 11759021

Query:      382 ATTGTATACAATGATGTG-----TTATTTATTAGCAATAAAATTTGGAATCTCAC 432
           |||
Sbjct:     11759022 ATTGTATACAATGATGTGTTTAGATAATTAGTTATTTAGCAATAAAATTTGGAATCTCAC 11759081

Query:      433 TTAATCCCAATCATTCGGTTTTTCGCCTTTGGTTCAGTACTCCATGAATTTTATTACATA 492
           |||
Sbjct:     11759082 TTAATCCCAATCATTCAGTTTTTCGCCTTTGGTTCAGTACTCCATGAATTTTATTACATA 11759141

Query:      493 TACACAACAATCAAATTTATGTGAATGGAACAATGGGCTGTATTAGGAGAACCGGTATA 552
           |||
Sbjct:     11759142 TACACAACAATCAAATTTATGTGAATGGAACAATGGGCTGTATTAGGAGAACCGGTATA 11759201

Query:      553 CATCTCAATTGAACCTACTAATTAAGGTATTGTTAGGTTTTGAGGGGGATT 603
           |||
Sbjct:     11759202 CATCTCAATTGAACCTACTAATTAAGGTATTGTTAGGTTTTGAGGGGGATT 11759252
    
```

### HSP 2

Identity= 162/167 (97.01%) , Positive= 162/167 (97.01%) Query Matches 39 to 205 Hit Matches = 11756140 to 11756306

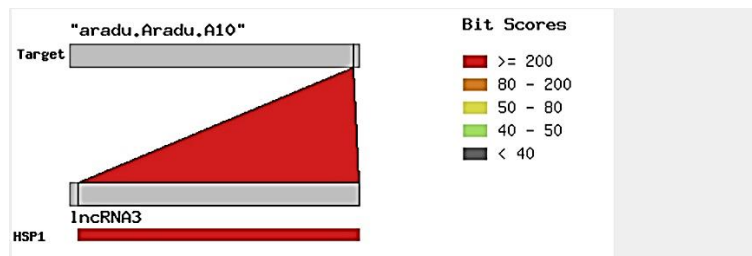
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Query:      39 GGTACAAAACCTCTGTCACATTTGGTCTGTGAGATTTTCGATTGAAACGGCAAAATCCAA 98
           |||
Sbjct:     11756140 GGTACAAAACCTCTGTCACATTTGGTCTGTGAGATTTCAATTGAAACGGCAAAATCCAA 11756199

Query:      99 GGATTAGAAGCAATGTTGATGTTGGAGCCATCCCAACCTTCCAAATCAGTTCTCTTTTT 158
           |||
Sbjct:     11756200 GGATTAGAAGCAATGCTGATGTTGGAGCCATCTCAACCTTCCAAATCAGTTCTCTTTTT 11756259

Query:      159 CAACAACCTTTCGGCCCTCCAACAAGCTCCTCCATCTCCACGAAGGT 205
           |||
Sbjct:     11756260 CAACAACCTTTCGGCCCTCCAACAAGCTCCTCCATCTCCATGAAGGT 11756306
    
```

# lncRNA3 against Aradu.A10: 107598427-107605282



## Alignment

### HSP 1

Identity= 337/338 (99.7%) , Positive= 337/338 (99.7%) Query Matches 11 to 348 Hit Matches = 107604926 to 107605263

```

Query:      11  CCAAGTTGTGTTGTCGAGAAATTCGGCTTGAGATCACGAAGGGGATTAGAAGATGTCCTTTG  70
           |||
Sbjct:     107604926  CCAAGTTGTGTTGTCGAGAAATTCGGCTTGAGATCACGAAGGGGATTAGAAGATGTCCTTTG  107604985

Query:      71  CAATTGGATCTTATTGTCATGATGTCGATGTAGATATAGATTCTCGTTTGTCTGAGTCA  130
           |||
Sbjct:     107604986  CAATTGGATCTTATTGTCATGATGTCGATGTAGATATAGATTCTCGTTTGTCTGAGTCA  107605045

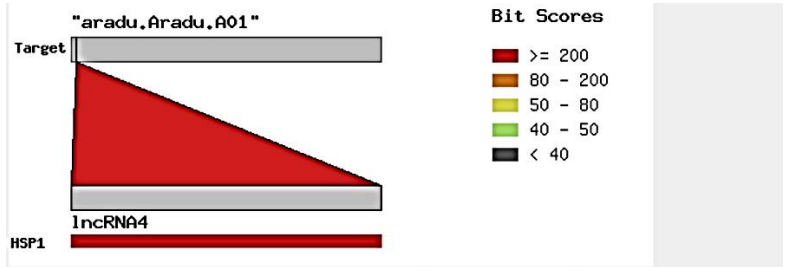
Query:     131  ATGATTCGGATCAAGTCAAAAAGAATTATCTCCTGTCTAAAGAGGTGAAGTCTTTTTTG  190
           |||
Sbjct:     107605046  ATGATTCGGATCAAGTCAAAAAGAATTATCTCCTGTCTAAAGAGGTGAAGTCTTTTTTG  107605105

Query:     191  ACCTAATTGAAGATCATCAACTCCGACAAAATGTAAGTCTATATCGACCTCAACTTCATG  250
           |||
Sbjct:     107605106  ACCTAATTGGAGATCATCAACTCCGACAAAATGTAAGTCTATATCGACCTCAACTTCATG  107605165

Query:     251  AGAAGCAAGAAGGAAAGAAACAATTATAAGTGGTTAGAAACCTAAAATGTTCCAAATTT  310
           |||
Sbjct:     107605166  AGAAGCAAGAAGGAAAGAAACAATTATAAGTGGTTAGAAACCTAAAATGTTCCAAATTT  107605225

Query:     311  TGTAGTAAATGGAAGGAATAGAGCAACCTGCATGACA  348
           |||
Sbjct:     107605226  TGTAGTAAATGGAAGGAATAGAGCAACCTGCATGACA  107605263
    
```

# lncRNA4 against Aradu.A01: 1874505-1875866



## Alignment

### HSP 1

Identity= 716/717 (99.86%), Positive= 716/717 (99.86%) Query Matches 1 to 717 Hit Matches = 1875138 to 1875854

```

Query:      1  TCCCACATGCAAGCTGAGACATTAATTGAGCACCAAAGGCTTTAAACTCTTACTACCA 60
            |
Sbjct:    1875138 TCCCACATGCAAGCTGAGACATTAATTGAGCACCAAAGGCTTTAAACTCTTACTACCA 1875197

Query:      61  TGTGAAATCTGAAGGCAATGGCAAAGAAACCAATTTACCATAGACATCAATACAAATGG 120
            |
Sbjct:    1875198 TGTGAAATCTGAAGGCAATGGCAAAGAAACCAATTTACCATAGACATCAATACAAATGG 1875257

Query:     121  TAGAAAAGCAAAGCTCCAAAGGTAAAAAGGATCCATGCCTCATTAGAATATGAGCAA 180
            |
Sbjct:    1875258 TAGAAAAGCAAAGCTCCAAAGGTAAAAAGGATCCATGCCTCATTAGAATATGAGCAA 1875317

Query:     181  GTGGGTAGTAGGAGGATCCCATAGAAAACCCCTAATGAGAAAACCTCCATATTTGGTAA 240
            |
Sbjct:    1875318 GTGGGTAGTAGGAGGATCCCATAGAAAACCCCTAATGAGAAAACCTCCATATTTGGTAA 1875377

Query:     241  TTTGATGTTGCACAGCTATGACTCGAAACGCTCCATTATTACAGGGAAGGCGATCTTA 300
            |
Sbjct:    1875378 TTTGATGTTGCACAGCTATGACTCGAAACGCTCCATTATTACAGGGAAGGCGATCTTA 1875437

Query:     301  AGGGCAGTGCITAGAAATCAGAGAATAAGAACCTTTGCACAAAATGGACATTCAAATA 360
            |
Sbjct:    1875438 AGGGCAGTGCITAGAAATCAGAGAATAAGAACCTTTGCACAAAATGGACATTCAAATA 1875497

Query:     361  ACAGAAAATCAAACAACTTTGGAGTATAGAATTATCTCACACGGATTCAAGAAACAAT 420
            |
Sbjct:    1875498 ACAGAAAATCAAACAACTTTGGAGTATAGAATTATCTCACACGGATTCAAGAAACAAT 1875557

Query:     421  GGATTGTAAAAACACATAATAACGATTTGAGAATCCCTCAGATTATTTTTCTCTCAAT 480
            |
Sbjct:    1875558 GGATTGTAAAAACACATAATAACGATTTGAGAATCCCTCAGATTATTTTTCTCTCAAT 1875617

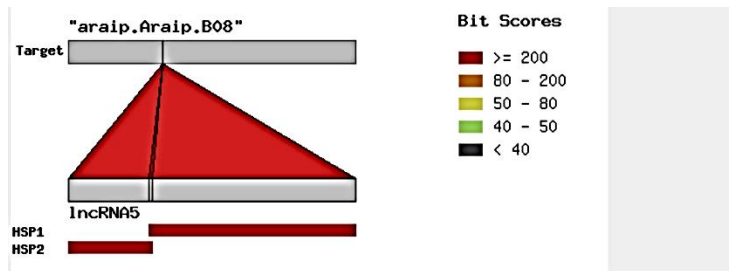
Query:     481  GGAATTCGGTCCACTACTTTAAATATTATAAATGTCACAGGGAAGCATTAAATATGICAT 540
            |
Sbjct:    1875618 GGAATTCGGTCCACTACTTTAAATATTATAAATGTCACAGGGAAGCATTAAATATGICAT 1875677

Query:     541  AAATCTGCATTAGAAATCAACCAAACCTCACCTAATCTTGAATACCGCCAAATAACAA 600
            |
Sbjct:    1875678 AAATCTGCATTAGAAATCAACCAAACCTCACCTAATCTTGAATACCGCCAAATAACAA 1875737

Query:     601  TTTTAAAAAATAATAATAAAGATATAAGAAAAGAAATTAATAAAAAGCATCCAAT 660
            |
Sbjct:    1875738 TTTTAAAAAATAATAATAAAGATATAAGAAAAGAAATTAATAAAAAGCATCCAAT 1875797

Query:     661  GAGATGAAAGAAATACTGAACAACTCTCTCTTAAGAAATCTCCGAAACCGCCGC 717
            |
Sbjct:    1875798 GAGATGAAAGAAATACTGAACAACTCTCTCTTAAGAAATCTCCGAAACCGCCGC 1875854
    
```

# lncRNA5 against Araip.B08: 42806631-42808445



## Alignment

### HSP 1

Identity= 694/695 (99.86%) , Positive= 694/695 (99.86%) Query Matches 274 to 968 Hit Matches = 42807350 to 42808044

```

Query:      274 CACACAGCAAAATCTCAAATATATTATTATTTTCATGAAAAGTGGAGAAGGTAATAGGGT 333
           |||
Sbjct:      42807350 CACACAGCAAAATCTCAAATATATTATTATTTTCATGAAAAGTGGAGAAGGTAATAGGGT 42807409

Query:      334 GTTGCTCAAAGTAACGAATGTTGGTAGTTTTCACAATCAGAATGGATTGGCTTGATG 393
           |||
Sbjct:      42807410 GTTGCTCAAAGTAACGAATGTTGGTAGTTTTCACAATCAGAATGGATTGGCTTGATG 42807469

Query:      394 TTGTTGATAAGCCTAGAGGCCAACAGCAATAGTGGGATAACAAATGAAATATTATAAAAT 453
           |||
Sbjct:      42807470 TTGTTGATAAGCCTAGAGGCCAACAGCAATAGTGGGATAACAAATGAAATATTATAAAAT 42807529

Query:      454 GAAACCTCATTGCAATCATGCATGGTTGTCACCTTGTTCATTGCAACATTGACGTGGTGGT 513
           |||
Sbjct:      42807530 GAAACCTCATTGCAATCATGCATGGTTGTCACCTTGTTCATTGCAACATTGACGTGGTGGT 42807589

Query:      514 GCTGAGCTAATACAGCTCCTCGGGAACCTGAAGACCTACATTATCTTAGTGGTATGAAT 573
           |||
Sbjct:      42807590 GCTGAGCTAATACAGCTCCTCGGGAACCTGAAGACCTACATTATCTTAGTGGTATGAAT 42807649

Query:      574 GCATACACTTGATTACCCCTTCATCATTCATCACACCCCTCAACTCGTGAATAAA 633
           |||
Sbjct:      42807650 GCATACACTTGATTACCCCTTCATCATTCATCACACCCCTCAACTCGTGAATAAA 42807709

Query:      634 GTTACAAAATCCTAAATGCTCCATATTTATTTATTTAAATTTCTCATTTTCTTTATTA 693
           |||
Sbjct:      42807710 GTTACAAAATCCTAAATGCTCCATATTTATTTATTTAAATTTCTCATTTTCTTTATTA 42807769

Query:      694 GATTCTTAGCTTTTAAATTTTACAACTGTGAGATAGATCAATTTTGTTCACCTGTA 753
           |||
Sbjct:      42807770 GATTCTTAGCTTTTAAATTTTACAACTGTGAGATAGATCAATTTTGTTCACCTGTA 42807829

Query:      754 AAAGTATGAAATAATAAGGACTAACATATGCTCTTTGTAATTTAGAAAATAATCTAGAT 813
           |||
Sbjct:      42807830 AAAGTATGAAATAATAAGGACTAACATATGCTCTTTGTAATTTAGAAAATAATCTAGAT 42807889

Query:      814 CATTATAAATTTTGAACTAATTAAGGGATAAATAAGACTAAAACTGAATGTTTTCAC 873
           |||
Sbjct:      42807890 CATTATAAATTTTGAACTAATTAAGGGATAAATAAGACTAAAACTGAATGTTTTCAC 42807949

Query:      874 TCAACAAAAAATAAATAAGTCTGAAGACCAATTTGAAATTTTCTCAAGAGTTATTCTC 933
           |||
Sbjct:      42807950 TCAACAAAAAATAAATAAGTCTGAAGACCAATTTGAAATTTTCTCAAGAGTTATTCTC 42808009

Query:      934 AATTTATAAATTTAAGTACCGATAAATCAACTGC 968
           |||
Sbjct:      42808010 AATTTATAAATTTAAGTACCGATAAATCAACTGC 42808044
    
```

### HSP 2

Identity= 283/284 (99.65%) , Positive= 283/284 (99.65%) Query Matches 1 to 284 Hit Matches = 42806712 to 42806995

```

Query:      1 TCATCACCTCTCCAAGTCACTGACCTCTATTCTACTCTTAATCTTTCACCTCATTGTTGCACTT 60
           |||
Sbjct:      42806712 TCATCACCTCTCCAAGTCACTGACCTCTATTCTACTCTTAATCTTTCACCTCATTGTTGCACTT 42806771

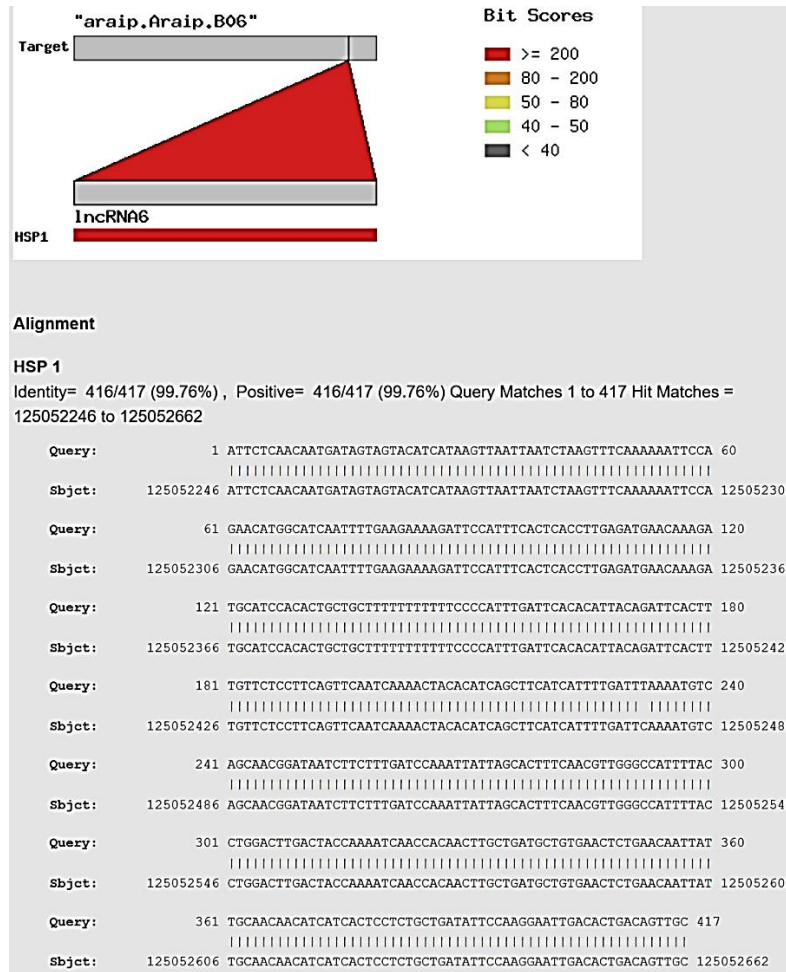
Query:      61 ACTCCCACTAAATCAAATAAATACTGAGAGTTAATTTAATTTGATTTTCATTTTTG 120
           |||
Sbjct:      42806772 ACTCCCACTAAATCAAATAAATACTGAGAGTTAATTTAATTTGATTTTCATTTTTG 42806831

Query:      121 TCTCTTAATAAATTTCTGCTTCTCAGTTCTATTTTTTTTTAAAAATATAAAAATGCAAAA 180
           |||
Sbjct:      42806832 TCTCTTAATAAATTTCTGCTTCTCAGTTCTATTTTTTTTTAAAAATATAAAAATGCAAAA 42806891

Query:      181 TAACATAATCCTAATAATTATAAATTTAGCTAATCTGTGCTTTTTTATGTAATTTT 240
           |||
Sbjct:      42806892 TAACATAATCCTAATAATTATAAATTTAGCTAATCTGTGCTTTTTTATGTAATTTT 42806951

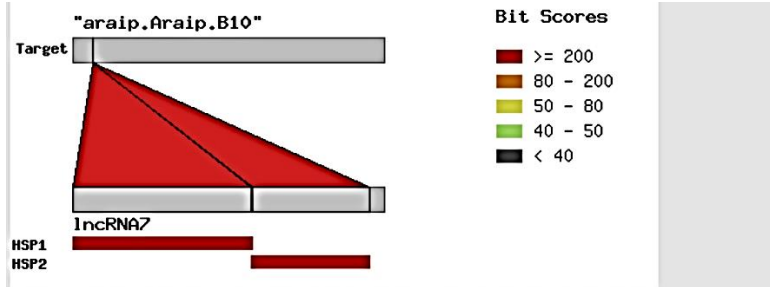
Query:      241 CGTAATTAACAACATTAATATGATTCTGAAGGCACACAGCAA 284
           |||
Sbjct:      42806952 CGTAATTAACAACATTAATATGATTCTGAAGGCACACAGCAA 42806995
    
```

# lncRNA6 against Araip.B06: 125052207-125052834





# lncRNA7 against Araip.B10: 9092728-9099715



The image above shows the relationship between query and target for this particular BLAST hit.

## Alignment

### HSP 1

Identity= 515/520 (99.04%) , Positive= 515/520 (99.04%) Query Matches 1 to 518 Hit Matches = 9092895 to 9093414

```

Query:          1  AACTACGAG-AACCGAAACCATACCATGGTCGATTCTCTCCCAATGTCAAAGCA-CITAC 58
                |||
Sbjct:    9092895  AACTACGAGAAACCGAAACCATACCATGGTCGATTCTCTCCCAATGTCAAAGCACCTAAC 9092954

Query:          59  ATCAAGCTTCCAGGACTCCAATCAATTCCAACAAGCTCTAATTTGCCAATTCAACACCG 118
                |||
Sbjct:    9092955  ATCAAGCTTCCAGGACTCCAATCAATTCCAACAAGCTCTAATTTGCCAATTCAACACCG 9093014

Query:          119  AATTCAACACAATTCAATCTATTTTCATGAAATTCACCAAAATTAAGTAGGGTTCACATA 178
                |||
Sbjct:    9093015  AATTCAACACAATTCAATCTATTTTCATGAAATTCACCAAAATTAAGTAGGGTTCACATA 9093074

Query:          179  TTGAATAACCGCTAGGGTTTAGAGTTTCCCTTACCTTACCCGACAGATTAATAGACAACC 238
                |||
Sbjct:    9093075  TTGAATAACCGCAAGGGTTTAGAGTTTCCCTTACCTTACCCGACAGATTAATAGACAACC 9093134

Query:          239  CTTATACTTATCCCACTAGAGTACCCTTAAACCATCAAATTAACAAAATCTCTCAATA 298
                |||
Sbjct:    9093135  CTTATACTTATCCCACTAGAGTACCCTTAAACCATCAAATTAACAAAATCTCTCAATA 9093194

Query:          299  CCAAGAATTCAAATCACGAACTGAAAAGGAAAGAAATGGACACAAAATCAGAATTTCTT 358
                |||
Sbjct:    9093195  CCAAGAATTCAAATCACGAACTGAAAAGGAAAGAAATGGACACAAAATCAGAATTTCTT 9093254

Query:          359  TACCAAATGTGAGTGTGTTTATAGAGAATCCGAGACGAACACGTGACTGTTGACGG 418
                |||
Sbjct:    9093255  TACCAAATGTGAGTGTGTTTATAGAGAATCCGAGACGAACACGTGACTGTTGACGG 9093314

Query:          419  CTCTCAATGGAGGGCTATAAGGATGATTTGGACTTGGAACTGGGTGATCGTTAGATT 478
                |||
Sbjct:    9093315  CTCTCAATGGAGGGCTATAAGGATGATTTGGACTTGGAACTGGGTGATCGTTAGATT 9093374

Query:          479  GTTGAGGCTCCAATACTAGATCCAGAACAATATATATCC 518
                |||
Sbjct:    9093375  GTTGAGGCTCCAATACTAGATCCAGAACAATATATATCC 9093414
    
```

### HSP 2

Identity= 341/342 (99.71%) , Positive= 341/342 (99.71%) Query Matches 517 to 858 Hit Matches = 9098042 to 9098383

```

Query:          517  CCCATAATCTTAGCGAAGACTGAAATCACACTTGCTGAAAGCTGTGCTTTGATCACCAA 576
                |||
Sbjct:    9098042  CCCATAATCTTAGCGAAGACTGAAATCACACTTGCTGAAAGCTGTGCTTTGATCACCAA 9098101

Query:          577  CCTTAAACACAAATGCCAAGAAGTAACATGTTGCAGTAGTAGTATAAAGCTATACCAA 636
                |||
Sbjct:    9098102  CCTTAAACACAAATGCCAAGAAGTAACATGTTGCAGTAGTAGTATAAAGCTATACCAA 9098161

Query:          637  ATATGATTAACAGTGGTTAGCCCAACATATATAACAAGTTCAACAAATGATGCACAA 696
                |||
Sbjct:    9098162  ATATGATTAACAGTGGTTAGCCCAACATATATAACAAGTTCAACAAATGATGCACAA 9098221

Query:          697  TAATATTTCCATTTTGCAAAGCCCTAATTATAAATCAGTAAATTCACATCGCAACTACG 756
                |||
Sbjct:    9098222  TAATATTTCCATTTTGCAAAGCCCTAATTATAAATCAGTAAATTCACATCGCAACTACG 9098281

Query:          757  CATTAAAAAATATAAACGGATCCTTTGGCAATCAATAATACCAAAAATACTTTTTCGCT 816
                |||
Sbjct:    9098282  CATTAAAAAATATAAACGGATCCTTTGGCAATCAATAATACCAAAAATACTTTTTCGCT 9098341

Query:          817  TGTTGCCTAATGGCACAAGAGTAGTAGATCCACTTCCACC 858
                |||
Sbjct:    9098342  TGTTGCCTAATGGCACAAGAGTAGTAGATCCACTTCCACC 9098383
    
```