Supplementary Dataset 4: Identification of LCDV-Sa in human enteric virome.

The data for this analysis was obtained from NCBI (SRA ID: PRJNA275568) and the name of the project is “Human stool virome in islet autoimmunity”. We report the BlastN hits that show a significant alignment with LCDV-Sa sequences. No significant hits were identified for LCDV-1, GIV and SGIV in this dataset. Human herpes virus and human parechovirus were used as controls. The full length reads that gave a significant hit for LCDV-Sa are reported at the end of the document.

1- LCDV-1

```
Query= NC_001824.1 Lymphocystis disease virus 1, complete genome

Length=102653


***** No hits found *****



Lambda      K        H
    1.33    0.621     1.12

Gapped
Lambda      K        H
    1.28    0.460    0.850

Effective search space used: 1986974652939930
```

2- LCDV-Sa

```
Query= NC_033423.1 Lymphocystis disease virus Sa isolate SA9, complete
genome

Length=208501
                                                                    Score     E
Sequences producing significant alignments:                        (Bits)  Value

SRR2298382.126301  126301 length=502                                 52.8    0.50
SRR2298382.124650  124650 length=156                                 52.8    0.50
SRR2298382.122212  122212 length=190                                 52.8    0.50
SRR2298382.118813  118813 length=192                                 52.8    0.50
SRR2298382.112002  112002 length=344                                 52.8    0.50
SRR2298382.111826  111826 length=502                                 52.8    0.50
SRR2298382.108909  108909 length=194                                 52.8    0.50
SRR2298382.106152  106152 length=342                                 52.8    0.50
SRR2298382.104887  104887 length=164                                 52.8    0.50
SRR2298382.99979  99979 length=252                                   52.8    0.50
SRR2298382.87062  87062 length=501                                   52.8    0.50
SRR2298382.83290  83290 length=502                                   52.8    0.50
SRR2298382.81661  81661 length=378                                   52.8    0.50
SRR2298382.81567  81567 length=266                                   52.8    0.50
SRR2298382.78124  78124 length=400                                   52.8    0.50
```

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SRR2298382.77844  77844 length=360                                     52.8    0.50
SRR2298382.71542  71542 length=356                                     52.8    0.50
SRR2298382.70519  70519 length=246                                     52.8    0.50
SRR2298382.69009  69009 length=420                                     52.8    0.50
SRR2298382.65644  65644 length=501                                     52.8    0.50
SRR2298382.63389  63389 length=501                                     52.8    0.50
SRR2298382.58758  58758 length=346                                     52.8    0.50
SRR2298382.58475  58475 length=501                                     52.8    0.50
SRR2298382.56894  56894 length=376                                     52.8    0.50
SRR2298382.52746  52746 length=236                                     52.8    0.50
SRR2298382.47829  47829 length=192                                     52.8    0.50
SRR2298382.47185  47185 length=501                                     52.8    0.50
SRR2298382.37617  37617 length=501                                     52.8    0.50
SRR2298382.35774  35774 length=500                                     52.8    0.50
SRR2298382.26484  26484 length=170                                     52.8    0.50
SRR2298382.25595  25595 length=500                                     52.8    0.50
SRR2298382.20988  20988 length=501                                     52.8    0.50
SRR2298382.18993  18993 length=498                                     52.8    0.50
SRR2298382.18914  18914 length=468                                     52.8    0.50
SRR2298382.6569  6569 length=366                                       52.8    0.50
SRR2298382.1706  1706 length=492                                       52.8    0.50
SRR2298290.411674  411674 length=502                                   52.8    0.50


>SRR2298382.126301 126301 length=502
Length=502

 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  73      GCAAGGACCTGTTGGACCTGCTGGACCT  100


 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Minus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  447     GCAAGGACCTGTTGGACCTGCTGGACCT  420


>SRR2298382.124650 124650 length=156
Length=156

 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  28      GCAAGGACCTGTTGGACCTGCTGGACCT  55


 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
```

```
 Strand=Plus/Minus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  129     GCAAGGACCTGTTGGACCTGCTGGACCT  102


>SRR2298382.122212 122212 length=190
Length=190

 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  28      GCAAGGACCTGTTGGACCTGCTGGACCT  55


 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Minus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  163     GCAAGGACCTGTTGGACCTGCTGGACCT  136


>SRR2298382.118813 118813 length=192
Length=192

 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Minus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  168     GCAAGGACCTGTTGGACCTGCTGGACCT  141


>SRR2298382.112002 112002 length=344
Length=344

 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  24      GCAAGGACCTGTTGGACCTGCTGGACCT  51


 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Minus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  321     GCAAGGACCTGTTGGACCTGCTGGACCT  294
```

```
>SRR2298382.111826 111826 length=502
Length=502

 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  188     GCAAGGACCTGTTGGACCTGCTGGACCT  215


 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Minus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  323     GCAAGGACCTGTTGGACCTGCTGGACCT  296


>SRR2298382.108909 108909 length=194
Length=194

 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  47      GCAAGGACCTGTTGGACCTGCTGGACCT  74


 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Minus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  148     GCAAGGACCTGTTGGACCTGCTGGACCT  121


>SRR2298382.106152 106152 length=342
Length=342

 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Minus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  133     GCAAGGACCTGTTGGACCTGCTGGACCT  106


 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Plus
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```
Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  210     GCAAGGACCTGTTGGACCTGCTGGACCT  237


>SRR2298382.104887 104887 length=164
Length=164

 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Minus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  68      GCAAGGACCTGTTGGACCTGCTGGACCT  41


 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  97      GCAAGGACCTGTTGGACCTGCTGGACCT  124


>SRR2298382.99979 99979 length=252
Length=252

 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Minus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  68      GCAAGGACCTGTTGGACCTGCTGGACCT  41


 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  185     GCAAGGACCTGTTGGACCTGCTGGACCT  212


>SRR2298382.87062 87062 length=501
Length=501

 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  204     GCAAGGACCTGTTGGACCTGCTGGACCT  231
```

```
 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Minus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  318     GCAAGGACCTGTTGGACCTGCTGGACCT  291


>SRR2298382.83290 83290 length=502
Length=502

 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  320     GCAAGGACCTGTTGGACCTGCTGGACCT  347


>SRR2298382.81661 81661 length=378
Length=378

 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Minus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  68      GCAAGGACCTGTTGGACCTGCTGGACCT  41


 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  311     GCAAGGACCTGTTGGACCTGCTGGACCT  338


>SRR2298382.81567 81567 length=266
Length=266

 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Minus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  51      GCAAGGACCTGTTGGACCTGCTGGACCT  24


 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Plus
```

```
Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  216     GCAAGGACCTGTTGGACCTGCTGGACCT  243


>SRR2298382.78124 78124 length=400
Length=400

 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Minus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  72      GCAAGGACCTGTTGGACCTGCTGGACCT  45


 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  329     GCAAGGACCTGTTGGACCTGCTGGACCT  356


>SRR2298382.77844 77844 length=360
Length=360

 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Minus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  112     GCAAGGACCTGTTGGACCTGCTGGACCT  85


 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  249     GCAAGGACCTGTTGGACCTGCTGGACCT  276


>SRR2298382.71542 71542 length=356
Length=356

 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Minus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  169     GCAAGGACCTGTTGGACCTGCTGGACCT  142
```

```
 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  188     GCAAGGACCTGTTGGACCTGCTGGACCT  215


>SRR2298382.70519 70519 length=246
Length=246

 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Minus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  40      GCAAGGACCTGTTGGACCTGCTGGACCT  13


 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  207     GCAAGGACCTGTTGGACCTGCTGGACCT  234


>SRR2298382.69009 69009 length=420
Length=420

 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Minus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  154     GCAAGGACCTGTTGGACCTGCTGGACCT  127


 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  267     GCAAGGACCTGTTGGACCTGCTGGACCT  294


>SRR2298382.65644 65644 length=501
Length=501

 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
```

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                ||||||||||||||||||||||||||||
Sbjct  334      GCAAGGACCTGTTGGACCTGCTGGACCT  361


>SRR2298382.63389 63389 length=501
Length=501

 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  403     GCAAGGACCTGTTGGACCTGCTGGACCT  430


>SRR2298382.58758 58758 length=346
Length=346

 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Minus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  224     GCAAGGACCTGTTGGACCTGCTGGACCT  197


>SRR2298382.58475 58475 length=501
Length=501

 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  77      GCAAGGACCTGTTGGACCTGCTGGACCT  104


 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Minus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  426     GCAAGGACCTGTTGGACCTGCTGGACCT  399


>SRR2298382.56894 56894 length=376
Length=376

 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  103     GCAAGGACCTGTTGGACCTGCTGGACCT  130
```

```
 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Minus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  274     GCAAGGACCTGTTGGACCTGCTGGACCT  247


>SRR2298382.52746 52746 length=236
Length=236

 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  36      GCAAGGACCTGTTGGACCTGCTGGACCT  63


 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Minus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  201     GCAAGGACCTGTTGGACCTGCTGGACCT  174


>SRR2298382.47829 47829 length=192
Length=192

 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Minus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  51      GCAAGGACCTGTTGGACCTGCTGGACCT  24


 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  142     GCAAGGACCTGTTGGACCTGCTGGACCT  169


>SRR2298382.47185 47185 length=501
Length=501

 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Plus
```

```
Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  36      GCAAGGACCTGTTGGACCTGCTGGACCT  63


>SRR2298382.37617 37617 length=501
Length=501

 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  113     GCAAGGACCTGTTGGACCTGCTGGACCT  140


 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Minus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  421     GCAAGGACCTGTTGGACCTGCTGGACCT  394


>SRR2298382.35774 35774 length=500
Length=500

 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  36      GCAAGGACCTGTTGGACCTGCTGGACCT  63


>SRR2298382.26484 26484 length=170
Length=170

 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Minus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  49      GCAAGGACCTGTTGGACCTGCTGGACCT  22


 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  122     GCAAGGACCTGTTGGACCTGCTGGACCT  149
```

```
>SRR2298382.25595 25595 length=500
Length=500

 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  182     GCAAGGACCTGTTGGACCTGCTGGACCT  209


 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Minus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  346     GCAAGGACCTGTTGGACCTGCTGGACCT  319


>SRR2298382.20988 20988 length=501
Length=501

 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  96      GCAAGGACCTGTTGGACCTGCTGGACCT  123


 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Minus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  460     GCAAGGACCTGTTGGACCTGCTGGACCT  433


>SRR2298382.18993 18993 length=498
Length=498

 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  63      GCAAGGACCTGTTGGACCTGCTGGACCT  90


 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Minus
```

```
Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  432     GCAAGGACCTGTTGGACCTGCTGGACCT  405


>SRR2298382.18914 18914 length=468
Length=468

 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Minus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  197     GCAAGGACCTGTTGGACCTGCTGGACCT  170


 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  272     GCAAGGACCTGTTGGACCTGCTGGACCT  299


>SRR2298382.6569 6569 length=366
Length=366

 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  38      GCAAGGACCTGTTGGACCTGCTGGACCT  65


 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Minus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  329     GCAAGGACCTGTTGGACCTGCTGGACCT  302


>SRR2298382.1706 1706 length=492
Length=492

 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  32      GCAAGGACCTGTTGGACCTGCTGGACCT  59
```

```
 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Minus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  461     GCAAGGACCTGTTGGACCTGCTGGACCT  434


>SRR2298290.411674 411674 length=502
Length=502

 Score = 52.8 bits (28),  Expect = 0.50
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Minus

Query  135821  GCAAGGACCTGTTGGACCTGCTGGACCT  135848
               ||||||||||||||||||||||||||||
Sbjct  39      GCAAGGACCTGTTGGACCTGCTGGACCT  12



Lambda      K        H
    1.33    0.621     1.12

Gapped
Lambda      K        H
    1.28    0.460    0.850

Effective search space used: 4022997847426584
```

3- SGIV

```
Query= NC_006549.1 Singapore grouper iridovirus, complete genome

Length=140131


***** No hits found *****



Lambda      K        H
    1.33    0.621     1.12

Gapped
Lambda      K        H
    1.28    0.460    0.850

Effective search space used: 2712675925101726
```

4- GIV

```
Query= AY666015.1 Grouper iridovirus, complete genome

Length=139793
```

```
***** No hits found *****



Lambda      K        H
    1.33    0.621     1.12

Gapped
Lambda      K        H
    1.28    0.460    0.850

Effective search space used: 2706131098003410
```

5- Human herpesvirus 7

```
Query= NC_001716.2 Human herpesvirus 7, complete genome

Length=153080


***** No hits found *****



Lambda      K        H
    1.33    0.621     1.12

Gapped
Lambda      K        H
    1.28    0.460    0.850

Effective search space used: 2963412511184844
```

6- Human parechovirus 1

```
Query= JX575746.1 Human parechovirus 1 isolate CAU10-NN, complete genome

Length=7348
                                                                          Score     E
Sequences producing significant alignments:                              (Bits)  Value

SRR2298578.40400  40400 length=500                                        499     5e-137
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SRR2298573.862030  862030 length=500                                      436     4e-118
SRR2298573.814921  814921 length=500                                      436     4e-118
SRR2298573.595924  595924 length=500                                      436     4e-118
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SRR2298573.846971  846971 length=500                                  424     3e-114
SRR2298573.840452  840452 length=500                                  424     3e-114
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SRR2298573.793320  793320 length=500                                  424     3e-114
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SRR2298573.773302  773302 length=500                                  424     3e-114
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SRR2298573.728669  728669 length=500                                  424     3e-114
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SRR2298573.714736  714736 length=500                                       424     3e-114
SRR2298573.708314  708314 length=500                                       424     3e-114
SRR2298573.705806  705806 length=500                                       424     3e-114
SRR2298573.700830  700830 length=500                                       424     3e-114
SRR2298573.696366  696366 length=500                                       424     3e-114
SRR2298573.688563  688563 length=500                                       424     3e-114
SRR2298573.685978  685978 length=500                                       424     3e-114
SRR2298573.685074  685074 length=500                                       424     3e-114
SRR2298573.682861  682861 length=500                                       424     3e-114


>SRR2298578.40400 40400 length=500
Length=500

 Score = 499 bits (270),  Expect = 5e-137
 Identities = 337/369 (91%), Gaps = 5/369 (1%)
 Strand=Plus/Plus

Query  2473  ATTATTTCTTAAATTTCAAGTCCATGAATGTGGATATCTTTACTGTTTCTCACACTAAAG  2532
             |||||||| ||||||||||||||||||||||||||||||| ||||||||||||||||| |
Sbjct  1     ATTATTTCCTAAATTTCAAGTCCATGAATGTGGATATCTTCACTGTTTCTCACACTAAGG  60

Query  2533  TAGACAATCTATTTGGAAGAGCTTGGTTTTACCAGGAACACACTTTCACCGATGAGGGGC  2592
             ||||||| ||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  61    TAGACAACCTATTTGGAAGAGCTTGGTTTTACCAGGAACACACTTTCACCGATGAAGGGC  120

Query  2593  AGTGGAGAGTTAATTTGGAATTCCCGAAACAAGGCCATGGTTCACTTTCCTTGCTATTCG  2652
             ||||||||||||  || || ||||||||||||||||||||||| ||||| ||| ||||||
Sbjct  121   AGTGGAGAGTTAGCTTAGAGTTCCCGAAACAAGGCCATGGTTCGCTTTCATTGTTATTCG  180

Query  2653  CTTACTTCACAGGTGAATTAAATATTCATGTTTTGTTCCTGGCTGAAAAGGGATTCCTTA  2712
             ||||||| ||||||||| |||||||||||||| ||||||| |||||||||||||| ||||
Sbjct  181   CTTACTTTACAGGTGAACTAAATATTCATGTTCTGTTCCTAGCTGAAAAGGGATTTCTTA  240

Query  2713  GAGT-----GGCCCACACTTATGACACATCAGCAGACAGAGTTAATTTCCTGTCATCCAA  2767
             ||||     ||||||||| ||||||||||||||| |||||||||| ||||||||||||||
Sbjct  241   GAGTAGAAGGGCCCACACCTATGACACATCAGCAAACAGAGTTAACTTCCTGTCATCCAA  300

Query  2768  TGGCGTTATTACAATCCCAGCTGGAGAACAAATGACACTATCTGCACCCTACTACTCAAA  2827
             |||||| || ||||||||||| ||||||||||||||| ||||||||||||||||||| ||
Sbjct  301   TGGCGTCATCACAATCCCAGCCGGAGAACAAATGACATTATCTGCACCCTACTACTCTAA  360

Query  2828  TAAACCCCT  2836
              ||| ||||
Sbjct  361   GAAATCCCT  369


>SRR2298573.122301 122301 length=500
Length=500

 Score = 440 bits (238),  Expect = 3e-119
 Identities = 251/257 (98%), Gaps = 1/257 (0%)
 Strand=Plus/Plus

Query  319   GCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAAC  378
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
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Sbjct  1    GCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAAC  60

Query  379  ATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGG  438
            ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGG  120

Query  439  GCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGA  498
            ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGA  180

Query  499  AGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAG  558
            ||||||||||||||| |||||||||||||| |||||||||||||||||||||||||||||
Sbjct  181  AGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAG  240

Query  559  GATGCCCAGAAGGTACC  575
            |||||||||| ||||||
Sbjct  241  GATGCCCAGA-GGTACC  256


 Score = 420 bits (227),  Expect = 4e-113
 Identities = 241/248 (97%), Gaps = 0/248 (0%)
 Strand=Plus/Minus

Query  328  TAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTG  387
            ||||||||||| | |||||||||||||||||||||||||||||||| |||||||||||||
Sbjct  498  TAGTAAGTTTGGGGGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTG  439

Query  388  CAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGC  447
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  438  TAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGC  379

Query  448  CAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTA  507
            |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  378  CAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTA  319

Query  508  GTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAG  567
            |||||| |||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  318  GTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAG  259

Query  568  AAGGTACC  575
            ||||||||
Sbjct  258  AAGGTACC  251


>SRR2298573.862030 862030 length=500
Length=500

 Score = 436 bits (236),  Expect = 4e-118
 Identities = 246/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  334  GTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGC  393
            |||||||||||||||||||||||||||||||||||||||| ||||||||||||| |||||
Sbjct  1    GTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGC  60

Query  394  ATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGT  453
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGT  120
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Query  454  CTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCT  513
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCT  180

Query  514  GCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTA  573
             |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTA  240

Query  574  CCCATAGGTAA  584
            |||||||||||
Sbjct  241  CCCATAGGTAA  251


 Score = 396 bits (214),  Expect = 7e-106
 Identities = 232/241 (96%), Gaps = 0/241 (0%)
 Strand=Plus/Minus

Query  389  AAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCC  448
            ||||| |||||||||| | |||||||| || |||||||||||||||||||||||||||||
Sbjct  490  AAAGCCTCCTATTGCCCGGGGAACAACCCCGGGTAACAGGTGCCTCTGGGGCCAAAAGCC  431

Query  449  AAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAG  508
            ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  430  AAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAG  371

Query  509  TACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGA  568
            ||||| |||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct  370  TACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGA  311

Query  569  AGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCT  628
            |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct  310  AGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCT  251

Query  629  T  629
            |
Sbjct  250  T  250


>SRR2298573.814921 814921 length=500
Length=500

 Score = 436 bits (236),  Expect = 4e-118
 Identities = 246/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  389  AAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCC  448
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  251  AAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCC  192

Query  449  AAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAG  508
            ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  191  AAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAG  132

Query  509  TACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGA  568
            ||||| |||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct  131  TACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGA  72

Query  569  AGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCT  628
            |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
```

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Sbjct  71   AGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCT  12

Query  629  TGGTGACCTGG  639
            |||||| ||||
Sbjct  11   TGGTGATCTGG  1


 Score = 398 bits (215),  Expect = 2e-106
 Identities = 237/248 (96%), Gaps = 0/248 (0%)
 Strand=Plus/Plus

Query  289  TACCACGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCT  348
            ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  251  TACCATGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCT  310

Query  349  GGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCG  408
            ||||||||||||||||||||||||| ||||||||||||| ||||||||||||||||||||
Sbjct  311  GGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCG  370

Query  409  GAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTA  468
            ||||||||||||||||||||||||||||||||||||| ||||||| ||||||||||||||
Sbjct  371  GAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAACCCAAGGTTTAACAAACCCTTTA  430

Query  469  GGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTA  528
            ||||||||||||||||||||||| |||||||||||||||||| || ||||||||| || |
Sbjct  431  GGATTGGTTCTAAACCTGAGATGGTGTGGAAGATACTTAGTAACTACCGATCTGGGAGGA  490

Query  529  CTGCAAAC  536
             |||||||
Sbjct  491  GTGCAAAC  498


>SRR2298573.595924 595924 length=500
Length=500

 Score = 436 bits (236),  Expect = 4e-118
 Identities = 246/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  396  CCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCT  455
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  251  CCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTT  192

Query  456  AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGC  515
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  191  AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTAC  132

Query  516  CGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACC  575
            ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  131  CGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACC  72

Query  576  CATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGAC  635
            ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  71   CATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGAT  12

Query  636  CTGGTTAAAAA  646
            |||||||||||
Sbjct  11   CTGGTTAAAAA  1
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 Score = 418 bits (226),  Expect = 2e-112
 Identities = 242/250 (97%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  345  GTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCC  404
            ||||||||||||||||||||||||||||| ||||||||||||| ||||||||||||||||
Sbjct  251  GTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCC  310

Query  405  AGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCC  464
            ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  311  AGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCC  370

Query  465  TTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGT  524
            ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  371  TTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGT  430

Query  525  AGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAA  584
            |||| |||||||||||||||||||||||||||||||||||||||||| ||||||||| ||
Sbjct  431  AGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGAACCCATAGGGAA  490

Query  585  CAAGTGACAC  594
            |||| |||||
Sbjct  491  CAAGCGACAC  500


>SRR2298573.482382 482382 length=500
Length=500

 Score = 436 bits (236),  Expect = 4e-118
 Identities = 246/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  320  CCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACA  379
            |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  251  CCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACA  192

Query  380  TTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGG  439
            |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  191  TTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGG  132

Query  440  CCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAA  499
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  131  CCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAA  72

Query  500  GATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGG  559
            |||||||||||||| |||||||||||||| ||||||||||||||||||||||||||||||
Sbjct  71   GATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGG  12

Query  560  ATGCCCAGAAG  570
            |||||||||||
Sbjct  11   ATGCCCAGAAG  1


 Score = 383 bits (207),  Expect = 6e-102
 Identities = 231/243 (95%), Gaps = 0/243 (0%)
 Strand=Plus/Plus

Query  283  GTGAGATACCACGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAG  342
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                 |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  251  GTGAGATACCATGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAG  310

Query  343  ACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTG  402
            ||||||||||||||||||||||||||||||| ||||||||||||| ||||||||||||||
Sbjct  311  ACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTG  370

Query  403  CCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAAC  462
            |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct  371  CCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAAC  430

Query  463  CCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTG  522
            ||||||||| |||| ||||||||||||||| ||||||||  ||||| |||| ||||| ||
Sbjct  431  CCTTTAGGAATGGTCCTAAACCTGAGATGTAGTGGAAGAACCTTAGAACCTACCGATTTG  490

Query  523  GTA  525
            |||
Sbjct  491  GTA  493


>SRR2298573.51148 51148 length=500
Length=500

 Score = 436 bits (236),  Expect = 4e-118
 Identities = 249/255 (98%), Gaps = 1/255 (0%)
 Strand=Plus/Plus

Query  322  ATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATT  381
            ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  1    ATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATT  60

Query  382  TTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCC  441
            |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCC  120

Query  442  AAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGA  501
            |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGA  180

Query  502  TACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGAT  561
            |||||||||||| |||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  181  TACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGAT  240

Query  562  GCCCAGAAGG-TACC  575
            |||||||||| ||||
Sbjct  241  GCCCAGAAGGGTACC  255


 Score = 409 bits (221),  Expect = 9e-110
 Identities = 248/261 (95%), Gaps = 2/261 (1%)
 Strand=Plus/Minus

Query  371  GAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTG  430
            ||| ||||||||||||| ||||| |||| ||||||||||| |||||||||||||||||||
Sbjct  500  GAAACAACATTTTGCTGTAAAGCCTCCTTTTGCCAGCGGACCAACACCTGGTAACAGGTG  441

Query  431  CCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGAT  490
            |||||||||| |||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  440  CCTCTGGGGCAAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGAT  381
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Query  491  GTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGC  550
            ||||||||||||||||||||||| |||||||||||||| |||||||||||||||||||||
Sbjct  380  GTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGC  321

Query  551  CCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGG  610
            |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Sbjct  320  CCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGG  261

Query  611  GGCCAGGTACCTCTATCTTGG  631
            ||||||||||| || ||| ||
Sbjct  260  GGCCAGGTACC-CT-TCTGGG  242


>SRR2298546.826318 826318 length=501
Length=501

 Score = 436 bits (236),  Expect = 4e-118
 Identities = 248/254 (98%), Gaps = 0/254 (0%)
 Strand=Plus/Plus

Query  1252  GTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTG  1311
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTG  60

Query  1312  GAGCATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATT  1371
             |||| |||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  61    GAGCGTTTACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATT  120

Query  1372  TATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGC  1431
             |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  121   TATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGC  180

Query  1432  AACTAAAAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTG  1491
             ||||||||||||||||||||||||||||||| ||||||||||||||||| ||||||||||
Sbjct  181   AACTAAAAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTG  240

Query  1492  ATGTAACCATATTG  1505
             |||| |||||||||
Sbjct  241   ATGTTACCATATTG  254


 Score = 387 bits (209),  Expect = 4e-103
 Identities = 237/251 (94%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  1365  GCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGAC  1424
             |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Sbjct  501   GCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGAC  442

Query  1425  TTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACA  1484
             ||||||||||||||||||||||||||||||||||||| |||||||||||||||| |||
Sbjct  441   TTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACA  382

Query  1485  CAAGTTGATGTAACCATATTGGGTAGTTTATTGCAATTGGACTTCCAAAATCCTAGGGTG  1544
             ||||||||||| |||||||||||||| ||||||||||||||||||||||||||| ||||
Sbjct  381   CAAGTTGATGTTACCATATTGGGTAGCTTATTGCAATTGGACTTCCAAAATCCTCGGGTA  322

Query  1545  TTTGGCCAAGACGTTGGTATCTATGATAATGCACCAACGCGGAAACAAAATCTTAAAAAG  1604
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             || || |||||||||||||| ||||| ||||||||||||||||| ||||||||||| ||
Sbjct  321   TTCGGTCAAGACGTTGGTATTTATGACAATGCACCAACGCGGAAGCAAAATCTTAAGAAA  262

Query  1605  ATTCTTACAAT  1615
             |||||||||||
Sbjct  261   ATTCTTACAAT  251


>SRR2298573.820409 820409 length=500
Length=500

 Score = 435 bits (235),  Expect = 2e-117
 Identities = 248/254 (98%), Gaps = 1/254 (0%)
 Strand=Plus/Minus

Query  380  TTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGG  439
            |||| ||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  253  TTTT-CTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGG  195

Query  440  CCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAA  499
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  194  CCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAA  135

Query  500  GATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGG  559
            |||||||||||||| |||||||||||||| ||||||||||||||||||||||||||||||
Sbjct  134  GATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGG  75

Query  560  ATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTA  619
            ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Sbjct  74   ATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTA  15

Query  620  CCTCTATCTTGGTG  633
            ||||||||||||||
Sbjct  14   CCTCTATCTTGGTG  1


 Score = 374 bits (202),  Expect = 3e-99
 Identities = 234/250 (94%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  372  AAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGC  431
            || ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  251  AAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGC  310

Query  432  CTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATG  491
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  311  CTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATG  370

Query  492  TTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCC  551
            |||||||||||||||||||||| |||||||||||||| ||||||||||||||||||||||
Sbjct  371  TTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCC  430

Query  552  CACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGG  611
            |||||||||||||||||||||||||| ||| || ||| ||| | ||||| | ||  ||||
Sbjct  431  CACGAAGGATGCCCAGAAGGTACCCAAAGGAAAAAAGGGACCCAATGGACCGGAATTGGG  490

Query  612  GCCAGGTACC  621
            |||||| |||
Sbjct  491  GCCAGGGACC  500
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>SRR2298573.724260 724260 length=500
Length=500

 Score = 435 bits (235),  Expect = 2e-117
 Identities = 245/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  303  ACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGA  362
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  251  ACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGA  310

Query  363  ACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGT  422
            ||||||||||| ||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  311  ACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGT  370

Query  423  AACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAA  482
            ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  371  AACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAA  430

Query  483  CCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGT  542
            ||||||||||||||||||||||||||||||| |||||||||||||| |||||||||||||
Sbjct  431  CCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGT  490

Query  543  TGTAAGGCCC  552
            ||||||||||
Sbjct  491  TGTAAGGCCC  500


 Score = 422 bits (228),  Expect = 1e-113
 Identities = 242/249 (97%), Gaps = 0/249 (0%)
 Strand=Plus/Minus

Query  309  TGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTAT  368
            ||| ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  249  TGCCCACACAGGCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTAT  190

Query  369  TGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGG  428
            ||||| ||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  189  TGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGG  130

Query  429  TGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAG  488
            ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  129  TGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAG  70

Query  489  ATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAG  548
            ||||||||||||||||||||||||| |||||||||||||| |||||||||||||||||||
Sbjct  69   ATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAG  10

Query  549  GCCCACGAA  557
            |||||||||
Sbjct  9    GCCCACGAA  1


>SRR2298573.708355 708355 length=500
Length=500

 Score = 435 bits (235),  Expect = 2e-117
```

```
 Identities = 245/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  326   TCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGC  385
             |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  1     TCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGC  60

Query  386   TGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAA  445
             || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    TGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAA  120

Query  446   GCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACT  505
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   GCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACT  180

Query  506   TAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCC  565
             |||||||| |||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  181   TAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCC  240

Query  566   AGAAGGTACC  575
             ||||||||||
Sbjct  241   AGAAGGTACC  250


 Score = 420 bits (227),  Expect = 4e-113
 Identities = 239/245 (98%), Gaps = 0/245 (0%)
 Strand=Plus/Minus

Query  358   TGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACAC  417
             |||||||||||||||| ||||||||||||| |||||||||||||||||||||||||||||
Sbjct  495   TGGGAACTTATTGGAAACAACATTTTGCTGGAAAGCATCCTATTGCCAGCGGAACAACAC  436

Query  418   CTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTT  477
             |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct  435   CTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTT  376

Query  478   CTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACA  537
             |||||||||||||||||||||||||||||||||||| |||||||||||||| ||||||||
Sbjct  375   CTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACA  316

Query  538   CTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTAT  597
             ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  315   CTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTAT  256

Query  598   GGATC  602
             |||||
Sbjct  255   GGATC  251


>SRR2298573.664456 664456 length=500
Length=500

 Score = 435 bits (235),  Expect = 2e-117
 Identities = 245/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  454   CTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCT  513
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  251   CTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCT  192
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Query  514  GCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTA  573
             |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  191  ACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTA  132

Query  574  CCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTG  633
            ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  131  CCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTG  72

Query  634  ACCTGGTTAAAAAGCGTCTAGTGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATT  693
            | ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  71   ATCTGGTTAAAAAACGTCTAGTGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATT  12

Query  694  TTATCAATGC  703
            ||||||||||
Sbjct  11   TTATCAATGC  2


 Score = 416 bits (225),  Expect = 6e-112
 Identities = 237/243 (98%), Gaps = 0/243 (0%)
 Strand=Plus/Plus

Query  389  AAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCC  448
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  253  AAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCC  312

Query  449  AAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAG  508
            ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  313  AAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAG  372

Query  509  TACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGA  568
            ||||| |||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct  373  TACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGA  432

Query  569  AGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCT  628
            |||||||||||||||||||| ||||| |||||||||||||||||||||| ||||||||||
Sbjct  433  AGGTACCCATAGGTAACAAGCGACACAATGGATCTGATCTGGGGCCAGGGACCTCTATCT  492

Query  629  TGG  631
            |||
Sbjct  493  TGG  495


>SRR2298573.584493 584493 length=500
Length=500

 Score = 435 bits (235),  Expect = 2e-117
 Identities = 245/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  322  ATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATT  381
            |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  251  ATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATT  310

Query  382  TTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCC  441
            |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  311  TTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCC  370

Query  442  AAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGA  501
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                |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  371   AAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGA  430

Query  502   TACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGAT  561
             |||||||||||| |||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  431   TACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGAT  490

Query  562   GCCCAGAAGG  571
             ||||||||||
Sbjct  491   GCCCAGAAGG  500


 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  322   ATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATT  381
             ||||| |||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  250   ATCCTTTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATT  191

Query  382   TTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCC  441
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  190   TTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCC  131

Query  442   AAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGA  501
             |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  130   AAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGA  71

Query  502   TACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGAT  561
             |||||||||||| |||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  70    TACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGAT  11

Query  562   GCCCAGAAGG  571
             ||||||||||
Sbjct  10    GCCCAGAAGG  1


>SRR2298573.530988 530988 length=500
Length=500

 Score = 435 bits (235),  Expect = 2e-117
 Identities = 245/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  382   TTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCC  441
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  500   TTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCC  441

Query  442   AAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGA  501
             |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  440   AAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGA  381

Query  502   TACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGAT  561
             |||||||||||| |||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  380   TACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGAT  321

Query  562   GCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACC  621
             ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  320   GCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACC  261
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Query  622  TCTATCTTGG  631
            ||||||||||
Sbjct  260  TCTATCTTGG  251


 Score = 414 bits (224),  Expect = 2e-111
 Identities = 236/242 (98%), Gaps = 0/242 (0%)
 Strand=Plus/Plus

Query  276  TCTACTAGTGAGATACCACGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGT  335
            |||| ||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  9    TCTATTAGTGAGATACCATGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGT  68

Query  336  TTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCAT  395
            |||||||||||||||||||||||||||||||||||||| ||||||||||||| |||||||
Sbjct  69   TTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCAT  128

Query  396  CCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCT  455
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  129  CCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTT  188

Query  456  AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGC  515
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  189  AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTAC  248

Query  516  CG  517
            ||
Sbjct  249  CG  250


>SRR2298573.512385 512385 length=500
Length=500

 Score = 435 bits (235),  Expect = 2e-117
 Identities = 247/253 (98%), Gaps = 0/253 (0%)
 Strand=Plus/Minus

Query  347  CTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAG  406
            ||||||||||||||||||||||||||| ||||||||||||| ||||||||||||||||||
Sbjct  253  CTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAG  194

Query  407  CGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTT  466
            ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  193  CGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTT  134

Query  467  TAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAG  526
            ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  133  TAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAG  74

Query  527  TACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACA  586
            || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  73   TAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACA  14

Query  587  AGTGACACTATGG  599
            || ||||||||||
Sbjct  13   AGCGACACTATGG  1
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 Score = 431 bits (233),  Expect = 2e-116
 Identities = 248/255 (97%), Gaps = 1/255 (0%)
 Strand=Plus/Plus

Query  312   TCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGG  371
             |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  247   TCAC-CAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGG  305

Query  372   AAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGC  431
             || ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  306   AAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGC  365

Query  432   CTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATG  491
             |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  366   CTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATG  425

Query  492   TTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCC  551
             |||||||||||||||||||||| |||||||||||||| ||||||||||||||||||||||
Sbjct  426   TTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCC  485

Query  552   CACGAAGGATGCCCA  566
             | |||||||||||||
Sbjct  486   CCCGAAGGATGCCCA  500


>SRR2298573.476602 476602 length=500
Length=500

 Score = 435 bits (235),  Expect = 2e-117
 Identities = 247/253 (98%), Gaps = 0/253 (0%)
 Strand=Plus/Plus

Query  409   GAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTA  468
             ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  1     GAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTA  60

Query  469   GGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTA  528
             ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  61    GGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTA  120

Query  529   CTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAG  588
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   GTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAG  180

Query  589   TGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGC  648
              ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||| |
Sbjct  181   CGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAAC  240

Query  649   GTCTAGTGGGCCA  661
             |||||||||||||
Sbjct  241   GTCTAGTGGGCCA  253


 Score = 385 bits (208),  Expect = 2e-102
 Identities = 236/250 (94%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  462   CCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCT  521
             ||||||||||||||||| ||||||| ||||||  |||||||||||||| ||| |||||||
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Sbjct  500  CCCTTTAGGATTGGTTCCAAACCTGGGATGTTTGGGAAGATACTTAGTCCCTACCGATCT  441

Query  522  GGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGG  581
            ||||||| || |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  440  GGTAGTAGTGAAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGG  381

Query  582  TAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTT  641
            ||||||| ||| ||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  380  TAACAAGCGACTCTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTT  321

Query  642  AAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTTTATCAAT  701
            ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  320  AAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTATCAAT  261

Query  702  GCTACAATGG  711
            || || ||||
Sbjct  260  GCCACTATGG  251


>SRR2298573.293144 293144 length=500
Length=500

 Score = 435 bits (235),  Expect = 2e-117
 Identities = 245/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  397  CTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTA  456
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  250  CTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTA  191

Query  457  ACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCC  516
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  190  ACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACC  131

Query  517  GATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCC  576
            |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  130  GATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCC  71

Query  577  ATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACC  636
            |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  70   ATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATC  11

Query  637  TGGTTAAAAA  646
            ||||||||||
Sbjct  10   TGGTTAAAAA  1


 Score = 401 bits (217),  Expect = 2e-107
 Identities = 239/250 (96%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  327  CTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCT  386
            ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  251  CTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCT  310

Query  387  GCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAG  446
            | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  311  GTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAG  370
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Query  447  CCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTT  506
            ||||||| |||||||||||||||||||||||||||||| ||||||||| |||||||||||
Sbjct  371  CCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCCGAGATGTTGGGGAAGATACTT  430

Query  507  AGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCA  566
            ||||||| |||||||||||||| || |||||||||||||||||||||||||||| |||| 
Sbjct  431  AGTACCTACCGATCTGGTAGTAGTGAAAACACTAGTTGTAAGGCCCACGAAGGAGGCCCC  490

Query  567  GAAGGTACCC  576
            ||||| ||||
Sbjct  491  GAAGGGACCC  500


>SRR2298573.260918 260918 length=500
Length=500

 Score = 435 bits (235),  Expect = 2e-117
 Identities = 248/254 (98%), Gaps = 1/254 (0%)
 Strand=Plus/Plus

Query  384  GCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAA  443
            |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAA  60

Query  444  AAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATA  503
            |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATA  120

Query  504  CTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGC  563
            |||||||||| |||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  121  CTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGC  180

Query  564  CCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTC  623
            ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  181  CCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTC  240

Query  624  TATCTTGGTG-ACC  636
            |||||||||| |||
Sbjct  241  TATCTTGGTGCACC  254


 Score = 424 bits (229),  Expect = 3e-114
 Identities = 246/254 (97%), Gaps = 1/254 (0%)
 Strand=Plus/Minus

Query  384  GCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAA  443
            |||| ||||||||||||||||||||||||||| || ||||||||||||||||||||||||
Sbjct  500  GCTGTAAAGCATCCTATTGCCAGCGGAACAACCCCGGGTAACAGGTGCCTCTGGGGCCAA  441

Query  444  AAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATA  503
            |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  440  AAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATA  381

Query  504  CTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGC  563
            |||||||||| |||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  380  CTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGC  321

Query  564  CCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTC  623
            ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
```

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Sbjct  320  CCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTC  261

Query  624  TATCTTGGTG-ACC  636
            |||||||||| |||
Sbjct  260  TATCTTGGTGCACC  247


>SRR2298573.165720 165720 length=500
Length=500

 Score = 435 bits (235),  Expect = 2e-117
 Identities = 245/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  309  TGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTAT  368
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTAT  60

Query  369  TGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGG  428
            ||||| ||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGG  120

Query  429  TGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAG  488
            ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  121  TGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAG  180

Query  489  ATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAG  548
            ||||||||||||||||||||||||| |||||||||||||| |||||||||||||||||||
Sbjct  181  ATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAG  240

Query  549  GCCCACGAAG  558
            ||||||||||
Sbjct  241  GCCCACGAAG  250


 Score = 407 bits (220),  Expect = 3e-109
 Identities = 240/250 (96%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  321  CATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACAT  380
            |||||||||||||||||||||||||   ||||||||||||||||||| ||||| ||||||
Sbjct  500  CATCCTCTAGTAAGTTTGTGAGACGGTGGGTGACGTGTGGGAACTTAATGGAAACAACAT  441

Query  381  TTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGC  440
            ||||||| ||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  440  TTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTTCCTCTGGGGC  381

Query  441  CAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAG  500
            ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  380  CAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAG  321

Query  501  ATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGA  560
            ||||||||||||| |||||||||||||| |||||||||||||||||||||||||||||||
Sbjct  320  ATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGA  261

Query  561  TGCCCAGAAG  570
            ||||||||||
Sbjct  260  TGCCCAGAAG  251
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>SRR2298573.147826 147826 length=500
Length=500

 Score = 435 bits (235),  Expect = 2e-117
 Identities = 245/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  420  GGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCT  479
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCT  60

Query  480  AAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACT  539
            |||||||||||||||||||||||||||||||||| ||||||||||||||| ||||||||||
Sbjct  61   AAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACT  120

Query  540  AGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGG  599
            ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  121  AGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGG  180

Query  600  ATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGC  659
            ||||||||||||||||||||||||||||||||||| ||||||||||| ||||||||||||
Sbjct  181  ATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGC  240

Query  660  CAAACCCggg  669
            ||||||||||
Sbjct  241  CAAACCCGGG  250


 Score = 326 bits (176),  Expect = 1e-84
 Identities = 220/242 (91%), Gaps = 0/242 (0%)
 Strand=Plus/Minus

Query  636  CTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTTT  695
            ||||||||||| | | | ||||||| |||||||||||| ||||||||||| |||||||||
Sbjct  492  CTGGTTAAAAAACCTTTTGTGGGCCCAACCCGGGGGGGTTCCCCGGTTTCTTTTTATTTT  433

Query  696  ATCAATGCTACAATGGAGACAATTAAAAGTATTGCAGATATGGCGACCGGAGTGGTCAGT  755
            | | |||| || ||||||||||||||| ||| ||||||||||||||||||||||||||||
Sbjct  432  AACCATGCCACTATGGAGACAATTAAGAGTTTTGCAGATATGGCGACCGGAGTGGTCAGT  373

Query  756  TCAGTTGATTCCACTATCAATGCAGTTAATGAGAGAGTAGAAAATGTGGGCAATGAAATT  815
            |||||||||||||||||||||| ||||||||||||||| |||||||| || |||||||||
Sbjct  372  TCAGTTGATTCCACTATCAATGTAGTTAATGAGAGAGTGGAAAATGTAGGTAATGAAATT  313

Query  816  GGAGGTAACCTATTAACCAAAGTAGCAGATGATGCTTCTAATGTGCTTGGACCAAATTGT  875
            ||||||||  ||||||||||||| ||||||||||||||||||||||| |||||||||||
Sbjct  312  GGAGGTAATTTATTAACCAAAGTTGCAGATGATGCTTCTAATGTGCTCGGACCAAATTGC  253

Query  876  TA  877
            ||
Sbjct  252  TA  251


>SRR2298573.138574 138574 length=500
Length=500

 Score = 435 bits (235),  Expect = 2e-117
 Identities = 245/250 (98%), Gaps = 0/250 (0%)
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 Strand=Plus/Minus

Query  382   TTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCC  441
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  500   TTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCC  441

Query  442   AAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGA  501
             |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  440   AAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGA  381

Query  502   TACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGAT  561
             |||||||||||| ||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  380   TACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGAT  321

Query  562   GCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACC  621
             ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  320   GCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACC  261

Query  622   TCTATCTTGG  631
             ||||||||||
Sbjct  260   TCTATCTTGG  251


 Score = 407 bits (220),  Expect = 3e-109
 Identities = 239/248 (96%), Gaps = 1/248 (0%)
 Strand=Plus/Plus

Query  330   GTA-AGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGC  388
             ||| ||||||||||||||||||||||||||||||||||||||||| ||||||||||||| 
Sbjct  4     GTATAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGT  63

Query  389   AAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCC  448
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  64    AAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCC  123

Query  449   AAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAG  508
             ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  124   AAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAG  183

Query  509   TACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGA  568
             ||||| |||||||||||||| ||||||| |||||||||||||| ||||||||||||||||
Sbjct  184   TACCTACCGATCTGGTAGTAGTGCAAACCCTAGTTGTAAGGCCAACGAAGGATGCCCAGA  243

Query  569   AGGTACCC  576
             ||| ||||
Sbjct  244   AGGAACCC  251


>SRR2298573.114824 114824 length=500
Length=500

 Score = 435 bits (235),  Expect = 2e-117
 Identities = 245/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  382   TTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCC  441
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  250   TTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCC  191
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Query  442   AAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGA  501
             |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  190   AAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGA  131

Query  502   TACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGAT  561
             |||||||||||| |||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  130   TACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGAT  71

Query  562   GCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACC  621
             ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  70    GCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACC  11

Query  622   TCTATCTTGG  631
             ||||||||||
Sbjct  10    TCTATCTTGG  1


 Score = 435 bits (235),  Expect = 2e-117
 Identities = 245/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  327   CTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCT  386
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  251   CTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCT  310

Query  387   GCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAG  446
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  311   GTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAG  370

Query  447   CCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTT  506
             ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  371   CCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTT  430

Query  507   AGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCA  566
             ||||||| |||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  431   AGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCA  490

Query  567   GAAGGTACCC  576
             ||||||||||
Sbjct  491   GAAGGTACCC  500


>SRR2298573.95695 95695 length=500
Length=500

 Score = 435 bits (235),  Expect = 2e-117
 Identities = 245/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  303   ACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGA  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     ACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGA  60

Query  363   ACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGT  422
             ||||||||||| ||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  61    ACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGT  120

Query  423   AACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAA  482
             ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
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Sbjct  121  AACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAA  180

Query  483  CCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGT  542
            ||||||||||||||||||||||||||||||| |||||||||||||| |||||||||||||
Sbjct  181  CCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGT  240

Query  543  TGTAAGGCCC  552
            ||||||||||
Sbjct  241  TGTAAGGCCC  250


 Score = 327 bits (177),  Expect = 3e-85
 Identities = 226/250 (90%), Gaps = 1/250 (0%)
 Strand=Plus/Minus

Query  420  GGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCT  479
            |||||| ||  |||  |||| |||| |||||||| ||| ||||||||| |||||||||||
Sbjct  496  GGTAACTGGGTCCTTCGGGGACAAAGGCCAAGGTTTAAAAAACCCTTTGGGATTGGTTCT  437

Query  480  AAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACT  539
            |||||||| ||  ||||||||||||||||| ||| |||||||||||||| ||||||| |
Sbjct  436  AAACCTGAAATTGTGTGGAAGATACTTAGTTCCTACCGATCTGGTAGTAGTGCAAACGCG  377

Query  540  AGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGG  599
            ||| |||||||||||||||||||||| |||||||||||||||||||||| ||||||||||
Sbjct  376  AGTGGTAAGGCCCACGAAGGATGCCCGGAAGGTACCCATAGGTAACAAGCGACACTATGG  317

Query  600  ATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGC  659
            ||||||||||||||||||||||||||||||||||| ||||||||||| ||||||||||||
Sbjct  316  ATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGC  257

Query  660  CAAACCCggg  669
            |||||| |||
Sbjct  256  CAAACC-GGG  248


>SRR2298566.272602 272602 length=500
Length=500

 Score = 435 bits (235),  Expect = 2e-117
 Identities = 245/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  1226  GAATGTTAACCAAGGAACAGCTGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGT  1285
             ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  500   GAATGTTAATCAAGGAACAGCTGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGT  441

Query  1286  GACATATGACTCAAAGTTAGAATTTGGAGCATTTACCAATTTACCACATGTATTGATGAA  1345
             |||||||||||||||||||||||||||||||||||||||| |||||||||| ||||||||
Sbjct  440   GACATATGACTCAAAGTTAGAATTTGGAGCATTTACCAATCTACCACATGTGTTGATGAA  381

Query  1346  TTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGT  1405
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  380   TTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGT  321

Query  1406  TAAAACGGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCTAT  1465
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  320   TAAAACAGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCCAT  261
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Query  1466  ACCTTCAGGT  1475
             ||||||||||
Sbjct  260   ACCTTCAGGT  251


 Score = 401 bits (217),  Expect = 2e-107
 Identities = 239/250 (96%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  1176  TCAAGATACTTTGCAGCAGTACGGTGTGGCTTTCATTTTCAGGTGCAAGTGAATGTTAAC  1235
             ||||||||||||||||||||||||||||| ||||||||||| || ||||||||||||||
Sbjct  1     TCAAGATACTTTGCAGCAGTACGGTGTGGTTTTCATTTTCAAGTACAAGTGAATGTTAAT  60

Query  1236  CAAGGAACAGCTGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGAC  1295
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    CAAGGAACAGCTGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGAC  120

Query  1296  TCAAAGTTAGAATTTGGAGCATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAG  1355
             |||||||||||||||||||||||||||||| |||||||||| ||||||||||||||||||
Sbjct  121   TCAAAGTTAGAATTTGGAGCATTTACCAATCTACCACATGTGTTGATGAATTTGGCTGAG  180

Query  1356  ACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGAT  1415
             || |||||||||||||||||||||||||||||||||| ||||||| |||||||||| |||
Sbjct  181   ACAACACAGGCTGATTTATGTATCCCCTATGTTGCTGCCACAAACAATGTTAAAACAGAT  240

Query  1416  TCGTCAGACT  1425
             |||||| |||
Sbjct  241   TCGTCAAACT  250


>SRR2298546.837218 837218 length=501
Length=501

 Score = 435 bits (235),  Expect = 2e-117
 Identities = 247/253 (98%), Gaps = 0/253 (0%)
 Strand=Plus/Minus

Query  1264  TGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCATTTACCA  1323
             |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  501   TGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCGTTTACCA  442

Query  1324  ATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCT  1383
             ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  441   ATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCT  382

Query  1384  ATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACTAAAAGTCT  1443
             |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Sbjct  381   ATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAACTAAAAGTCT  322

Query  1444  ATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGATGTAACCATAT  1503
             ||||||||||||||||||| ||||||||||||||||| |||||||||||||| |||||||
Sbjct  321   ATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGATGTTACCATAT  262

Query  1504  TGGGTAGTTTATT  1516
             |||||||||||||
Sbjct  261   TGGGTAGTTTATT  249


 Score = 403 bits (218),  Expect = 4e-108
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 Identities = 240/251 (96%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  1096  GGGCTAGAGGACATCAGATAACCCATGTGGAATTGCCAAAAGTCTTTTGGGACAAAAACA  1155
             ||||| |||||||||||||||||||||||||| | |||||||||||||||||||||||||
Sbjct  1     GGGCTGGAGGACATCAGATAACCCATGTGGAACTACCAAAAGTCTTTTGGGACAAAAACA  60

Query  1156  GTAAGCCAGCCTATGGCCAATCAAGATACTTTGCAGCAGTACGGTGTGGCTTTCATTTTC  1215
             | ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  61    GCAAGCCAGCCTATGGCCAATCAAGATACTTTGCAGCAGTACGGTGTGGTTTTCATTTTC  120

Query  1216  AGGTGCAAGTGAATGTTAACCAAGGAACAGCTGGTAGTGCATTGGTGGTGTATGAACCCA  1275
             | || |||||||||||||| ||||||||||| ||||||||||||||||||||||||||||
Sbjct  121   AAGTACAAGTGAATGTTAATCAAGGAACAGCCGGTAGTGCATTGGTGGTGTATGAACCCA  180

Query  1276  AACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCATTTACCAATTTACCACATG  1335
             |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  181   AACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCGTTTACCAATTTACCACATG  240

Query  1336  TATTGATGAAT  1346
             | |||||||||
Sbjct  241   TGTTGATGAAT  251


>SRR2298546.758593 758593 length=500
Length=500

 Score = 435 bits (235),  Expect = 2e-117
 Identities = 247/253 (98%), Gaps = 0/253 (0%)
 Strand=Plus/Minus

Query  1256  ATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGC  1315
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  253   ATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGC  194

Query  1316  ATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTTATG  1375
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  193   GTTTACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATTTATG  134

Query  1376  TATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACT  1435
             |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct  133   TATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAACT  74

Query  1436  AAAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGATGT  1495
             |||||||||||||||||||||||||| ||||||||||||||||| |||||||||||||||
Sbjct  73    AAAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGATGT  14

Query  1496  AACCATATTGGGT  1508
              ||||||||||||
Sbjct  13    TACCATATTGGGT  1


 Score = 422 bits (228),  Expect = 1e-113
 Identities = 244/252 (97%), Gaps = 0/252 (0%)
 Strand=Plus/Plus

Query  1172  CCAATCAAGATACTTTGCAGCAGTACGGTGTGGCTTTCATTTTCAGGTGCAAGTGAATGT  1231
             ||||||||||||||||||||||||||||||||| ||||||||||| || |||||||||||
Sbjct  249   CCAATCAAGATACTTTGCAGCAGTACGGTGTGGTTTTCATTTTCAAGTACAAGTGAATGT  308
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Query  1232  TAACCAAGGAACAGCTGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATA  1291
             ||| ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  309   TAATCAAGGAACAGCCGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATA  368

Query  1292  TGACTCAAAGTTAGAATTTGGAGCATTTACCAATTTACCACATGTATTGATGAATTTGGC  1351
             |||||||||||||||||||||||| |||||||||||||||||||| ||||||||||||||
Sbjct  369   TGACTCAAAGTTAGAATTTGGAGCGTTTACCAATTTACCACATGTGTTGATGAATTTGGC  428

Query  1352  TGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAAC  1411
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  429   TGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAAC  488

Query  1412  GGATTCGTCAGA  1423
              |||||||||||
Sbjct  489   AGATTCGTCAGA  500


>SRR2298546.171832 171832 length=502
Length=502

 Score = 435 bits (235),  Expect = 2e-117
 Identities = 248/254 (98%), Gaps = 1/254 (0%)
 Strand=Plus/Plus

Query  1248  GGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAA  1307
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2     GGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAA  61

Query  1308  TTTGGAGCATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCT  1367
             |||||||| |||||||||||||||||||| ||||||||||||||||||||||||||||||
Sbjct  62    TTTGGAGCGTTTACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCT  121

Query  1368  GATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTA  1427
             |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Sbjct  122   GATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTA  181

Query  1428  GGGCAACTAAAAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAA  1487
             ||||||||||||||||||||||||||||||||||| ||||||||||||||||| ||||||
Sbjct  182   GGGCAACTAAAAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAA  241

Query  1488  GTTGATGT-AACCA  1500
             |||||||| |||||
Sbjct  242   GTTGATGTTAACCA  255


 Score = 399 bits (216),  Expect = 6e-107
 Identities = 240/252 (95%), Gaps = 0/252 (0%)
 Strand=Plus/Minus

Query  1476  TCTGCGACACAAGTTGATGTAACCATATTGGGTAGTTTATTGCAATTGGACTTCCAAAAT  1535
             ||||| |||||||||||||| |||||||||||||| ||||||||||||||||||||||||
Sbjct  502   TCTGCTACACAAGTTGATGTTACCATATTGGGTAGCTTATTGCAATTGGACTTCCAAAAT  443

Query  1536  CCTAGGGTGTTTGGCCAAGACGTTGGTATCTATGATAATGCACCAACGCGGAAACAAAAT  1595
             |||||||| || || |||||||||||||| ||||| ||||||| ||||||||| ||||||
Sbjct  442   CCTAGGGTATTCGGTCAAGACGTTGGTATTTATGACAATGCACAAACGCGGAAGCAAAAT  383

Query  1596  CTTAAAAAGATTCTTACAATGAGCACTAAATACAAGTGGACTAGGGGAAAAATTGACATT  1655
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             ||||| || |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  382   CTTAAGAAAATTCTTACAATGAGCACTAAATACAAGTGGACTAGGGGAAAAATTGACATT  323

Query  1656  GCAGAAGGGCCAGGTTCTATGAACATGGCGAACGTATTGAGTACCACTGCAGCGCAATCA  1715
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  322   GCAGAAGGGCCAGGTTCTATGAACATGGCGAACGTATTGAGTACCACTGCAGCGCAATCA  263

Query  1716  ATTGCTTTGGTT  1727
             ||||||||||||
Sbjct  262   ATTGCTTTGGTT  251


>SRR2298546.85661 85661 length=502
Length=502

 Score = 435 bits (235),  Expect = 2e-117
 Identities = 247/253 (98%), Gaps = 0/253 (0%)
 Strand=Plus/Plus

Query  1259  GGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCATT  1318
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  1     GGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCGTT  60

Query  1319  TACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTAT  1378
             |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  61    TACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTAT  120

Query  1379  CCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACTAAA  1438
             ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  121   CCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAACTAAA  180

Query  1439  AGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGATGTAAC  1498
             |||||||||||||||||||||||| ||||||||||||||||| |||||||||||||| ||
Sbjct  181   AGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGATGTTAC  240

Query  1499  CATATTGGGTAGT  1511
             |||||||||||||
Sbjct  241   CATATTGGGTAGT  253


 Score = 407 bits (220),  Expect = 3e-109
 Identities = 240/250 (96%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  1321  CCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTATCC  1380
             |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  502   CCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTATCC  443

Query  1381  CCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACTAAAAG  1440
             ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  442   CCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAACTAAAAG  383

Query  1441  TCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGATGTAACCA  1500
             |||||||||||||||||||||| ||||||||||||||||| |||||||||||||| ||||
Sbjct  382   TCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGATGTTACCA  323

Query  1501  TATTGGGTAGTTTATTGCAATTGGACTTCCAAAATCCTAGGGTGTTTGGCCAAGACGTTG  1560
             |||||||||| |||||||||||||||||||||||||||||||| || || ||||||||||
Sbjct  322   TATTGGGTAGCTTATTGCAATTGGACTTCCAAAATCCTAGGGTATTCGGTCAAGACGTTG  263
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Query  1561  GTATCTATGA  1570
             |||| |||||
Sbjct  262   GTATTTATGA  253


>SRR2298382.81982 81982 length=502
Length=502

 Score = 435 bits (235),  Expect = 2e-117
 Identities = 247/253 (98%), Gaps = 0/253 (0%)
 Strand=Plus/Minus

Query  373  AGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCC  432
            ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  253  AGCAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCC  194

Query  433  TCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGT  492
            ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  193  TCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGT  134

Query  493  TGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCC  552
            ||||||||||||||||||||| |||||||||||||| |||||||||||||||||||||||
Sbjct  133  TGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCC  74

Query  553  ACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGG  612
            |||||||| ||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct  73   ACGAAGGAGGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGG  14

Query  613  CCAGGTACCTCTA  625
            |||||||||||||
Sbjct  13   CCAGGTACCTCTA  1


 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  347  CTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAG  406
            ||||||||||||||||||||||||||| ||||||||||||| ||||||||||||||||||
Sbjct  252  CTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAG  311

Query  407  CGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTT  466
            ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  312  CGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTT  371

Query  467  TAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAG  526
            ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  372  TAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAG  431

Query  527  TACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACA  586
            || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  432  TAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACA  491

Query  587  AGTGACACTA  596
            || |||||||
Sbjct  492  AGCGACACTA  501
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>SRR2298573.824788 824788 length=500
Length=500

 Score = 433 bits (234),  Expect = 5e-117
 Identities = 246/252 (98%), Gaps = 0/252 (0%)
 Strand=Plus/Plus

Query  436   GGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGT  495
             |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGT  60

Query  496   GGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACG  555
             |||||||||||||||||| |||||||||||||| ||||||||||||||||||||||||||
Sbjct  61    GGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACG  120

Query  556   AAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCA  615
             ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  121   AAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCA  180

Query  616   GGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggAT  675
             ||||||||||||||||||| ||||||||||| ||||||||||||||||||||||||||||
Sbjct  181   GGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGAT  240

Query  676   CCCCGGTTTCCT  687
             ||||||||||||
Sbjct  241   CCCCGGTTTCCT  252


 Score = 340 bits (184),  Expect = 3e-89
 Identities = 234/258 (91%), Gaps = 4/258 (2%)
 Strand=Plus/Minus

Query  668   ggggggATCCCCGGTTTCCTTTTATTTTATCA--ATGCTACAATGGAGACAATTAAAAGT  725
             ||||||||||||||||||||||| |||| |||  |||| ||  |||||||||||||  ||
Sbjct  500   GGGGGGATCCCCGGTTTCCTTTT-TTTT-TCACCATGCCACTGTGGAGACAATTAAGGGT  443

Query  726   ATTGCAGATATGGCGACCGGAGTGGTCAGTTCAGTTGATTCCACTATCAATGCAGTTAAT  785
             ||||||| | |||| ||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  442   ATTGCAGTTTTGGCCACCGGAGTGGTCAGTTCAGTTGATTCCACTATCAATGTAGTTAAT  383

Query  786   GAGAGAGTAGAAAATGTGGGCAATGAAATTGGAGGTAACCTATTAACCAAAGTAGCAGAT  845
             |||||||| |||||| | || |||||||||||||||||  ||||||||||||| ||||||
Sbjct  382   GAGAGAGTGGAAAATTTAGGTAATGAAATTGGAGGTAATTTATTAACCAAAGTTGCAGAT  323

Query  846   GATGCTTCTAATGTGCTTGGACCAAATTGTTATGCTACAACAGCTGAACCAGAGAACAAA  905
             ||||||||||||||||| ||||||||||| ||||||||||||||||||||||||||||||
Sbjct  322   GATGCTTCTAATGTGCTCGGACCAAATTGCTATGCTACAACAGCTGAACCAGAGAACAAA  263

Query  906   GATGTGGTACAGGCAACC  923
             ||||| ||||||| ||||
Sbjct  262   GATGTAGTACAGGAAACC  245


>SRR2298573.800813 800813 length=500
Length=500

 Score = 433 bits (234),  Expect = 5e-117
 Identities = 244/249 (98%), Gaps = 0/249 (0%)
 Strand=Plus/Plus
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Query  327   CTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCT  386
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  1     CTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCT  60

Query  387   GCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAG  446
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    GTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAG  120

Query  447   CCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTT  506
             ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   CCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTT  180

Query  507   AGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCA  566
             ||||||| |||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  181   AGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCA  240

Query  567   GAAGGTACC  575
             |||||||||
Sbjct  241   GAAGGTACC  249


 Score = 424 bits (229),  Expect = 3e-114
 Identities = 243/250 (97%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  352   GACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAA  411
             |||||||||||||||||||||| ||||||||||||| |||||||||||||||||||||||
Sbjct  500   GACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAA  441

Query  412   CAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGA  471
             |||| ||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Sbjct  440   CAACCCCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGA  381

Query  472   TTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTG  531
             |||||||||||||||||||||||||||||||||||||||||| |||||||||||||| ||
Sbjct  380   TTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTG  321

Query  532   CAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGA  591
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  320   CAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGA  261

Query  592   CACTATGGAT  601
             ||||||||||
Sbjct  260   CACTATGGAT  251


>SRR2298573.779215 779215 length=500
Length=500

 Score = 433 bits (234),  Expect = 5e-117
 Identities = 244/249 (98%), Gaps = 0/249 (0%)
 Strand=Plus/Minus

Query  455   TAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTG  514
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  250   TAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTA  191

Query  515   CCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTAC  574
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            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  190  CCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTAC  131

Query  575  CCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGA  634
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  130  CCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGA  71

Query  635  CCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTT  694
             ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  70   TCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTT  11

Query  695  TATCAATGC  703
            |||||||||
Sbjct  10   TATCAATGC  2


 Score = 412 bits (223),  Expect = 7e-111
 Identities = 241/250 (96%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  356  TGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAAC  415
            |||||| ||||||||||| ||||||||||||| |||||||||||||||||||||||||||
Sbjct  251  TGTGGGCACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAAC  310

Query  416  ACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGG  475
            |||||||||||||||||||||||||||||||||||||| || ||||||||||||||||||
Sbjct  311  ACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTACCAAACCCTTTAGGATTGG  370

Query  476  TTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAA  535
            |||||||||||||||||||||||||||||||||||||| |||||||||||||| ||||||
Sbjct  371  TTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAA  430

Query  536  CACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACT  595
            |||||||||||||||||||||||||||||||||||||||||||||| |||||| ||||||
Sbjct  431  CACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGGAACAAGGGACACT  490

Query  596  ATGGATCTGA  605
            ||||||||||
Sbjct  491  ATGGATCTGA  500


>SRR2298573.758263 758263 length=500
Length=500

 Score = 433 bits (234),  Expect = 5e-117
 Identities = 244/249 (98%), Gaps = 0/249 (0%)
 Strand=Plus/Minus

Query  455  TAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTG  514
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  249  TAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTA  190

Query  515  CCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTAC  574
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  189  CCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTAC  130

Query  575  CCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGA  634
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  129  CCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGA  70
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Query  635   CCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTT  694
              ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  69    TCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTT  10

Query  695   TATCAATGC  703
             |||||||||
Sbjct  9     TATCAATGC  1


 Score = 414 bits (224),  Expect = 2e-111
 Identities = 242/251 (96%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  449   AAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAG  508
             ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  250   AAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAG  309

Query  509   TACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGA  568
             ||||| |||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct  310   TACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGA  369

Query  569   AGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCT  628
             |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct  370   AGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCT  429

Query  629   TGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTT  688
             |||||| ||||||||||| ||||||| |||||||||||||||||||||||||| ||||||
Sbjct  430   TGGTGATCTGGTTAAAAAACGTCTAGGGGGCCAAACCCGGGGGGGATCCCCGGGTTCCTT  489

Query  689   TTATTTTATCA  699
             ||||||| |||
Sbjct  490   TTATTTTTTCA  500


>SRR2298573.736368 736368 length=500
Length=500

 Score = 433 bits (234),  Expect = 5e-117
 Identities = 244/249 (98%), Gaps = 0/249 (0%)
 Strand=Plus/Minus

Query  330   GTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCA  389
             |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||| |
Sbjct  249   GTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTA  190

Query  390   AAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCA  449
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  189   AAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCA  130

Query  450   AGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGT  509
             |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  129   AGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGT  70

Query  510   ACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAA  569
             |||| |||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  69    ACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAA  10

Query  570   GGTACCCAT  578
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             |||||||||
Sbjct  9     GGTACCCAT  1


 Score = 405 bits (219),  Expect = 1e-108
 Identities = 239/249 (96%), Gaps = 0/249 (0%)
 Strand=Plus/Plus

Query  251   GGGGTGGCAGATGGCGTGCCATAATTCTACTAGTGAGATACCACGCTTGTGGACCTTATG  310
             ||||||| |||||||||||||||  |||| ||||||||||||| ||||||||||||||||
Sbjct  251   GGGGTGGTAGATGGCGTGCCATAGCTCTATTAGTGAGATACCATGCTTGTGGACCTTATG  310

Query  311   CTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTG  370
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  311   CTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTG  370

Query  371   GAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTG  430
             ||| ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  371   GAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTG  430

Query  431   CCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGAT  490
             |||||||||||||||||| |||| ||||||||||||||||||||||||||||||||||||
Sbjct  431   CCTCTGGGGCCAAAAGCCCAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGAT  490

Query  491   GTTGTGGAA  499
             |||| ||||
Sbjct  491   GTTGGGGAA  499


>SRR2298573.593802 593802 length=500
Length=500

 Score = 433 bits (234),  Expect = 5e-117
 Identities = 246/252 (98%), Gaps = 0/252 (0%)
 Strand=Plus/Plus

Query  277   CTACTAGTGAGATACCACGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTT  336
             ||| ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  249   CTATTAGTGAGATACCATGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTT  308

Query  337   TGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATC  396
             ||||||||||||||||||||||||||||||||||||| ||||||||||||| ||||||||
Sbjct  309   TGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATC  368

Query  397   CTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTA  456
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  369   CTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTA  428

Query  457   ACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCC  516
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  429   ACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACC  488

Query  517   GATCTGGTAGTA  528
             ||||||||||||
Sbjct  489   GATCTGGTAGTA  500


 Score = 418 bits (226),  Expect = 2e-112
 Identities = 242/250 (97%), Gaps = 0/250 (0%)
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 Strand=Plus/Minus

Query  333  AGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAG  392
            |||||| |||||||||||||||||||||||||||||||||| |||| |||||||| ||||
Sbjct  250  AGTTTGGGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACTTTTTGCTGTAAAG  191

Query  393  CATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGG  452
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  190  CATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGG  131

Query  453  TCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACC  512
            | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  130  TTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACC  71

Query  513  TGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGT  572
            | |||||||||||||| |||||||||||||||||||||||||||||||||||||| ||||
Sbjct  70   TACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGGAGGT  11

Query  573  ACCCATAGGT  582
            ||||||||||
Sbjct  10   ACCCATAGGT  1


>SRR2298573.582811 582811 length=500
Length=500

 Score = 433 bits (234),  Expect = 5e-117
 Identities = 246/252 (98%), Gaps = 0/252 (0%)
 Strand=Plus/Plus

Query  449  AAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAG  508
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  249  AAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAG  308

Query  509  TACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGA  568
            ||||| |||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct  309  TACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGA  368

Query  569  AGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCT  628
            |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct  369  AGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCT  428

Query  629  TGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTT  688
            ||| || ||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  429  TGGGGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTT  488

Query  689  TTATTTTATCAA  700
            ||||||||||||
Sbjct  489  TTATTTTATCAA  500


 Score = 399 bits (216),  Expect = 6e-107
 Identities = 238/249 (96%), Gaps = 0/249 (0%)
 Strand=Plus/Minus

Query  476  TTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAA  535
            ||||||||||| ||||||||||||||| |||||| ||| |||||||||||||| ||||||
Sbjct  249  TTCTAAACCTGGGATGTTGTGGAAGATCCTTAGTTCCTACCGATCTGGTAGTAGTGCAAA  190
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Query  536   CACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACT  595
             ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  189   CACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACT  130

Query  596   ATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGT  655
             ||||||||||||||||||||||||||||||||||||||| ||||||||||| ||||||||
Sbjct  129   ATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGT  70

Query  656   GGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTTTATCAATGCTACAATGGAGAC  715
             |||||||||||||||||||||||||||||||||||||||||||||||| || ||||||||
Sbjct  69    GGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTATCAATGCCACTATGGAGAC  10

Query  716   AATTAAAAG  724
             |||||| ||
Sbjct  9     AATTAAGAG  1


>SRR2298573.563998 563998 length=500
Length=500

 Score = 433 bits (234),  Expect = 5e-117
 Identities = 244/249 (98%), Gaps = 0/249 (0%)
 Strand=Plus/Minus

Query  385   CTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAA  444
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  249   CTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAA  190

Query  445   AGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATAC  504
             ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  189   AGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATAC  130

Query  505   TTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCC  564
             ||||||||| |||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  129   TTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCC  70

Query  565   CAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCT  624
             |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  69    CAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCT  10

Query  625   ATCTTGGTG  633
             |||||||||
Sbjct  9     ATCTTGGTG  1


 Score = 396 bits (214),  Expect = 7e-106
 Identities = 238/250 (95%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  349   GGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCG  408
             ||||||||||||||||||||||||| ||||||||||||| ||||||||||||||||||||
Sbjct  251   GGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCG  310

Query  409   GAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTA  468
             ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  311   GAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTA  370

Query  469   GGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTA  528
             |||||||||||||||||||||||||||||||||||||||| |||| ||||||||||||||
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Sbjct  371  GGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGAACCTACCGATCTGGTAGTA  430

Query  529  CTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAG  588
             |||||||||||||||||||||||||||||||||||||||||| |||| ||||||  || 
Sbjct  431  GTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGAACCCCTAGGTACAAAA  490

Query  589  TGACACTATG  598
             |||||||||
Sbjct  491  CGACACTATG  500


>SRR2298573.544508 544508 length=500
Length=500

 Score = 433 bits (234),  Expect = 5e-117
 Identities = 244/249 (98%), Gaps = 0/249 (0%)
 Strand=Plus/Minus

Query  298  TGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTG  357
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  249  TGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTG  190

Query  358  TGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACAC  417
            |||||||||||||||| ||||||||||||| |||||||||||||||||||||||||||||
Sbjct  189  TGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACAC  130

Query  418  CTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTT  477
            |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct  129  CTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTT  70

Query  478  CTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACA  537
            |||||||||||||||||||||||||||||||||||| |||||||||||||| ||||||||
Sbjct  69   CTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACA  10

Query  538  CTAGTTGTA  546
            |||||||||
Sbjct  9    CTAGTTGTA  1


 Score = 412 bits (223),  Expect = 7e-111
 Identities = 239/247 (97%), Gaps = 0/247 (0%)
 Strand=Plus/Plus

Query  277  CTACTAGTGAGATACCACGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTT  336
            ||| ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  251  CTATTAGTGAGATACCATGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTT  310

Query  337  TGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATC  396
            ||||||||||||||||||||||||||||||||||||| ||||||||||||| ||||||||
Sbjct  311  TGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATC  370

Query  397  CTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTA  456
            ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||| ||
Sbjct  371  CTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCCAAAGCCAAGGTTTA  430

Query  457  ACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCC  516
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  431  ACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACC  490
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Query  517  GATCTGG  523
            | |||||
Sbjct  491  GGTCTGG  497


>SRR2298573.509938 509938 length=500
Length=500

 Score = 433 bits (234),  Expect = 5e-117
 Identities = 244/249 (98%), Gaps = 0/249 (0%)
 Strand=Plus/Plus

Query  455  TAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTG  514
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  2    TAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTA  61

Query  515  CCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTAC  574
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  62   CCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTAC  121

Query  575  CCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGA  634
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  122  CCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGA  181

Query  635  CCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTT  694
             ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  182  TCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTT  241

Query  695  TATCAATGC  703
            |||||||||
Sbjct  242  TATCAATGC  250


 Score = 390 bits (211),  Expect = 3e-104
 Identities = 237/250 (95%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  476  TTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAA  535
            ||||||||||||||||||| ||||| | |||||| ||| |||||| ||||||| ||||||
Sbjct  500  TTCTAAACCTGAGATGTTGGGGAAGTTTCTTAGTTCCTACCGATCGGGTAGTAGTGCAAA  441

Query  536  CACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACT  595
            ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  440  CACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACT  381

Query  596  ATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGT  655
            ||||||||||||||||||||||||||||||||||||||| ||||||||||| ||||||||
Sbjct  380  ATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGT  321

Query  656  GGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTTTATCAATGCTACAATGGAGAC  715
            |||||||||||||||||||||||||||||||||||||||||||||||| || ||||||||
Sbjct  320  GGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTATCAATGCCACTATGGAGAC  261

Query  716  AATTAAAAGT  725
            |||||| |||
Sbjct  260  AATTAAGAGT  251


>SRR2298573.486398 486398 length=500
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Length=500

 Score = 433 bits (234),  Expect = 5e-117
 Identities = 244/249 (98%), Gaps = 0/249 (0%)
 Strand=Plus/Minus

Query  323  TCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTT  382
            ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  249  TCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTT  190

Query  383  TGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCA  442
            ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  189  TGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCA  130

Query  443  AAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGAT  502
            ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  129  AAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGAT  70

Query  503  ACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATG  562
            ||||||||||| |||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  69   ACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATG  10

Query  563  CCCAGAAGG  571
            |||||||||
Sbjct  9    CCCAGAAGG  1


 Score = 387 bits (209),  Expect = 4e-103
 Identities = 235/248 (95%), Gaps = 0/248 (0%)
 Strand=Plus/Plus

Query  295  GCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGAC  354
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  250  GCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGAC  309

Query  355  GTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAA  414
            ||||||||||||||||||| ||||||||||||| ||||||||||||||||||||||||||
Sbjct  310  GTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAA  369

Query  415  CACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTG  474
            ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  370  CACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTG  429

Query  475  GTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAA  534
            |||||| ||||||| |||||||||||| |||||||| |  ||||||||| ||||  ||||
Sbjct  430  GTTCTACACCTGAGCTGTTGTGGAAGAAACTTAGTAACAACCGATCTGGCAGTAGGGCAA  489

Query  535  ACACTAGT  542
            | ||||||
Sbjct  490  AAACTAGT  497


>SRR2298573.462636 462636 length=500
Length=500

 Score = 433 bits (234),  Expect = 5e-117
 Identities = 242/246 (98%), Gaps = 0/246 (0%)
 Strand=Plus/Minus
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Query  389   AAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCC  448
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  248   AAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCC  189

Query  449   AAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAG  508
             ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  188   AAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAG  129

Query  509   TACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGA  568
             ||||| |||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct  128   TACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGA  69

Query  569   AGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCT  628
             |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct  68    AGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCT  9

Query  629   TGGTGA  634
             ||||||
Sbjct  8     TGGTGA  3


 Score = 394 bits (213),  Expect = 3e-105
 Identities = 237/249 (95%), Gaps = 0/249 (0%)
 Strand=Plus/Plus

Query  336   TTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCAT  395
             ||| |||||||||||||||||||||||||||||||||| ||||||||||||| |||||||
Sbjct  252   TTGAGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCAT  311

Query  396   CCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCT  455
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  312   CCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTT  371

Query  456   AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGC  515
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  372   AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTAC  431

Query  516   CGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACC  575
             ||||||||||||| |||||||||||||||||||| |||| |||||  ||||||||| |||
Sbjct  432   CGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGGCCACAAAGGAGTCCCAGAAGGGACC  491

Query  576   CATAGGTAA  584
             || ||||||
Sbjct  492   CAAAGGTAA  500


>SRR2298573.451956 451956 length=500
Length=500

 Score = 433 bits (234),  Expect = 5e-117
 Identities = 244/249 (98%), Gaps = 0/249 (0%)
 Strand=Plus/Plus

Query  296   CTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACG  355
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     CTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACG  60

Query  356   TGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAAC  415
             |||||||||||||||||| |||||||||||||| |||||||||||||||||||||||||||
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Sbjct  61   TGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAAC  120

Query  416  ACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGG  475
            |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Sbjct  121  ACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGG  180

Query  476  TTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAA  535
            |||||||||||||||||||||||||||||||||||||| |||||||||||||| ||||||
Sbjct  181  TTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAA  240

Query  536  CACTAGTTG  544
            |||||||||
Sbjct  241  CACTAGTTG  249


 Score = 418 bits (226),  Expect = 2e-112
 Identities = 240/247 (97%), Gaps = 0/247 (0%)
 Strand=Plus/Minus

Query  357  GTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACA  416
            ||||||||||||||||| ||||||||||||| ||||||||||||||||||||||||||| 
Sbjct  496  GTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACC  437

Query  417  CCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGT  476
            ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct  436  CCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGT  377

Query  477  TCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAAC  536
            ||||||||||||||||||||||||||||||||||||| |||||||||||||| |||||||
Sbjct  376  TCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAAC  317

Query  537  ACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTA  596
            |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  316  ACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTA  257

Query  597  TGGATCT  603
            |||||||
Sbjct  256  TGGATCT  250


>SRR2298573.406175 406175 length=500
Length=500

 Score = 433 bits (234),  Expect = 5e-117
 Identities = 246/252 (98%), Gaps = 0/252 (0%)
 Strand=Plus/Minus

Query  444  AAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATA  503
            |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  500  AAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATA  441

Query  504  CTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGC  563
            |||||||||| |||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  440  CTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGC  381

Query  564  CCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTC  623
            ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  380  CCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTC  321
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Query  624  TATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTT  683
            ||||||||||| ||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  320  TATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTT  261

Query  684  TCCTTTTATTTT  695
            ||||||||||||
Sbjct  260  TCCTTTTATTTT  249


 Score = 424 bits (229),  Expect = 3e-114
 Identities = 243/250 (97%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  414  ACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATT  473
            |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  1    ACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATT  60

Query  474  GGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCA  533
            |||||||||||||||||||||||||||||||||||||||| |||||||||||||| ||||
Sbjct  61   GGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCA  120

Query  534  AACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACA  593
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  121  AACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACA  180

Query  594  CTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTA  653
            |||||||||||||||||||||||||||||||||||||| || ||||||||||| ||||||
Sbjct  181  CTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGGGATCTGGTTAAAAAACGTCTA  240

Query  654  GTGGGCCAAA  663
            ||||||||||
Sbjct  241  GTGGGCCAAA  250


>SRR2298573.401580 401580 length=500
Length=500

 Score = 433 bits (234),  Expect = 5e-117
 Identities = 244/249 (98%), Gaps = 0/249 (0%)
 Strand=Plus/Plus

Query  455  TAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTG  514
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  2    TAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTA  61

Query  515  CCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTAC  574
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  62   CCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTAC  121

Query  575  CCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGA  634
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  122  CCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGA  181

Query  635  CCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTT  694
             ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  182  TCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTT  241

Query  695  TATCAATGC  703
            |||||||||
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Sbjct  242  TATCAATGC  250


 Score = 363 bits (196),  Expect = 7e-96
 Identities = 230/247 (93%), Gaps = 0/247 (0%)
 Strand=Plus/Minus

Query  657  GGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTTTATCAATGCTACAATGGAGACA  716
            |||||| ||||||||||||||||||||||||||||||||| |||||| || |||||| ||
Sbjct  499  GGCCAACCCCGGGGGGGATCCCCGGTTTCCTTTTATTTTAGCAATGCCACTATGGAGCCA  440

Query  717  ATTAAAAGTATTGCAGATATGGCGACCGGAGTGGTCAGTTCAGTTGATTCCACTATCAAT  776
            ||||| ||||||||| ||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  439  ATTAAGAGTATTGCAAATATGGCTACCGGAGTGGTCAGTTCAGTTGATTCCACTATCAAT  380

Query  777  GCAGTTAATGAGAGAGTAGAAAATGTGGGCAATGAAATTGGAGGTAACCTATTAACCAAA  836
            | ||||||||||||||| |||||||| || |||||||||||||||||  |||||||||||
Sbjct  379  GTAGTTAATGAGAGAGTGGAAAATGTAGGTAATGAAATTGGAGGTAATTTATTAACCAAA  320

Query  837  GTAGCAGATGATGCTTCTAATGTGCTTGGACCAAATTGTTATGCTACAACAGCTGAACCA  896
            || ||||||||||||||||||||||| ||||||||||| |||||||||||||||||||||
Sbjct  319  GTTGCAGATGATGCTTCTAATGTGCTCGGACCAAATTGCTATGCTACAACAGCTGAACCA  260

Query  897  GAGAACA  903
            |||||||
Sbjct  259  GAGAACA  253


>SRR2298573.350726 350726 length=500
Length=500

 Score = 433 bits (234),  Expect = 5e-117
 Identities = 244/249 (98%), Gaps = 0/249 (0%)
 Strand=Plus/Minus

Query  455  TAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTG  514
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  249  TAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTA  190

Query  515  CCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTAC  574
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  189  CCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTAC  130

Query  575  CCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGA  634
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  129  CCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGA  70

Query  635  CCTGGTTAAAAAGCGTCTAGTGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTT  694
             ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  69   TCTGGTTAAAAAACGTCTAGTGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTT  10

Query  695  TATCAATGC  703
            |||||||||
Sbjct  9    TATCAATGC  1


 Score = 348 bits (188),  Expect = 2e-91
 Identities = 230/251 (92%), Gaps = 0/251 (0%)
 Strand=Plus/Plus
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Query  390  AAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCA  449
            |||||||||||||||||||||||| |||||||||||||||||||||||||||||| ||||
Sbjct  249  AAGCATCCTATTGCCAGCGGAACACCACCTGGTAACAGGTGCCTCTGGGGCCAAAGGCCA  308

Query  450  AGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGT  509
            |||| |||| |||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  309  AGGTTTAACCAACCCTCTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGT  368

Query  510  ACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAA  569
            |||| |||||||||||||| |||||||||||||||||||||||| |||||| ||||||||
Sbjct  369  ACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCATGAAGGAGGCCCAGAA  428

Query  570  GGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTT  629
            || ||||||||| || ||| ||| ||||||| | |||||||||||||| ||| ||| |||
Sbjct  429  GGAACCCATAGGAAAAAAGCGACCCTATGGAACGGATCTGGGGCCAGGGACCCCTACCTT  488

Query  630  GGTGACCTGGT  640
            || || |||||
Sbjct  489  GGGGATCTGGT  499


>SRR2298573.330438 330438 length=500
Length=500

 Score = 433 bits (234),  Expect = 5e-117
 Identities = 244/249 (98%), Gaps = 0/249 (0%)
 Strand=Plus/Minus

Query  340  GAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTA  399
            |||||||||||||||||||||||||||||||||| ||||||||||||| |||||||||||
Sbjct  250  GAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTA  191

Query  400  TTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACA  459
            |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  190  TTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACA  131

Query  460  AACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGAT  519
            |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  130  AACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGAT  71

Query  520  CTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATA  579
            ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  70   CTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATA  11

Query  580  GGTAACAAG  588
            |||||||||
Sbjct  10   GGTAACAAG  2


 Score = 337 bits (182),  Expect = 4e-88
 Identities = 227/249 (91%), Gaps = 1/249 (0%)
 Strand=Plus/Plus

Query  151  TGCCTGGTCTCCACTGGTTGAAGGCAACTTGCAATAAAATGAGTGGGAACAAGACGCTTA  210
            ||||||||||||||| |||||||||||||||||||||||||||||| |||||||||||||
Sbjct  251  TGCCTGGTCTCCACTAGTTGAAGGCAACTTGCAATAAAATGAGTGGAAACAAGACGCTTA  310

Query  211  AAGCATGGTGTGAACTAAC-TTTCTAACCCACATTTTGTGTGGGGTGGCAGATGGCGTGC  269
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            |||||||| || |  || | ||||||||||||||||||||||||||||||||||||||||
Sbjct  311  AAGCATGGGGTAATTTAGCTTTTCTAACCCACATTTTGTGTGGGGTGGCAGATGGCGTGC  370

Query  270  CATAATTCTACTAGTGAGATACCACGCTTGTGGACCTTATGCTCACACAGCCATCCTCTA  329
            ||||  |||  ||||||||||||| |||||||||||||||||||||||||||||||||| 
Sbjct  371  CATAGCTCTCTTAGTGAGATACCATGCTTGTGGACCTTATGCTCACACAGCCATCCTCTG  430

Query  330  GTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCA  389
            |||| ||||||||||||||||  ||||| ||||||||||||| |  |||||||||||| |
Sbjct  431  GTAAATTTGTGAGACGTCTGGGAACGTGGGGGAACTTATTGGCAAAAACATTTTGCTGTA  490

Query  390  AAGCATCCT  398
            |||||||||
Sbjct  491  AAGCATCCT  499


>SRR2298573.321918 321918 length=500
Length=500

 Score = 433 bits (234),  Expect = 5e-117
 Identities = 244/249 (98%), Gaps = 0/249 (0%)
 Strand=Plus/Minus

Query  296  CTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACG  355
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  249  CTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACG  190

Query  356  TGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAAC  415
            |||||||||||||||||| ||||||||||||| |||||||||||||||||||||||||||
Sbjct  189  TGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAAC  130

Query  416  ACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGG  475
            |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Sbjct  129  ACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGG  70

Query  476  TTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAA  535
            |||||||||||||||||||||||||||||||||||||| |||||||||||||| ||||||
Sbjct  69   TTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAA  10

Query  536  CACTAGTTG  544
            |||||||||
Sbjct  9    CACTAGTTG  1


 Score = 412 bits (223),  Expect = 7e-111
 Identities = 241/250 (96%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  277  CTACTAGTGAGATACCACGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTT  336
            ||| ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  251  CTATTAGTGAGATACCATGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTT  310

Query  337  TGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATC  396
            ||||||||||||||||||||||||||||||||||||| ||||||||||||| ||||||||
Sbjct  311  TGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATC  370

Query  397  CTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTA  456
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Sbjct  371  CTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGGTTA  430
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Query  457  ACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCC  516
            ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||| ||
Sbjct  431  ACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGAGACTTAGTACCTACC  490

Query  517  GATCTGGTAG  526
            | ||||||||
Sbjct  491  GTTCTGGTAG  500


>SRR2298573.300070 300070 length=500
Length=500

 Score = 433 bits (234),  Expect = 5e-117
 Identities = 253/262 (97%), Gaps = 2/262 (1%)
 Strand=Plus/Plus

Query  313  CACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGA  372
            ||||| | || |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CACAC-GTCA-CCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGA  298

Query  373  AGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCC  432
            | ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  299  AACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCC  358

Query  433  TCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGT  492
            ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||| 
Sbjct  359  TCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGG  418

Query  493  TGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCC  552
            ||||||||||||||||||||| |||||||||||||||| |||||||||||||||||||||||
Sbjct  419  TGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCC  478

Query  553  ACGAAGGATGCCCAGAAGGTAC  574
            ||||||||||||||||||||||
Sbjct  479  ACGAAGGATGCCCAGAAGGTAC  500


 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  349  GGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCG  408
            ||||||||||||||||||||||||| ||||||||||||| ||||||||||||||||||||
Sbjct  251  GGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCG  192

Query  409  GAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTA  468
            ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  191  GAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTA  132

Query  469  GGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTA  528
            ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  131  GGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTA  72

Query  529  CTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAG  588
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  71   GTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAG  12

Query  589  TGACACTATGG  599
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                ||||||||||| 
Sbjct  11   CGACACTATGG  1


>SRR2298573.280250 280250 length=500
Length=500

 Score = 433 bits (234),  Expect = 5e-117
 Identities = 248/255 (97%), Gaps = 0/255 (0%)
 Strand=Plus/Plus

Query  439  GCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGA  498
            ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGA  60

Query  499  AGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAG  558
            ||||||||||||||| |||||||||||||| |||||||||||||||||||||||||||||
Sbjct  61   AGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAG  120

Query  559  GATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGT  618
            |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Sbjct  121  GATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGT  180

Query  619  ACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCC  678
            |||||||||||||||| ||||||||||| |||||||||||||||||||||||||||||||
Sbjct  181  ACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCC  240

Query  679  CGGTTTCCTTTTATT  693
            ||||||||||| |||
Sbjct  241  CGGTTTCCTTTAATT  255


 Score = 398 bits (215),  Expect = 2e-106
 Identities = 239/251 (95%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  472  TTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTG  531
            ||||||||||||||| ||||||| ||||| | ||| |||||| |||||||||||||| ||
Sbjct  499  TTGGTTCTAAACCTGGGATGTTGGGGAAGCTGCTTTGTACCTACCGATCTGGTAGTAGTG  440

Query  532  CAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGA  591
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  439  CAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGA  380

Query  592  CACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTC  651
            |||||||||||||||||||||||||||||||||||||||||| |||||||||||| ||||
Sbjct  379  CACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTC  320

Query  652  TAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTTTATCAATGCTACAATGG  711
            |||||||||||||||||||||||||||||||||||||||||||||||||||| || ||||
Sbjct  319  TAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTATCAATGCCACTATGG  260

Query  712  AGACAATTAAA  722
            |||||||||||
Sbjct  259  AGACAATTAAA  249


>SRR2298573.250564 250564 length=500
Length=500
```

```
 Score = 433 bits (234),  Expect = 5e-117
 Identities = 244/249 (98%), Gaps = 0/249 (0%)
 Strand=Plus/Plus

Query  296   CTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACG  355
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     CTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACG  60

Query  356   TGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAAC  415
             |||||||||||||||||| ||||||||||||| |||||||||||||||||||||||||||
Sbjct  61    TGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAAC  120

Query  416   ACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGG  475
             |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Sbjct  121   ACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGG  180

Query  476   TTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAA  535
             |||||||||||||||||||||||||||||||||||||| |||||||||||||| ||||||
Sbjct  181   TTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAA  240

Query  536   CACTAGTTG  544
             |||||||||
Sbjct  241   CACTAGTTG  249


 Score = 366 bits (198),  Expect = 6e-97
 Identities = 229/244 (94%), Gaps = 2/244 (1%)
 Strand=Plus/Minus

Query  357   GTGGGAACTTATTGGAAGCAACATTT-TGCTGCAAAGCATCCTATTGCCAGCGGAACAAC  415
             |||||||||| |||||| |||||||| || || |||| ||||| ||||| | ||||||||
Sbjct  493   GTGGGAACTTTTTGGAAACAACATTTGTGTTG-AAAGGATCCTTTTGCCCGGGGAACAAC  435

Query  416   ACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGG  475
              ||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Sbjct  434   CCCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGG  375

Query  476   TTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAA  535
             ||||||||||||||||||| |||||||||||||||||| |||||||||||||| ||||||
Sbjct  374   TTCTAAACCTGAGATGTTGGGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAA  315

Query  536   CACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACT  595
             ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  314   CACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACT  255

Query  596   ATGG  599
             ||||
Sbjct  254   ATGG  251


>SRR2298573.191538 191538 length=500
Length=500

 Score = 433 bits (234),  Expect = 5e-117
 Identities = 246/252 (98%), Gaps = 0/252 (0%)
 Strand=Plus/Plus

Query  435   TGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTG  494
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            ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  249  TGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTG  308

Query  495  TGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCAC  554
            ||||||||||||||||||| |||||||||||||| |||||||||||||||||||||||||
Sbjct  309  TGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCAC  368

Query  555  GAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCC  614
            |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  369  GAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCC  428

Query  615  AGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggA  674
            |||||||||||||||||||| ||||||||||| |||||||||||||||||||||||||||
Sbjct  429  AGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGA  488

Query  675  TCCCCGGTTTCC  686
            ||||||||||||
Sbjct  489  TCCCCGGTTTCC  500


 Score = 420 bits (227),  Expect = 4e-113
 Identities = 241/248 (97%), Gaps = 0/248 (0%)
 Strand=Plus/Minus

Query  515  CCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTAC  574
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  248  CCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTAC  189

Query  575  CCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGA  634
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  188  CCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGA  129

Query  635  CCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTT  694
             ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  128  TCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTT  69

Query  695  TATCAATGCTACAATGGAGACAATTAAAAGTATTGCAGATATGGCGACCGGAGTGGTCAG  754
            ||||||||| || |||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  68   TATCAATGCCACTATGGAGACAATTAAGAGTATTGCAGATATGGCGACCGGAGTGGTCAG  9

Query  755  TTCAGTTG  762
            ||||||||
Sbjct  8    TTCAGTTG  1


>SRR2298573.142735 142735 length=500
Length=500

 Score = 433 bits (234),  Expect = 5e-117
 Identities = 244/249 (98%), Gaps = 0/249 (0%)
 Strand=Plus/Minus

Query  375  CAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTC  434
            ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  249  CAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTC  190

Query  435  TGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTG  494
            ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  189  TGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTG  130
```

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Query  495  TGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCAC  554
            ||||||||||||||||||| |||||||||||||| |||||||||||||||||||||||||
Sbjct  129  TGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCAC  70

Query  555  GAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCC  614
            |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  69   GAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCC  10

Query  615  AGGTACCTC  623
            |||||||||
Sbjct  9    AGGTACCTC  1


 Score = 414 bits (224),  Expect = 2e-111
 Identities = 242/251 (96%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  336  TTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCAT  395
            |||||||||||||||||||||||||||||||||||||| ||||||||||||| |||||||
Sbjct  250  TTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCAT  309

Query  396  CCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCT  455
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  310  CCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTT  369

Query  456  AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGC  515
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  370  AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTAC  429

Query  516  CGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACC  575
            ||||||||||||| ||||||||||||||||||||||| ||||||||| |||||||| |||
Sbjct  430  CGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCCCGAAGGATGACCAGAAGGGACC  489

Query  576  CATAGGTAACA  586
            || ||||||||
Sbjct  490  CAAAGGTAACA  500


>SRR2298573.100807 100807 length=500
Length=500

 Score = 433 bits (234),  Expect = 5e-117
 Identities = 244/249 (98%), Gaps = 0/249 (0%)
 Strand=Plus/Minus

Query  327  CTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCT  386
            ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  249  CTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCT  190

Query  387  GCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAG  446
            | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  189  GTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAG  130

Query  447  CCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTT  506
            ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  129  CCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTT  70

Query  507  AGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCA  566
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            ||||||| |||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  69   AGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCA  10

Query  567  GAAGGTACC  575
            |||||||||
Sbjct  9    GAAGGTACC  1


 Score = 390 bits (211),  Expect = 3e-104
 Identities = 237/250 (95%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  317  CAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCA  376
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  251  CAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACA  310

Query  377  ACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTG  436
            ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  311  ACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTG  370

Query  437  GGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTG  496
            ||||||||||||||||| ||||||||||||||||||||||||||| ||||||||||||||
Sbjct  371  GGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAACCCTGAGATGTTGTG  430

Query  497  GAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGA  556
            ||||||||||||||||| |||| |||||||||  ||||| || ||||| |||| ||||||
Sbjct  431  GAAGATACTTAGTACCTACCGAACTGGTAGTAGGGCAAAAACCAGTTGAAAGGGCCACGA  490

Query  557  AGGATGCCCA  566
            |||| |||||
Sbjct  491  AGGAGGCCCA  500


>SRR2298573.93103 93103 length=500
Length=500

 Score = 433 bits (234),  Expect = 5e-117
 Identities = 244/249 (98%), Gaps = 0/249 (0%)
 Strand=Plus/Plus

Query  338  GTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCC  397
            |||||||||||||||||||||||||||||||||||| ||||||||||||| |||||||||
Sbjct  252  GTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCC  311

Query  398  TATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAA  457
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  312  TATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAA  371

Query  458  CAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCG  517
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  372  CAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCG  431

Query  518  ATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCA  577
            ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  432  ATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCA  491

Query  578  TAGGTAACA  586
            |||||||||
Sbjct  492  TAGGTAACA  500
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```
 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  382  TTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCC  441
            |||||| ||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  250  TTGCTGTAAAGCCTCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCC  191

Query  442  AAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGA  501
            |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  190  AAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGA  131

Query  502  TACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGAT  561
            |||||||||||| |||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  130  TACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGAT  71

Query  562  GCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACC  621
            ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  70   GCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACC  11

Query  622  TCTATCTTGG  631
            ||||||||||
Sbjct  10   TCTATCTTGG  1


>SRR2298573.59417 59417 length=500
Length=500

 Score = 433 bits (234),  Expect = 5e-117
 Identities = 244/249 (98%), Gaps = 0/249 (0%)
 Strand=Plus/Plus

Query  455  TAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTG  514
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  2    TAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTA  61

Query  515  CCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTAC  574
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  62   CCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTAC  121

Query  575  CCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGA  634
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  122  CCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGA  181

Query  635  CCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTT  694
             ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  182  TCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTT  241

Query  695  TATCAATGC  703
            |||||||||
Sbjct  242  TATCAATGC  250


 Score = 387 bits (209),  Expect = 4e-103
 Identities = 235/248 (95%), Gaps = 0/248 (0%)
 Strand=Plus/Minus
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Query  483  CCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGT  542
            |||| ||||||||||||||| |||||  ||| ||| |||||||||| |||||||||||||
Sbjct  498  CCTGGGATGTTGTGGAAGATTCTTAGGTCCTACCGGTCTGGTAGTAGTGCAAACACTAGT  439

Query  543  TGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATC  602
            |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Sbjct  438  TGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATC  379

Query  603  TGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAA  662
            |||||||||||||||||||||||||||||||| |||||||||||| ||||||||||||||
Sbjct  378  TGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAA  319

Query  663  ACCCgggggggATCCCCGGTTTCCTTTTATTTTATCAATGCTACAATGGAGACAATTAAA  722
            ||||||||||||||||||||||||||||||||||||||||| || ||||||||||||||
Sbjct  318  ACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTATCAATGCCACTATGGAGACAATTAAG  259

Query  723  AGTATTGC  730
            ||||||||
Sbjct  258  AGTATTGC  251


>SRR2298573.13345 13345 length=500
Length=500

 Score = 433 bits (234),  Expect = 5e-117
 Identities = 246/252 (98%), Gaps = 0/252 (0%)
 Strand=Plus/Minus

Query  330  GTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCA  389
            ||||||||| |||||||||||||||||||||||||||||||||| ||||||||||||| |
Sbjct  500  GTAAGTTTGGGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTA  441

Query  390  AAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCA  449
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  440  AAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCA  381

Query  450  AGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGT  509
            |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  380  AGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGT  321

Query  510  ACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAA  569
            |||| |||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  320  ACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAA  261

Query  570  GGTACCCATAGG  581
            ||||||||||||
Sbjct  260  GGTACCCATAGG  249


 Score = 431 bits (233),  Expect = 2e-116
 Identities = 250/258 (97%), Gaps = 1/258 (0%)
 Strand=Plus/Plus

Query  327  CTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCT  386
            ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  1    CTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCT  60

Query  387  GCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAG  446
            | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  61   GTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAG  120

Query  447  CCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTT  506
            ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTT  180

Query  507  AGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCA  566
            ||||||| |||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  181  AGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCA  240

Query  567  GAAGGTACCC-ATAGGTA  583
             ||||||||| || ||||
Sbjct  241  AAAGGTACCCTATGGGTA  258


>SRR2298546.925026 925026 length=502
Length=502

 Score = 433 bits (234),  Expect = 5e-117
 Identities = 246/252 (98%), Gaps = 0/252 (0%)
 Strand=Plus/Minus

Query  1255  CATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAG  1314
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  252   CATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAG  193

Query  1315  CATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTTAT  1374
             | |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  192   CGTTTACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATTTAT  133

Query  1375  GTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAAC  1434
             ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct  132   GTATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAAC  73

Query  1435  TAAAAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGATG  1494
             |||||||||||||||||||||||||||| |||||||||||||||| ||||||||||||||
Sbjct  72    TAAAAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGATG  13

Query  1495  TAACCATATTGG  1506
             | ||||||||||
Sbjct  12    TTACCATATTGG  1


 Score = 416 bits (225),  Expect = 6e-112
 Identities = 250/262 (95%), Gaps = 1/262 (0%)
 Strand=Plus/Plus

Query  1086  ACACCAAC-ATGGGCTAGAGGACATCAGATAACCCATGTGGAATTGCCAAAAGTCTTTTG  1144
             |||||| | |||||||||||||||||||||||||||||||||| | ||||||||||||||
Sbjct  241   ACACCACCAATGGGCTAGAGGACATCAGATAACCCATGTGGAACTACCAAAAGTCTTTTG  300

Query  1145  GGACAAAAACAGTAAGCCAGCCTATGGCCAATCAAGATACTTTGCAGCAGTACGGTGTGG  1204
             |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   GGACAAAAACAGCAAGCCAGCCTATGGCCAATCAAGATACTTTGCAGCAGTACGGTGTGG  360

Query  1205  CTTTCATTTTCAGGTGCAAGTGAATGTTAACCAAGGAACAGCTGGTAGTGCATTGGTGGT  1264
              ||||||||||| || ||||||||||||| ||||||||||| ||||||||||||||||||
Sbjct  361   TTTTCATTTTCAAGTACAAGTGAATGTTAATCAAGGAACAGCCGGTAGTGCATTGGTGGT  420
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Query  1265  GTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCATTTACCAA  1324
             ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  421   GTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCGTTTACCAA  480

Query  1325  TTTACCACATGTATTGATGAAT  1346
             |||||||||||| |||||||||
Sbjct  481   TTTACCACATGTGTTGATGAAT  502


>SRR2298546.917017 917017 length=500
Length=500

 Score = 433 bits (234),  Expect = 5e-117
 Identities = 246/252 (98%), Gaps = 0/252 (0%)
 Strand=Plus/Minus

Query  1253  TGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGG  1312
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  500   TGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGG  441

Query  1313  AGCATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTT  1372
             ||| |||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  440   AGCGTTTACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATTT  381

Query  1373  ATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCA  1432
             ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  380   ATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCA  321

Query  1433  ACTAAAAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGA  1492
             |||||||||||||||||||||||||||||| ||||||||||||||||| |||||||||||
Sbjct  320   ACTAAAAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGA  261

Query  1493  TGTAACCATATT  1504
             ||| ||||||||
Sbjct  260   TGTTACCATATT  249


 Score = 416 bits (225),  Expect = 6e-112
 Identities = 241/249 (97%), Gaps = 0/249 (0%)
 Strand=Plus/Plus

Query  1175  ATCAAGATACTTTGCAGCAGTACGGTGTGGCTTTCATTTTCAGGTGCAAGTGAATGTTAA  1234
             |||||||||||||||||||||||||||||| ||||||||||| || ||||||||||||||
Sbjct  1     ATCAAGATACTTTGCAGCAGTACGGTGTGGTTTTCATTTTCAAGTACAAGTGAATGTTAA  60

Query  1235  CCAAGGAACAGCTGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGA  1294
              ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    TCAAGGAACAGCCGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGA  120

Query  1295  CTCAAAGTTAGAATTTGGAGCATTTACCAATTTACCACATGTATTGATGAATTTGGCTGA  1354
             ||||||||||||||||||||| |||||||||||||||||||| |||||||||||||||||
Sbjct  121   CTCAAAGTTAGAATTTGGAGCGTTTACCAATTTACCACATGTGTTGATGAATTTGGCTGA  180

Query  1355  GACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGA  1414
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  181   GACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGA  240

Query  1415  TTCGTCAGA  1423
             |||||||||
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Sbjct  241   TTCGTCAGA  249


>SRR2298546.733295 733295 length=502
Length=502

 Score = 433 bits (234),  Expect = 5e-117
 Identities = 246/252 (98%), Gaps = 0/252 (0%)
 Strand=Plus/Plus

Query  1244  AGCTGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTT  1303
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  251   AGCCGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTT  310

Query  1304  AGAATTTGGAGCATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACA  1363
             |||||||||||| |||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  311   AGAATTTGGAGCGTTTACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACA  370

Query  1364  GGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGA  1423
             |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  371   GGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGA  430

Query  1424  CTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGAC  1483
             ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||| ||
Sbjct  431   CTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTAC  490

Query  1484  ACAAGTTGATGT  1495
             ||||||||||||
Sbjct  491   ACAAGTTGATGT  502


 Score = 409 bits (221),  Expect = 9e-110
 Identities = 241/251 (96%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  1319  TACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTAT  1378
             |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  251   TACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTAT  192

Query  1379  CCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACTAAA  1438
             ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  191   CCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAACTAAA  132

Query  1439  AGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGATGTAAC  1498
             |||||||||||||||||||||||| ||||||||||||||||| |||||||||||||| ||
Sbjct  131   AGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGATGTTAC  72

Query  1499  CATATTGGGTAGTTTATTGCAATTGGACTTCCAAAATCCTAGGGTGTTTGGCCAAGACGT  1558
             |||||||||||| |||||||||||||||||||||||||||||||| || || ||||||||
Sbjct  71    CATATTGGGTAGCTTATTGCAATTGGACTTCCAAAATCCTAGGGTATTCGGTCAAGACGT  12

Query  1559  TGGTATCTATG  1569
             |||||| ||||
Sbjct  11    TGGTATTTATG  1


>SRR2298546.572666 572666 length=502
Length=502
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 Score = 433 bits (234),  Expect = 5e-117
 Identities = 246/252 (98%), Gaps = 0/252 (0%)
 Strand=Plus/Minus

Query  1257  TTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCA  1316
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  252   TTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCG  193

Query  1317  TTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGT  1376
             |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct  192   TTTACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGT  133

Query  1377  ATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACTA  1436
             ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  132   ATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAACTA  73

Query  1437  AAAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGATGTA  1496
             |||||||||||||||||||||||||| ||||||||||||||||| |||||||||||||| 
Sbjct  72    AAAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGATGTT  13

Query  1497  ACCATATTGGGT  1508
             ||||||||||||
Sbjct  12    ACCATATTGGGT  1


 Score = 414 bits (224),  Expect = 2e-111
 Identities = 242/251 (96%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  1196  ACGGTGTGGCTTTCATTTTCAGGTGCAAGTGAATGTTAACCAAGGAACAGCTGGTAGTGC  1255
             ||||||||| ||||||||||| || |||||||||||||| ||||||||||| ||||||||
Sbjct  252   ACGGTGTGGTTTTCATTTTCAAGTACAAGTGAATGTTAATCAAGGAACAGCCGGTAGTGC  311

Query  1256  ATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGC  1315
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  312   ATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGC  371

Query  1316  ATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTTATG  1375
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  372   GTTTACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATTTATG  431

Query  1376  TATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACT  1435
             ||| ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  432   TATACCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAACT  491

Query  1436  AAAAGTCTATG  1446
             |||||||||||
Sbjct  492   AAAAGTCTATG  502


>SRR2298546.570152 570152 length=501
Length=501

 Score = 433 bits (234),  Expect = 5e-117
 Identities = 246/252 (98%), Gaps = 0/252 (0%)
 Strand=Plus/Plus

Query  1256  ATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGC  1315
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  250   ATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGC  309

Query  1316  ATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTTATG  1375
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  310   GTTTACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATTTATG  369

Query  1376  TATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACT  1435
             |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct  370   TATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAACT  429

Query  1436  AAAAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGATGT  1495
             ||||||||||||||||||||||||||| ||||||||||||||||| ||||||||||||||
Sbjct  430   AAAAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGATGT  489

Query  1496  AACCATATTGGG  1507
              |||||||||||
Sbjct  490   TACCATATTGGG  501


 Score = 390 bits (211),  Expect = 3e-104
 Identities = 237/250 (95%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  1405  TTAAAACGGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCTA  1464
             ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  250   TTAAAACAGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCCA  191

Query  1465  TACCTTCAGGTTCTGCGACACAAGTTGATGTAACCATATTGGGTAGTTTATTGCAATTGG  1524
             |||||||||||||||| |||||||||||||| |||||||||||||| |||||||||||||
Sbjct  190   TACCTTCAGGTTCTGCTACACAAGTTGATGTTACCATATTGGGTAGCTTATTGCAATTGG  131

Query  1525  ACTTCCAAAATCCTAGGGTGTTTGGCCAAGACGTTGGTATCTATGATAATGCACCAACGC  1584
             ||||||||||||||||||| || || |||||||||||||| ||||| |||||||||||||
Sbjct  130   ACTTCCAAAATCCTAGGGTATTCGGTCAAGACGTTGGTATTTATGACAATGCACCAACGC  71

Query  1585  GGAAACAAAATCTTAAAAAGATTCTTACAATGAGCACTAAATACAAGTGGACTAGGGGAA  1644
             |||| ||||||||||| || ||||||||||||||||||||||||||||||||||||||||
Sbjct  70    GGAAGCAAAATCTTAAGAAAATTCTTACAATGAGCACTAAATACAAGTGGACTAGGGGAA  11

Query  1645  AAATTGACAT  1654
             ||||||||||
Sbjct  10    AAATTGACAT  1


>SRR2298546.467110 467110 length=502
Length=502

 Score = 433 bits (234),  Expect = 5e-117
 Identities = 246/252 (98%), Gaps = 0/252 (0%)
 Strand=Plus/Minus

Query  1258  TGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCAT  1317
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  502   TGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCGT  443

Query  1318  TTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTA  1377
             ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  442   TTACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTA  383
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Query  1378  TCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACTAA  1437
             |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  382   TCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAACTAA  323

Query  1438  AAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGATGTAA  1497
             ||||||||||||||||||||||||| ||||||||||||||||| |||||||||||||| |
Sbjct  322   AAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGATGTTA  263

Query  1498  CCATATTGGGTA  1509
             ||||||||||||
Sbjct  262   CCATATTGGGTA  251


 Score = 422 bits (228),  Expect = 1e-113
 Identities = 244/252 (97%), Gaps = 0/252 (0%)
 Strand=Plus/Plus

Query  1176  TCAAGATACTTTGCAGCAGTACGGTGTGGCTTTCATTTTCAGGTGCAAGTGAATGTTAAC  1235
             ||||||||||||||||||||||||||||| ||||||||||| || ||||||||||||||
Sbjct  1     TCAAGATACTTTGCAGCAGTACGGTGTGGTTTTCATTTTCAAGTACAAGTGAATGTTAAT  60

Query  1236  CAAGGAACAGCTGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGAC  1295
             ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    CAAGGAACAGCCGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGAC  120

Query  1296  TCAAAGTTAGAATTTGGAGCATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAG  1355
             |||||||||||||||||||| |||||||||||||||||||| ||||||||||||||||||
Sbjct  121   TCAAAGTTAGAATTTGGAGCGTTTACCAATTTACCACATGTGTTGATGAATTTGGCTGAG  180

Query  1356  ACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGAT  1415
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  181   ACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGAT  240

Query  1416  TCGTCAGACTTA  1427
             ||||||||||||
Sbjct  241   TCGTCAGACTTA  252


>SRR2298546.362559 362559 length=502
Length=502

 Score = 433 bits (234),  Expect = 5e-117
 Identities = 246/252 (98%), Gaps = 0/252 (0%)
 Strand=Plus/Plus

Query  1254  GCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGA  1313
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  251   GCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGA  310

Query  1314  GCATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTTA  1373
             || |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  311   GCGTTTACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATTTA  370

Query  1374  TGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAA  1433
             |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Sbjct  371   TGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAA  430

Query  1434  CTAAAAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGAT  1493
             ||||||||||||||||||||||||||||| ||||||||||||||||| ||||||||||||
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Sbjct  431   CTAAAAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGAT  490

Query  1494  GTAACCATATTG  1505
             || |||||||||
Sbjct  491   GTTACCATATTG  502


 Score = 401 bits (217),  Expect = 2e-107
 Identities = 239/250 (96%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  1321  CCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTATCC  1380
             |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  251   CCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTATCC  192

Query  1381  CCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACTAAAAG  1440
             ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  191   CCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAACTAAAAG  132

Query  1441  TCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGATGTAACCA  1500
             |||||||||||||||||||||| ||||||||||||||||| |||||||||||||| ||||
Sbjct  131   TCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGATGTTACCA  72

Query  1501  TATTGGGTAGTTTATTGCAATTGGACTTCCAAAATCCTAGGGTGTTTGGCCAAGACGTTG  1560
             |||||||||| |||||||||||||||||||||||||||||||| || || ||||| ||||
Sbjct  71    TATTGGGTAGCTTATTGCAATTGGACTTCCAAAATCCTAGGGTATTCGGTCAAGATGTTG  12

Query  1561  GTATCTATGA  1570
             |||| |||||
Sbjct  11    GTATTTATGA  2


>SRR2298546.103054 103054 length=502
Length=502

 Score = 433 bits (234),  Expect = 5e-117
 Identities = 246/252 (98%), Gaps = 0/252 (0%)
 Strand=Plus/Minus

Query  1225  TGAATGTTAACCAAGGAACAGCTGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTG  1284
             |||||||||| ||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  502   TGAATGTTAATCAAGGAACAGCCGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTG  443

Query  1285  TGACATATGACTCAAAGTTAGAATTTGGAGCATTTACCAATTTACCACATGTATTGATGA  1344
             |||||||||||||||||||||||||||||| ||||||||||||||||||||| |||||||
Sbjct  442   TGACATATGACTCAAAGTTAGAATTTGGAGCGTTTACCAATTTACCACATGTGTTGATGA  383

Query  1345  ATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATG  1404
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  382   ATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATG  323

Query  1405  TTAAAACGGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCTA  1464
             ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  322   TTAAAACAGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCCA  263

Query  1465  TACCTTCAGGTT  1476
             ||||||||||||
Sbjct  262   TACCTTCAGGTT  251
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 Score = 416 bits (225),  Expect = 6e-112
 Identities = 241/249 (97%), Gaps = 0/249 (0%)
 Strand=Plus/Plus

Query  1191  GCAGTACGGTGTGGCTTTCATTTTCAGGTGCAAGTGAATGTTAACCAAGGAACAGCTGGT  1250
             |||||||||||||| ||||||||||| || |||||||||||||| ||||||||||| |||
Sbjct  3     GCAGTACGGTGTGGTTTTCATTTTCAAGTACAAGTGAATGTTAATCAAGGAACAGCCGGT  62

Query  1251  AGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTT  1310
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  63    AGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTT  122

Query  1311  GGAGCATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGAT  1370
             ||||| |||||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  123   GGAGCGTTTACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGAT  182

Query  1371  TTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGG  1430
             ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  183   TTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGG  242

Query  1431  CAACTAAAA  1439
             |||||||||
Sbjct  243   CAACTAAAA  251


>SRR2298578.1030338 1030338 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 247/254 (97%), Gaps = 0/254 (0%)
 Strand=Plus/Plus

Query  349  GGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCG  408
            ||||||||||||||||||||||||| ||||||||||||| ||||||||||||||||||||
Sbjct  1    GGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCG  60

Query  409  GAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTA  468
            ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  61   GAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTA  120

Query  469  GGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTA  528
            ||||||||||||||||||||||||||| ||||||||||||||||| ||||||||||||||
Sbjct  121  GGATTGGTTCTAAACCTGAGATGTTGTAGAAGATACTTAGTACCTACCGATCTGGTAGTA  180

Query  529  CTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAG  588
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAG  240

Query  589  TGACACTATGGATC  602
             |||||||||||||
Sbjct  241  CGACACTATGGATC  254


 Score = 399 bits (216),  Expect = 6e-107
 Identities = 234/243 (96%), Gaps = 0/243 (0%)
 Strand=Plus/Minus

Query  360  GGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCT  419
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            |||||||| ||||| |||||||||| || |||||||||||||||||||||||||||||||
Sbjct  493  GGAACTTAGTGGAAACAACATTTTGGTGTAAAGCATCCTATTGCCAGCGGAACAACACCT  434

Query  420  GGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCT  479
            |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  433  GGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCT  374

Query  480  AAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACT  539
            |||||||||||||||| ||||||||||||||||| |||||||||||||| ||||||||||
Sbjct  373  AAACCTGAGATGTTGTAGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACT  314

Query  540  AGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGG  599
            ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  313  AGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGG  254

Query  600  ATC  602
            |||
Sbjct  253  ATC  251


>SRR2298578.535032 535032 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  1258  TGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCAT  1317
             ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  251   TGGTGGTGTATGAACCCAAACCCGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCAT  192

Query  1318  TTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTA  1377
             |||||||| |||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  191   TTACCAATCTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTA  132

Query  1378  TCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACTAA  1437
             |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  131   TCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAACTAA  72

Query  1438  AAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGATGTAA  1497
             ||||||||||||||||||||||||| ||||||||||||||||| ||||||||||||||||
Sbjct  71    AAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGATGTAA  12

Query  1498  CCATATTGGGT  1508
             |||||||||||
Sbjct  11    CCATATTGGGT  1


 Score = 388 bits (210),  Expect = 1e-103
 Identities = 239/253 (94%), Gaps = 1/253 (0%)
 Strand=Plus/Plus

Query  1234  ACCAAGGAACAGCTGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATG  1293
             ||| ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  248   ACC-AGGAACAGCTGGTAGTGCATTGGTGGTGTATGAACCCAAACCCGTTGTGACATATG  306

Query  1294  ACTCAAAGTTAGAATTTGGAGCATTTACCAATTTACCACATGTATTGATGAATTTGGCTG  1353
             |||||||||||||||||||||||||||||||| |||||||||| ||||||||||||||||
Sbjct  307   ACTCAAAGTTAGAATTTGGAGCATTTACCAATCTACCACATGTGTTGATGAATTTGGCTG  366
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Query  1354  AGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGG  1413
             ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||| |
Sbjct  367   AGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACAATGTTAAAACAG  426

Query  1414  ATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCTATACCTTCAG  1473
             ||||||||||||||||| ||||||||| | ||||||||  ||||||||| ||||||||||
Sbjct  427   ATTCGTCAGACTTAGGGTAACTAAAAGCCAATGTTTGGCAACCTTTATCCATACCTTCAG  486

Query  1474  GTTCTGCGACACA  1486
             ||| ||| |||||
Sbjct  487   GTTTTGCTACACA  499


>SRR2298573.869794 869794 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  396  CCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCT  455
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  1    CCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTT  60

Query  456  AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGC  515
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  61   AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTAC  120

Query  516  CGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACC  575
            ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACC  180

Query  576  CATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGAC  635
            ||||||||||||| |||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  181  CATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGGGAT  240

Query  636  CTGGTTAAAAA  646
            |||||||||||
Sbjct  241  CTGGTTAAAAA  251


 Score = 368 bits (199),  Expect = 2e-97
 Identities = 229/244 (94%), Gaps = 0/244 (0%)
 Strand=Plus/Minus

Query  557  AGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAG  616
            ||| ||||| | |||| ||||||||||||||| ||| || ||||||||||||||||||||
Sbjct  494  AGGGTGCCCCGGAGGTCCCCATAGGTAACAAGCGACCCTTTGGATCTGATCTGGGGCCAG  435

Query  617  GTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATC  676
            |||||||||||||||||| ||||||||||| |||||||||||||||||||||||||||||
Sbjct  434  GTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATC  375

Query  677  CCCGGTTTCCTTTTATTTTATCAATGCTACAATGGAGACAATTAAAAGTATTGCAGATAT  736
            ||||||||||||||||||||||||||| || |||||||||||||| |||||||||||||||
Sbjct  374  CCCGGTTTCCTTTTATTTTATCAATGCCACTATGGAGACAATTAAGAGTATTGCAGATAT  315

Query  737  GGCGACCGGAGTGGTCAGTTCAGTTGATTCCACTATCAATGCAGTTAATGAGAGAGTAGA  796
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                |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||| ||
Sbjct  314  GGCGACCGGAGTGGTCAGTTCAGTTGATTCCACTATCAATGTAGTTAATGAGAGAGTGGA  255

Query  797  AAAT  800
            | ||
Sbjct  254  AGAT  251


>SRR2298573.825070 825070 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 243/248 (98%), Gaps = 0/248 (0%)
 Strand=Plus/Minus

Query  297  TTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGT  356
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  498  TTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGT  439

Query  357  GTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACA  416
            ||||||||||||||||| ||||||||||||| ||||||||||||||||||||||||||||
Sbjct  438  GTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACA  379

Query  417  CCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGT  476
            ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct  378  CCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGT  319

Query  477  TCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAAC  536
            ||||||||||||||||||||||||||||||||||||| |||||||||||||| |||||||
Sbjct  318  TCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAAC  259

Query  537  ACTAGTTG  544
            ||||||||
Sbjct  258  ACTAGTTG  251


 Score = 392 bits (212),  Expect = 9e-105
 Identities = 236/248 (95%), Gaps = 0/248 (0%)
 Strand=Plus/Plus

Query  296  CTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACG  355
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACG  60

Query  356  TGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAAC  415
            |||||||||||||||||| ||||||||||||| |||||||||||||||||||||||||||
Sbjct  61   TGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAAC  120

Query  416  ACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGG  475
            |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Sbjct  121  ACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGG  180

Query  476  TTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAA  535
            |||||||||||||||||||||||||| |||||| |||  |||| |||| || | ||||||
Sbjct  181  TTCTAAACCTGAGATGTTGTGGAAGAAACTTAGAACCAACCGACCTGGAAGAAGTGCAAA  240

Query  536  CACTAGTT  543
            ||| ||||
Sbjct  241  CACAAGTT  248
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>SRR2298573.781063 781063 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  461  ACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATC  520
            ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  250  ACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATC  309

Query  521  TGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAG  580
            |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  310  TGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAG  369

Query  581  GTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGT  640
            |||||||| ||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  370  GTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGT  429

Query  641  TAAAAAGCGTCTAGTGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTTTATCAA  700
            |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  430  TAAAAAACGTCTAGTGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTATCAA  489

Query  701  TGCTACAATGG  711
            ||| |||||||
Sbjct  490  TGCCACAATGG  500


 Score = 411 bits (222),  Expect = 3e-110
 Identities = 240/249 (96%), Gaps = 0/249 (0%)
 Strand=Plus/Minus

Query  473  TGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGC  532
            |||||||||||||||| ||||||||||||| |||||||||| |||||||||||||| |||
Sbjct  250  TGGTTCTAAACCTGAGGTGTTGTGGAAGATTCTTAGTACCTTCCGATCTGGTAGTAGTGC  191

Query  533  AAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGAC  592
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  190  AAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGAC  131

Query  593  ACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCT  652
            |||||||||||||||||||||||||||||||||||||||||| ||||||||||| |||||
Sbjct  130  ACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCT  71

Query  653  AGTGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTTTATCAATGCTACAATGGA  712
            ||||||||||||||||||||||||||||||||||||||||||||||||||| || |||||
Sbjct  70   AGTGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTATCAATGCCACTATGGA  11

Query  713  GACAATTAA  721
            |||||||||
Sbjct  10   GACAATTAA  2


>SRR2298573.780853 780853 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
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 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  443  AAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGAT  502
            ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  251  AAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGAT  192

Query  503  ACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATG  562
            ||||||||||| |||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  191  ACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATG  132

Query  563  CCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCT  622
            |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  131  CCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCT  72

Query  623  CTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCggggggATCCCCGGT  682
            |||||||||||| ||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  71   CTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGATCCCCGGT  12

Query  683  TTCCTTTTATT  693
            |||||||||||
Sbjct  11   TTCCTTTTATT  1


 Score = 424 bits (229),  Expect = 3e-114
 Identities = 243/250 (97%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  422  TAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAA  481
            |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Sbjct  251  TAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAA  310

Query  482  ACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAG  541
            |||||||||||||||||||||||||||||||| |||||||||||||| ||||||||||||
Sbjct  311  ACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAG  370

Query  542  TTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGAT  601
            ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  371  TTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGAT  430

Query  602  CTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCA  661
            |||||||||||||||||||||||||||||| || ||||||||||| ||||||||||||||
Sbjct  431  CTGATCTGGGGCCAGGTACCTCTATCTTGGGGATCTGGTTAAAAAACGTCTAGTGGGCCA  490

Query  662  AACCCggggg  671
            ||||||||||
Sbjct  491  AACCCGGGGG  500


>SRR2298573.769703 769703 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 254/264 (96%), Gaps = 1/264 (0%)
 Strand=Plus/Minus

Query  327  CTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCT  386
            |||||||||||||||||||||||||||||| |||||||||||||||| ||||||||||||
Sbjct  499  CTAGTAAGTTTGTGAGACGTCTGGTGACGTTTGGGAACTTATTGGAAACAACATTTTGCT  440
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Query  387  GCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAG  446
            | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  439  GTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAG  380

Query  447  CCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTT  506
            ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  379  CCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTT  320

Query  507  AGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCA  566
            ||||||| |||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  319  AGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCA  260

Query  567  GAAGGTACCCA-TAGGTAACAAGT  589
            ||||||||||  ||||||  ||||
Sbjct  259  GAAGGTACCCGGTAGGTACTAAGT  236


 Score = 409 bits (221),  Expect = 9e-110
 Identities = 235/242 (97%), Gaps = 0/242 (0%)
 Strand=Plus/Plus

Query  276  TCTACTAGTGAGATACCACGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGT  335
            |||| ||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  9    TCTATTAGTGAGATACCATGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGT  68

Query  336  TTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCAT  395
            |||||||||||||||||||||||||||||||||||||| ||||||||||||| |||||||
Sbjct  69   TTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCAT  128

Query  396  CCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCT  455
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  129  CCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTT  188

Query  456  AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGC  515
            |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||| |
Sbjct  189  AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGAAACTTAGTACCTAC  248

Query  516  CG  517
            ||
Sbjct  249  CG  250


>SRR2298573.746679 746679 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 243/248 (98%), Gaps = 0/248 (0%)
 Strand=Plus/Minus

Query  335  TTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCA  394
            ||||||||||||||||||||||||||||||||||||||| ||||||||||||| ||||||
Sbjct  498  TTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCA  439

Query  395  TCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTC  454
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  438  TCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTT  379

Query  455  TAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTG  514
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            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  378  TAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTA  319

Query  515  CCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTAC  574
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  318  CCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTAC  259

Query  575  CCATAGGT  582
            ||||||||
Sbjct  258  CCATAGGT  251


 Score = 412 bits (223),  Expect = 7e-111
 Identities = 242/251 (96%), Gaps = 1/251 (0%)
 Strand=Plus/Plus

Query  334  GTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGC  393
            |||||||||||||||||||||||||||||||||||||||| ||||||||||||| |||||
Sbjct  11   GTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGC  70

Query  394  ATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGT  453
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  71   ATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGT  130

Query  454  CTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCT  513
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  131  TTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCT  190

Query  514  GCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTA  573
             |||||||||||||| |||||||||||||||||||||||||||||||||||||||||| |
Sbjct  191  ACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGGA  250

Query  574  CCC-ATAGGTA  583
             || || ||||
Sbjct  251  ACCTATGGGTA  261


>SRR2298573.740334 740334 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  396  CCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCT  455
            |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||| |
Sbjct  251  CCTATTGCCAGCGGAACAACCCCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTT  192

Query  456  AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGC  515
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  191  AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTAC  132

Query  516  CGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACC  575
            ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  131  CGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACC  72

Query  576  CATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGAC  635
            ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  71   CATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGAT  12
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```
Query  636  CTGGTTAAAAA  646
            |||||||||||
Sbjct  11   CTGGTTAAAAA  1


 Score = 379 bits (205),  Expect = 7e-101
 Identities = 227/238 (95%), Gaps = 0/238 (0%)
 Strand=Plus/Plus

Query  333  AGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAG  392
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||||| ||||
Sbjct  263  AGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAG  322

Query  393  CATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGG  452
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  323  CATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGG  382

Query  453  TCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACC  512
            | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  383  TTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACC  442

Query  513  TGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAG  570
            | ||||||||||  ||  |||||||| ||||||||||||| || ||||||||||||||
Sbjct  443  TACCGATCTGGTGTTAGGGCAAACACAAGTTGTAAGGCCCCCGCAGGATGCCCAGAAG  500


>SRR2298573.710464 710464 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 243/248 (98%), Gaps = 0/248 (0%)
 Strand=Plus/Plus

Query  456  AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGC  515
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  1    AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTAC  60

Query  516  CGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACC  575
            ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACC  120

Query  576  CATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGAC  635
            ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  121  CATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGAT  180

Query  636  CTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTTT  695
            ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTT  240

Query  696  ATCAATGC  703
            ||||||||
Sbjct  241  ATCAATGC  248


 Score = 385 bits (208),  Expect = 2e-102
 Identities = 236/250 (94%), Gaps = 0/250 (0%)
 Strand=Plus/Minus
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Query  475  GTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAA  534
            |||||||||||||||||||| ||||| | |||||  ||| ||||| |||||||| |||||
Sbjct  500  GTTCTAAACCTGAGATGTTGGGGAAGGTTCTTAGGTCCTTCCGATTTGGTAGTAGTGCAA  441

Query  535  ACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACAC  594
            |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  440  ACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACAC  381

Query  595  TATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAG  654
            |||||||||||||||||||||||||||||||||||||||| ||||||||||| |||||||
Sbjct  380  TATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAG  321

Query  655  TGGGCCAAACCCggggggATCCCCGGTTTCCTTTTATTTTATCAATGCTACAATGGAGA  714
            ||||||||||||||||||||||||||||||||||||||||||||||||| || |||||||
Sbjct  320  TGGGCCAAACCCGGGGGGATCCCCGGTTTCCTTTTATTTTATCAATGCCACTATGGAGA  261

Query  715  CAATTAAAAG  724
            ||||||| ||
Sbjct  260  CAATTAAGAG  251


>SRR2298573.706510 706510 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 248/255 (97%), Gaps = 1/255 (0%)
 Strand=Plus/Plus

Query  277  CTACTAGTGAGATACCACGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTT  336
            ||| ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTATTAGTGAGATACCATGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTT  60

Query  337  TGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATC  396
            ||||||||||||||||||||||||||||||||||||| ||||||||||||| ||||||||
Sbjct  61   TGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATC  120

Query  397  CTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTA  456
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  121  CTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTA  180

Query  457  ACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCC  516
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  181  ACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACC  240

Query  517  GATCTGGTAG-TACT  530
            |||||||||| ||||
Sbjct  241  GATCTGGTAGCTACT  255


 Score = 387 bits (209),  Expect = 4e-103
 Identities = 235/248 (95%), Gaps = 0/248 (0%)
 Strand=Plus/Minus

Query  281  TAGTGAGATACCACGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTG  340
            ||| || || ||| ||| ||||||||||||||| |  |||||||||||||||||||||||
Sbjct  499  TAGGGAAATCCCATGCTGGTGGACCTTATGCTCCCCAAGCCATCCTCTAGTAAGTTTGTG  440

Query  341  AGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTAT  400
            ||||||||||||||||||||||||||||||||| ||||||||||||| ||||||||||||
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Sbjct  439  AGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTAT  380

Query  401  TGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAA  460
            ||||||||||||||||||||||||||||||||||||||| ||||||||||||| ||||||
Sbjct  379  TGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGACAAAAGCCAAGGTTTAACAA  320

Query  461  ACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATC  520
            ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  319  ACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATC  260

Query  521  TGGTAGTA  528
            ||||||||
Sbjct  259  TGGTAGTA  252


>SRR2298573.647887 647887 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 247/254 (97%), Gaps = 0/254 (0%)
 Strand=Plus/Plus

Query  433  TCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGT  492
            ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGT  60

Query  493  TGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCC  552
            ||||||||||||||||||||| |||||||||||||| |||||||||||||||||||||||
Sbjct  61   TGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCC  120

Query  553  ACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGG  612
            |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct  121  ACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGG  180

Query  613  CCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggg  672
            |||||||||||||||||||||| ||||||||||| |||||||||||||||||||||||||
Sbjct  181  CCAGGTACCTCTATCTTGGTGAACTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGG  240

Query  673  gATCCCCGGTTTCC  686
            |||||||||| |||
Sbjct  241  GATCCCCGGTCTCC  254


 Score = 383 bits (207),  Expect = 6e-102
 Identities = 235/249 (94%), Gaps = 0/249 (0%)
 Strand=Plus/Minus

Query  499  AGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAG  558
            ||||||||||| ||| ||| ||||||||||  |||||| |||||| ||||||||||||||
Sbjct  499  AGATACTTAGTTCCTACCGGTCTGGTAGTAGGGCAAACCCTAGTTTTAAGGCCCACGAAG  440

Query  559  GATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGT  618
            |||||||||||||||||||||||||||||| ||||||| |||||||||||||||||||||
Sbjct  439  GATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTAGGGATCTGATCTGGGGCCAGGT  380

Query  619  ACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCC  678
            |||||||||||||||| ||||||||||| |||||||||||||||||||||||||||||||
Sbjct  379  ACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCC  320
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Query  679  CGGTTTCCTTTTATTTTATCAATGCTACAATGGAGACAATTAAAAGTATTGCAGATATGG  738
            ||||||||||||||||||||||||| || |||||||||||||| ||||||||||||||||
Sbjct  319  CGGTTTCCTTTTATTTTATCAATGCCACTATGGAGACAATTAAGAGTATTGCAGATATGG  260

Query  739  CGACCGGAG  747
            |||||||||
Sbjct  259  CGACCGGAG  251


>SRR2298573.588383 588383 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  430  GCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGA  489
            |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  251  GCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGA  192

Query  490  TGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGG  549
            |||||||||||||||||||||||| |||||||||||||| ||||||||||||||||||||
Sbjct  191  TGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGG  132

Query  550  CCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTG  609
            ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  131  CCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTG  72

Query  610  GGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCggg  669
            ||||||||||||||||||||||||| ||||||||||| ||||||||||||||||||||||
Sbjct  71   GGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGG  12

Query  670  ggggATCCCCG  680
            |||||||||||
Sbjct  11   GGGGATCCCCG  1


 Score = 390 bits (211),  Expect = 3e-104
 Identities = 237/250 (95%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  364  CTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTA  423
            |||||||||| ||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  251  CTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTA  310

Query  424  ACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAAC  483
            |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Sbjct  311  ACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAAC  370

Query  484  CTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTT  543
            |||||||||||||||||||||||||||||| |||||||||||||| ||||||||||||||
Sbjct  371  CTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTT  430

Query  544  GTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCT  603
            |||||||||||||||||||||||||||| ||| | ||| || ||  ||||| ||||||||
Sbjct  431  GTAAGGCCCACGAAGGATGCCCAGAAGGAACCAAAAGGAAAAAAACGACACAATGGATCT  490

Query  604  GATCTGGGGC  613
            ||||||||||
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Sbjct  491  GATCTGGGGC  500


>SRR2298573.550702 550702 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  338  GTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCC  397
            |||||||||||||||||||||||||||||||||||| ||||||||||||| |||||||||
Sbjct  251  GTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCC  192

Query  398  TATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAA  457
            |||||||||||||||||| ||||||||||||||||||||||||||||||||||||| |||
Sbjct  191  TATTGCCAGCGGAACAACGCCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAA  132

Query  458  CAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCG  517
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  131  CAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCG  72

Query  518  ATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCA  577
            ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  71   ATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCA  12

Query  578  TAGGTAACAAG  588
            |||||||||||
Sbjct  11   TAGGTAACAAG  1


 Score = 370 bits (200),  Expect = 4e-98
 Identities = 224/236 (95%), Gaps = 0/236 (0%)
 Strand=Plus/Plus

Query  336  TTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCAT  395
            |||||||||||||||||||||||||||||||||||||| ||||||||||||| |||||||
Sbjct  260  TTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCAT  319

Query  396  CCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCT  455
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  320  CCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTT  379

Query  456  AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGC  515
            |||||||||||||||||||||||||||||||||||||||||||||| |||| | |||| |
Sbjct  380  AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGAAACTTCGAACCTAC  439

Query  516  CGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGG  571
            ||||||||||| | |||||||||  || ||||||||||||||||||||||||||||
Sbjct  440  CGATCTGGTAGCAGTGCAAACACAGGTGGTAAGGCCCACGAAGGATGCCCAGAAGG  495


>SRR2298573.529564 529564 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Minus
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Query  357  GTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACA  416
            ||||||||||||||||| ||||||||||||| ||||||||||||||||||||||||||||
Sbjct  251  GTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACA  192

Query  417  CCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGT  476
            ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct  191  CCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGT  132

Query  477  TCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAAC  536
            ||||||||||||||||||||||||||||||||||||| |||||||||||||| |||||||
Sbjct  131  TCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAAC  72

Query  537  ACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTA  596
            |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  71   ACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTA  12

Query  597  TGGATCTGATC  607
            |||||||||||
Sbjct  11   TGGATCTGATC  1


 Score = 409 bits (221),  Expect = 9e-110
 Identities = 241/251 (96%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  303  ACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGA  362
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  250  ACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGA  309

Query  363  ACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGT  422
            ||||||||||| ||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  310  ACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGT  369

Query  423  AACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAA  482
            ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  370  AACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAA  429

Query  483  CCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGT  542
            |||||||||||| |||||||||||||||||| ||||||||||||||  |||||||  || 
Sbjct  430  CCTGAGATGTTGGGGAAGATACTTAGTACCTACCGATCTGGTAGTAGGGCAAACAACAGG  489

Query  543  TGTAAGGCCCA  553
            |||||||||||
Sbjct  490  TGTAAGGCCCA  500


>SRR2298573.498005 498005 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  357  GTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACA  416
            ||||||||||||||||| ||||||||||||| ||||||||||||||||||||||||||||
Sbjct  251  GTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACA  192

Query  417  CCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGT  476
            ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
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Sbjct  191  CCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGT  132

Query  477  TCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAAC  536
            ||||||||||||||||||||||||||||||||||||| |||||||||||||| |||||||
Sbjct  131  TCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAAC  72

Query  537  ACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTA  596
            |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  71   ACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTA  12

Query  597  TGGATCTGATC  607
            |||||||||||
Sbjct  11   TGGATCTGATC  1


 Score = 379 bits (205),  Expect = 7e-101
 Identities = 231/244 (95%), Gaps = 0/244 (0%)
 Strand=Plus/Plus

Query  332  AAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAA  391
            ||||||||||||||||||| |||||||||||||||||||||| ||||||||||||| |||
Sbjct  257  AAGTTTGTGAGACGTCTGGCGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAA  316

Query  392  GCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAG  451
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  317  GCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAG  376

Query  452  GTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTAC  511
            || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  377  GTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTAC  436

Query  512  CTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGG  571
            || ||||||||||||||  ||||| |||||||| ||||||| ||||||| ||||| ||||
Sbjct  437  CTACCGATCTGGTAGTAGGGCAAAAACTAGTTGAAAGGCCCCCGAAGGAGGCCCAAAAGG  496

Query  572  TACC  575
             |||
Sbjct  497  AACC  500


>SRR2298573.468266 468266 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 243/248 (98%), Gaps = 0/248 (0%)
 Strand=Plus/Plus

Query  456  AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGC  515
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  251  AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTAC  310

Query  516  CGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACC  575
            ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  311  CGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACC  370

Query  576  CATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGAC  635
            ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  371  CATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGAT  430
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Query  636  CTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTTT  695
            ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  431  CTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTT  490

Query  696  ATCAATGC  703
            ||||||||
Sbjct  491  ATCAATGC  498


 Score = 414 bits (224),  Expect = 2e-111
 Identities = 240/248 (97%), Gaps = 0/248 (0%)
 Strand=Plus/Minus

Query  515  CCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTAC  574
            |||||||||||||| |||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  248  CCGATCTGGTAGTAGTGCAAACACTTGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTAC  189

Query  575  CCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGA  634
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  188  CCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGA  129

Query  635  CCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTT  694
             ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  128  TCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTT  69

Query  695  TATCAATGCTACAATGGAGACAATTAAAAGTATTGCAGATATGGCGACCGGAGTGGTCAG  754
            ||||||||| || |||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  68   TATCAATGCCACTATGGAGACAATTAAGAGTATTGCAGATATGGCGACCGGAGTGGTCAG  9

Query  755  TTCAGTTG  762
            ||||||||
Sbjct  8    TTCAGTTG  1


>SRR2298573.423667 423667 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  377  ACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTG  436
            ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    ACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTG  60

Query  437  GGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTG  496
            ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTG  120

Query  497  GAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGA  556
            ||||||||||||||||| |||||||||||||| |||||||||||||||||||||||||||
Sbjct  121  GAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGA  180

Query  557  AGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAG  616
            |||||||||||||||||||||||||||||||| ||||| |||||||||||||||||||||
Sbjct  181  AGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACAATGGATCTGATCTGGGGCCAG  240

Query  617  GTACCTCTATC  627
            |||||||||||
```

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Sbjct  241  GTACCTCTATC  251


 Score = 379 bits (205),  Expect = 7e-101
 Identities = 235/250 (94%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  515  CCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTAC  574
            ||||||||| |||| ||||||| |||||||  ||||||| ||||| ||||||||||||||
Sbjct  498  CCGATCTGGGAGTAGTGCAAACCCTAGTTGGTAGGCCCAAGAAGGTTGCCCAGAAGGTAC  439

Query  575  CCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGA  634
            |||||||||||||| |||||||||||| | ||||||||||||||||||||||||||||||
Sbjct  438  CCATAGGTAACAAGCGACACTATGGATTTTATCTGGGGCCAGGTACCTCTATCTTGGTGA  379

Query  635  CCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTT  694
             ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  378  TCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTT  319

Query  695  TATCAATGCTACAATGGAGACAATTAAAAGTATTGCAGATATGGCGACCGGAGTGGTCAG  754
            ||||||||| || |||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  318  TATCAATGCCACTATGGAGACAATTAAGAGTATTGCAGATATGGCGACCGGAGTGGTCAG  259

Query  755  TTCAGTTGAT  764
            ||||||||||
Sbjct  258  TTCAGTTGAT  249


>SRR2298573.403271 403271 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 243/248 (98%), Gaps = 0/248 (0%)
 Strand=Plus/Minus

Query  384  GCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAA  443
            |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  248  GCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAA  189

Query  444  AAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATA  503
            |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  188  AAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATA  129

Query  504  CTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGC  563
            |||||||||| |||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  128  CTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGC  69

Query  564  CCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTC  623
            ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  68   CCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTC  9

Query  624  TATCTTGG  631
            ||||||||
Sbjct  8    TATCTTGG  1


 Score = 399 bits (216),  Expect = 6e-107
 Identities = 238/249 (96%), Gaps = 0/249 (0%)
 Strand=Plus/Plus
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Query  383  TGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCA  442
            ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  249  TGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCA  308

Query  443  AAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGAT  502
            ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  309  AAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGAT  368

Query  503  ACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATG  562
            ||||||||||| |||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  369  ACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATG  428

Query  563  CCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCT  622
            |||||||||||||||||||||||||| ||| | ||||||| || ||||||||||| |||
Sbjct  429  CCCAGAAGGTACCCATAGGTAACAAGCGACCCAATGGATCGGACCTGGGGCCAGGGACCC  488

Query  623  CTATCTTGG  631
            |||||||||
Sbjct  489  CTATCTTGG  497


>SRR2298573.379421 379421 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  327  CTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCT  386
            ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  1    CTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCT  60

Query  387  GCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAG  446
            | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAG  120

Query  447  CCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTT  506
            ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTT  180

Query  507  AGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCA  566
            ||||||| |||||||||||||| ||||||||||||||||||||||||||||||| |||||
Sbjct  181  AGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGAGGCCCA  240

Query  567  GAAGGTACCCA  577
            |||||||||||
Sbjct  241  GAAGGTACCCA  251


 Score = 420 bits (227),  Expect = 4e-113
 Identities = 248/258 (96%), Gaps = 1/258 (0%)
 Strand=Plus/Minus

Query  380  TTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGG  439
            |||||||| |||||||||| ||||||||||||| || |||||||||||||||||||||||
Sbjct  499  TTTTGCTGTAAAGCATCCTTTTGCCAGCGGAACTACGCCTGGTAACAGGTGCCTCTGGGG  440

Query  440  CCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAA  499
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            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  439  CCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAA  380

Query  500  GATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGG  559
            |||||||||||||| |||||||||||||| ||||||||||||||||||||||||||||||
Sbjct  379  GATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGG  320

Query  560  ATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTA  619
            ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Sbjct  319  ATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTA  260

Query  620  CCTCTATCTTGGTGACCT  637
            ||||||||| ||| ||||
Sbjct  259  CCTCTATCTGGGT-ACCT  243


>SRR2298573.374775 374775 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  439  GCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGA  498
            ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGA  60

Query  499  AGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAG  558
            ||||||||||||||| |||||||||||||| |||||||||||||||||||||||||||||
Sbjct  61   AGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAG  120

Query  559  GATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGT  618
            |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Sbjct  121  GATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGT  180

Query  619  ACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCggggggGATCCC  678
            |||||||||||||||| ||||||||||| |||||||||||||||||||||||||||||||
Sbjct  181  ACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCC  240

Query  679  CGGTTTCCTTT  689
            |||||||||||
Sbjct  241  CGGTTTCCTTT  251


 Score = 370 bits (200),  Expect = 4e-98
 Identities = 233/249 (94%), Gaps = 2/249 (1%)
 Strand=Plus/Minus

Query  488  GATGTTGTGGAAGATACTT-AGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTA  546
            ||||||  ||||||| ||| ||| ||| ||| | |||||||| |||||||||||||||||
Sbjct  498  GATGTTTGGGAAGATTCTTAAGT-CCTACCGGTTTGGTAGTAGTGCAAACACTAGTTGTA  440

Query  547  AGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGAT  606
            |||||||||||||||||||||||||||||||||||||||||| | |||||||||||||||
Sbjct  439  AGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGGCACTATGGATCTGAT  380

Query  607  CTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCC  666
            |||||||||||||||||||||||||||| ||||||||||| |||||||||||||||||||
Sbjct  379  CTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCC  320
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Query  667  gggggggATCCCCGGTTTCCTTTTATTTTATCAATGCTACAATGGAGACAATTAAAAGTA  726
            ||||||||||||||||||||||||||||||||||||| || |||||||||||||| ||||
Sbjct  319  GGGGGGGATCCCCGGTTTCCTTTTATTTTATCAATGCCACTATGGAGACAATTAAGAGTA  260

Query  727  TTGCAGATA  735
            |||||||||
Sbjct  259  TTGCAGATA  251


>SRR2298573.349802 349802 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 243/248 (98%), Gaps = 0/248 (0%)
 Strand=Plus/Minus

Query  336  TTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCAT  395
            |||||||||||||||||||||||||||||||||||||| ||||||||||||| |||||||
Sbjct  248  TTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCAT  189

Query  396  CCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCT  455
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  188  CCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTT  129

Query  456  AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGC  515
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  128  AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTAC  69

Query  516  CGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACC  575
            ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  68   CGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACC  9

Query  576  CATAGGTA  583
            ||||||||
Sbjct  8    CATAGGTA  1


 Score = 390 bits (211),  Expect = 3e-104
 Identities = 237/250 (95%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  310  GCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATT  369
            ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  251  GCTCACACAGCCATCCTCTAGTAAGCTTGTGAGACGTCTGGTGACGTGTGGGAACTTATT  310

Query  370  GGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGT  429
            |||| ||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  311  GGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGT  370

Query  430  GCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGA  489
            |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  371  GCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGA  430

Query  490  TGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGG  549
            ||||||||||||||||||  |||| ||||||||||||||  ||||||||  | |||||||
Sbjct  431  TGTTGTGGAAGATACTTAAAACCTACCGATCTGGTAGTAGGGCAAACACCTGGTGTAAGG  490

Query  550  CCCACGAAGG  559
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            ||| ||||||
Sbjct  491  CCCCCGAAGG  500


>SRR2298573.317178 317178 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  453  TCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACC  512
            |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Sbjct  252  TCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGGGGAAGATACTTAGTACC  193

Query  513  TGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGT  572
            | |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  192  TACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGT  133

Query  573  ACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGT  632
            |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  132  ACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGT  73

Query  633  GACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCggggggATCCCCGGTTTCCTTTTAT  692
            || ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  72   GATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGATCCCCGGTTTCCTTTTAT  13

Query  693  TTTATCAATGC  703
            |||||||||||
Sbjct  12   TTTATCAATGC  2


 Score = 379 bits (205),  Expect = 7e-101
 Identities = 235/250 (94%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  409  GAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTA  468
            ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  251  GAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTA  310

Query  469  GGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTA  528
            ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  311  GGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTA  370

Query  529  CTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAG  588
             ||||||||||||||||||| |||||||||||||||||||||| |||||||||||| |||
Sbjct  371  GTGCAAACACTAGTTGTAAGTCCCACGAAGGATGCCCAGAAGGAACCCATAGGTAAAAAG  430

Query  589  TGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGC  648
              |||||||||| |||| ||||||||||| ||| ||||||||||| |||||||||||| |
Sbjct  431  CAACACTATGGACCTGACCTGGGGCCAGGGACCCCTATCTTGGTGTCCTGGTTAAAAAAC  490

Query  649  GTCTAGTGGG  658
            | ||||||||
Sbjct  491  GCCTAGTGGG  500


>SRR2298573.316987 316987 length=500
Length=500
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 Score = 431 bits (233),  Expect = 2e-116
 Identities = 243/248 (98%), Gaps = 0/248 (0%)
 Strand=Plus/Plus

Query  334  GTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGC  393
            |||||||||||||||||||||||||||||||||||||||| ||||||||||||| |||||
Sbjct  1    GTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGC  60

Query  394  ATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGT  453
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGT  120

Query  454  CTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCT  513
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCT  180

Query  514  GCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTA  573
             |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTA  240

Query  574  CCCATAGG  581
            ||||||||
Sbjct  241  CCCATAGG  248


 Score = 424 bits (229),  Expect = 3e-114
 Identities = 243/250 (97%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  354  CGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACA  413
            |||||||||||||||||||| ||||||||||||| |||||||||||||||||||||||||
Sbjct  499  CGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACA  440

Query  414  ACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATT  473
            || ||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  439  ACGCCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATT  380

Query  474  GGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCA  533
            |||||||||||||||||||||||||||||||||||||||| |||||||||||||| ||||
Sbjct  379  GGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCA  320

Query  534  AACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACA  593
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  319  AACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACA  260

Query  594  CTATGGATCT  603
            ||||||||||
Sbjct  259  CTATGGATCT  250


>SRR2298573.312469 312469 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 248/255 (97%), Gaps = 1/255 (0%)
 Strand=Plus/Plus

Query  335  TTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCA  394
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            ||||||||||||||||||||||||||||||||||||||| ||||||||||||| ||||||
Sbjct  1    TTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCA  60

Query  395  TCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTC  454
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  61   TCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTT  120

Query  455  TAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTG  514
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  121  TAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTA  180

Query  515  CCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTAC  574
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTAC  240

Query  575  CCATAGGTAAC-AAG  588
            ||||||| ||| |||
Sbjct  241  CCATAGGAAACCAAG  255


 Score = 398 bits (215),  Expect = 2e-106
 Identities = 239/251 (95%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  382  TTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCC  441
            |||| | |||||  |||||  || |||||||||| |||||||||||||||||||||||||
Sbjct  500  TTGCGGTAAAGCTCCCTATGTCCGGCGGAACAACCCCTGGTAACAGGTGCCTCTGGGGCC  441

Query  442  AAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGA  501
            |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  440  AAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGA  381

Query  502  TACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGAT  561
            |||||||||||| |||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  380  TACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGAT  321

Query  562  GCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACC  621
            ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  320  GCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACC  261

Query  622  TCTATCTTGGT  632
            |||||||||||
Sbjct  260  TCTATCTTGGT  250


>SRR2298573.312255 312255 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  384  GCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAA  443
            |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAA  60

Query  444  AAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATA  503
            |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATA  120
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Query  504   CTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGC  563
             |||||||||| |||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  121   CTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGC  180

Query  564   CCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTC  623
             ||||||||||||||||||||||||| ||||| ||||||||||||||||||||||||||||
Sbjct  181   CCAGAAGGTACCCATAGGTAACAAGCGACACAATGGATCTGATCTGGGGCCAGGTACCTC  240

Query  624   TATCTTGGTGA  634
             |||||||||||
Sbjct  241   TATCTTGGTGA  251


 Score = 418 bits (226),  Expect = 2e-112
 Identities = 240/247 (97%), Gaps = 0/247 (0%)
 Strand=Plus/Minus

Query  395   TCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTC  454
             |||| |||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  497   TCCTTTTGCCAGCGGAACAACCCCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTT  438

Query  455   TAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTG  514
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  437   TAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTA  378

Query  515   CCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTAC  574
             |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  377   CCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTAC  318

Query  575   CCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGA  634
             |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  317   CCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGA  258

Query  635   CCTGGTT  641
              ||||||
Sbjct  257   TCTGGTT  251


>SRR2298573.293391 293391 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 248/255 (97%), Gaps = 1/255 (0%)
 Strand=Plus/Plus

Query  367   ATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACA  426
             ||||||| ||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  1     ATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACA  60

Query  427   GGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTG  486
             ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  61    GGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTG  120

Query  487   AGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTA  546
             ||||||||||||||||||||||||||| |||||||||||||| |||||||||||||||||
Sbjct  121   AGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTA  180

Query  547   AGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGAT  606
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                ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Sbjct  181  AGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGAT  240

Query  607  CTGGGGCCAGGTACC  621
            ||||||||||| |||
Sbjct  241  CTGGGGCCAGG-ACC  254


 Score = 346 bits (187),  Expect = 7e-91
 Identities = 230/251 (92%), Gaps = 1/251 (0%)
 Strand=Plus/Minus

Query  502  TACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGAT  561
            ||||| || ||| |||  ||||| ||| ||| ||| || |||  ||||||||||||||||
Sbjct  500  TACTT-GTCCCTACCGTACTGGTTGTAGTGCCAACCCTTGTTTGAAGGCCCACGAAGGAT  442

Query  562  GCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACC  621
            |||||| |||||||||||||||||||| ||| ||||||||||||||||||||||||||||
Sbjct  441  GCCCAGGAGGTACCCATAGGTAACAAGCGACCCTATGGATCTGATCTGGGGCCAGGTACC  382

Query  622  TCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCggggggATCCCCGG  681
            ||||||||||||| ||||||||||| |||||||||| |||||||||||||||||||||||
Sbjct  381  TCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGACCAAACCCGGGGGGATCCCCGG  322

Query  682  TTTCCTTTTATTTTATCAATGCTACAATGGAGACAATTAAAAGTATTGCAGATATGGCGA  741
            |||||||||||||||||||||| || |||||||||||||| |||||||||||||||||||
Sbjct  321  TTTCCTTTTATTTTATCAATGCCACTATGGAGACAATTAAGAGTATTGCAGATATGGCGA  262

Query  742  CCGGAGTGGTC  752
            |||||||||||
Sbjct  261  CCGGAGTGGTC  251


>SRR2298573.278399 278399 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 254/264 (96%), Gaps = 1/264 (0%)
 Strand=Plus/Minus

Query  327  CTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCT  386
            ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  499  CTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCT  440

Query  387  GCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAG  446
            | ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Sbjct  439  GTAAAGCATCCTATTGCCAGCGGAACAACCCCTGGTAACAGGTGCCTCTGGGGCCAAAAG  380

Query  447  CCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTT  506
            ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  379  CCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTT  320

Query  507  AGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCA  566
            ||||||| |||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  319  AGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCA  260

Query  567  GAAGGTACCCA-TAGGTAACAAGT  589
            ||||||||||  ||||||  ||||
Sbjct  259  GAAGGTACCCGGTAGGTACTAAGT  236
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 Score = 414 bits (224),  Expect = 2e-111
 Identities = 236/242 (98%), Gaps = 0/242 (0%)
 Strand=Plus/Plus

Query  276  TCTACTAGTGAGATACCACGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGT  335
            |||| ||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  9    TCTATTAGTGAGATACCATGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGT  68

Query  336  TTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCAT  395
            |||||||||||||||||||||||||||||||||||||| ||||||||||||| |||||||
Sbjct  69   TTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCAT  128

Query  396  CCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCT  455
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  129  CCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTT  188

Query  456  AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGC  515
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  189  AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTAC  248

Query  516  CG  517
            ||
Sbjct  249  CG  250


>SRR2298573.240500 240500 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  374  GCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCT  433
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  250  GCAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCT  309

Query  434  CTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTT  493
            |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct  310  CTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTT  369

Query  494  GTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCA  553
            |||||||||||||||||||| |||||||||||||| ||||||||||||||||||||||||
Sbjct  370  GTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCA  429

Query  554  CGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGC  613
            ||||||||||||||||||||||||||||||||||| |||||||||||||||| |||||||
Sbjct  430  CGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGACCTGGGGC  489

Query  614  CAGGTACCTCT  624
            |||||||||||
Sbjct  490  CAGGTACCTCT  500


 Score = 416 bits (225),  Expect = 6e-112
 Identities = 241/249 (97%), Gaps = 0/249 (0%)
 Strand=Plus/Minus
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Query  417  CCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGT  476
            |||||||| |||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct  249  CCTGGTAAAAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGT  190

Query  477  TCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAAC  536
            | ||||||||||||||||||||||||||||||||||| |||||||||||||| |||||||
Sbjct  189  TTTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTTCCGATCTGGTAGTAGTGCAAAC  130

Query  537  ACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTA  596
            |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  129  ACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTA  70

Query  597  TGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTG  656
            |||||||||||||||||||||||||||||||||||||| ||||||||||| |||||||||
Sbjct  69   TGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTG  10

Query  657  GGCCAAACC  665
            |||||||||
Sbjct  9    GGCCAAACC  1


>SRR2298573.235938 235938 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  377  ACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTG  436
            ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    ACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTG  60

Query  437  GGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTG  496
            ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTG  120

Query  497  GAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGA  556
             |||||||||||||||| |||||||||||||| |||||||||||||||||||||||||||
Sbjct  121  AAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGA  180

Query  557  AGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAG  616
            |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Sbjct  181  AGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAG  240

Query  617  GTACCTCTATC  627
            |||||||||||
Sbjct  241  GTACCTCTATC  251


 Score = 379 bits (205),  Expect = 7e-101
 Identities = 233/247 (94%), Gaps = 0/247 (0%)
 Strand=Plus/Minus

Query  426  AGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCT  485
            ||| ||| | |||||||||||||||||  |||||||||| ||||||||||||||||||||
Sbjct  497  AGGGGCCCCGGGGGCCAAAAGCCAAGGGTTAACAAACCCGTTAGGATTGGTTCTAAACCT  438

Query  486  GAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGT  545
            ||||||||||| ||||| |||||||||| |||||||||||||| ||||||||||||||||
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Sbjct  437  GAGATGTTGTGAAAGATTCTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGT  378

Query  546  AAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGA  605
            ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct  377  AAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGA  318

Query  606  TCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACC  665
            |||||||||||||||||||| |||||||| ||||||||||| ||||||||||||||||||
Sbjct  317  TCTGGGGCCAGGTACCTCTAGCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACC  258

Query  666  Cgggggg  672
            |||||||
Sbjct  257  CGGGGGG  251


>SRR2298573.227970 227970 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 243/248 (98%), Gaps = 0/248 (0%)
 Strand=Plus/Minus

Query  384  GCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAA  443
            |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  498  GCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAA  439

Query  444  AAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATA  503
            |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  438  AAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATA  379

Query  504  CTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGC  563
            |||||||||| |||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  378  CTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGC  319

Query  564  CCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTC  623
            ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  318  CCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTC  259

Query  624  TATCTTGG  631
            ||||||||
Sbjct  258  TATCTTGG  251


 Score = 418 bits (226),  Expect = 2e-112
 Identities = 240/247 (97%), Gaps = 0/247 (0%)
 Strand=Plus/Plus

Query  385  CTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAA  444
            ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAA  60

Query  445  AGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATAC  504
            ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATAC  120

Query  505  TTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCC  564
            ||||||||| |||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  121  TTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCC  180
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Query  565  CAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCT  624
            |||||||||||||||||||||||| |||||||||||||||| ||||||||||| ||||||
Sbjct  181  CAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGAACTGGGGCCAGGAACCTCT  240

Query  625  ATCTTGG  631
            |||||||
Sbjct  241  ATCTTGG  247


>SRR2298573.171554 171554 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  304  CCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAA  363
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAA  60

Query  364  CTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTA  423
            ||||||| || ||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  61   CTTATTGAAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTA  120

Query  424  ACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAAC  483
            |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Sbjct  121  ACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAAC  180

Query  484  CTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTT  543
            |||||||||||||||||||||||||||||| |||||||||||||| ||||||||||||||
Sbjct  181  CTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTT  240

Query  544  GTAAGGCCCAC  554
            |||||||||||
Sbjct  241  GTAAGGCCCAC  251


 Score = 396 bits (214),  Expect = 7e-106
 Identities = 238/250 (95%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  541  GTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGA  600
            ||||||||||||  ||||| |||||||||||||||||||||||||||| ||| |||||||
Sbjct  500  GTTGTAAGGCCCCAGAAGGGTGCCCAGAAGGTACCCATAGGTAACAAGCGACCCTATGGA  441

Query  601  TCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCC  660
            |||||||||||||||||||||| ||||||||||| ||||||||||| |||||||||||||
Sbjct  440  TCTGATCTGGGGCCAGGTACCTTTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCC  381

Query  661  AAACCCgggggggATCCCCGGTTTCCTTTTATTTTATCAATGCTACAATGGAGACAATTA  720
            ||||||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Sbjct  380  AAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTATCAATGCCACTATGGAGACAATTA  321

Query  721  AAAGTATTGCAGATATGGCGACCGGAGTGGTCAGTTCAGTTGATTCCACTATCAATGCAG  780
            | ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  320  AGAGTATTGCAGATATGGCGACCGGAGTGGTCAGTTCAGTTGATTCCACTATCAATGTAG  261

Query  781  TTAATGAGAG  790
            ||||||||||
```

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Sbjct  260  TTAATGAGAG  251


>SRR2298573.169771 169771 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  438  GGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGG  497
            |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGG  60

Query  498  AAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAA  557
            |||||||||||||||| |||||||||||||| ||||||||||||||||||||||||||||
Sbjct  61   AAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAA  120

Query  558  GGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGG  617
            ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  121  GGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGG  180

Query  618  TACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCC  677
            ||||||||||||||||| ||||||||||| ||||||||||||||||||||||||||||||
Sbjct  181  TACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCC  240

Query  678  CCGGTTTCCTT  688
            |||||||||||
Sbjct  241  CCGGTTTCCTT  251


 Score = 418 bits (226),  Expect = 2e-112
 Identities = 242/250 (97%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  504  CTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGC  563
            |||||||||| |||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  500  CTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGC  441

Query  564  CCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTC  623
            ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  440  CCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTC  381

Query  624  TATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTT  683
            ||||||||||| ||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  380  TATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTT  321

Query  684  TCCTTTTATTTTATCAATGCTACAATGGAGACAATTAAAAGTATTGCAGATATGGCGACC  743
            |||||||||||||||||||| || ||||||||||||||| ||||||||||||||||||||
Sbjct  320  TCCTTTTATTTTATCAATGCCACTATGGAGACAATTAAGAGTATTGCAGATATGGCGACC  261

Query  744  GGAGTGGTCA  753
            ||||||||||
Sbjct  260  GGAGTGGTCA  251


>SRR2298573.140309 140309 length=500
Length=500
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 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  428  GTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGA  487
            |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  1    GTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGA  60

Query  488  GATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAA  547
            |||||||||||||||||||||||||| |||||||||||||| ||||||||||||||||||
Sbjct  61   GATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAA  120

Query  548  GGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATC  607
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  121  GGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATC  180

Query  608  TGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCg  667
            ||||||||||||||||||||||||||| ||||||||||| ||||||||||||||||||||
Sbjct  181  TGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCG  240

Query  668  ggggggATCCC  678
            |||||||||||
Sbjct  241  GGGGGGATCCC  251


 Score = 401 bits (217),  Expect = 2e-107
 Identities = 239/250 (96%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  483  CCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGT  542
            |||| || ||||||||||||||||||||||| | |||||||||||| |||||||||||||
Sbjct  500  CCTGGGAGGTTGTGGAAGATACTTAGTACCTACAGATCTGGTAGTAGTGCAAACACTAGT  441

Query  543  TGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATC  602
            |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Sbjct  440  TGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATC  381

Query  603  TGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAA  662
            |||||||||||||||||||||||||||||||| ||||||||||| |||||||||||||||
Sbjct  380  TGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAA  321

Query  663  ACCCgggggggATCCCCGGTTTCCTTTTATTTTATCAATGCTACAATGGAGACAATTAAA  722
            ||||||||||||||||||||||||||||||||||||||||| || ||||||||||||||
Sbjct  320  ACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTATCAATGCCACTATGGAGACAATTAAG  261

Query  723  AGTATTGCAG  732
            ||||||||||
Sbjct  260  AGTATTGCAG  251


>SRR2298573.137408 137408 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  285  GAGATACCACGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGAC  344
            ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  1    GAGATACCATGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGAC  60

Query  345  GTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCC  404
            ||||||||||||||||||||||||||||| ||||||||||||| ||||||||||||||||
Sbjct  61   GTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCC  120

Query  405  AGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCC  464
            ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  121  AGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCC  180

Query  465  TTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGT  524
            ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  181  TTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGT  240

Query  525  AGTACTGCAAA  535
            |||| ||||||
Sbjct  241  AGTAGTGCAAA  251


 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  380  TTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGG  439
            |||||||| |||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  499  TTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCGGGGG  440

Query  440  CCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAA  499
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  439  CCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAA  380

Query  500  GATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGG  559
            |||||||||||||| |||||||||||||| ||||||||||||||||||||||||||||||
Sbjct  379  GATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGG  320

Query  560  ATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTA  619
            ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Sbjct  319  ATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTA  260

Query  620  CCTCTATCTT  629
            ||||||||||
Sbjct  259  CCTCTATCTT  250


>SRR2298573.125219 125219 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 243/248 (98%), Gaps = 0/248 (0%)
 Strand=Plus/Plus

Query  456  AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGC  515
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  1    AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTAC  60

Query  516  CGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACC  575
            ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACC  120
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Query  576  CATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGAC  635
            ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  121  CATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGAT  180

Query  636  CTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTTT  695
            ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTT  240

Query  696  ATCAATGC  703
            ||||||||
Sbjct  241  ATCAATGC  248


 Score = 412 bits (223),  Expect = 7e-111
 Identities = 241/250 (96%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  476  TTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAA  535
            |||||||||||||||||||||||||||||||||| ||| |||||||||||||| ||||||
Sbjct  500  TTCTAAACCTGAGATGTTGTGGAAGATACTTAGTCCCTACCGATCTGGTAGTAGTGCAAA  441

Query  536  CACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACT  595
            ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  440  CACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACT  381

Query  596  ATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGT  655
            ||||||||||||||||||||||||||||||||||||||| ||||||||||| ||||||||
Sbjct  380  ATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGT  321

Query  656  GGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTTTATCAATGCTACAATGGAGAC  715
            |||||||||||||||||||||||||||||||||||||||||||||||| || ||||||||
Sbjct  320  GGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTATCAATGCCACTATGGAGAC  261

Query  716  AATTAAAAGT  725
            |||||| |||
Sbjct  260  AATTAAGAGT  251


>SRR2298573.38478 38478 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  450  AGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGT  509
            |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  250  AGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGT  309

Query  510  ACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAA  569
            |||| |||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  310  ACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAA  369

Query  570  GGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTT  629
            ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  370  GGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTT  429

Query  630  GGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTT  689
            ||||| ||||||||||| ||||||||||||||||||||||||||||||||||||||||||
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Sbjct  430   GGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTT  489

Query  690   TATTTTATCAA  700
             |||||||||||
Sbjct  490   TATTTTATCAA  500


 Score = 403 bits (218),  Expect = 4e-108
 Identities = 236/245 (96%), Gaps = 0/245 (0%)
 Strand=Plus/Minus

Query  530   TGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGT  589
             ||||||| || |||| |||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  245   TGCAAACCCTGGTTGGAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGC  186

Query  590   GACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCG  649
             ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||| ||
Sbjct  185   GACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACG  126

Query  650   TCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTTTATCAATGCTACAAT  709
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| || ||
Sbjct  125   TCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTATCAATGCCACTAT  66

Query  710   GGAGACAATTAAAAGTATTGCAGATATGGCGACCGGAGTGGTCAGTTCAGTTGATTCCAC  769
             |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  65    GGAGACAATTAAGAGTATTGCAGATATGGCGACCGGAGTGGTCAGTTCAGTTGATTCCAC  6

Query  770   TATCA  774
             |||||
Sbjct  5     TATCA  1


>SRR2298573.11925 11925 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 246/252 (98%), Gaps = 1/252 (0%)
 Strand=Plus/Plus

Query  450   AGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGT  509
             |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     AGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGT  60

Query  510   ACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAA  569
             |||| |||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  61    ACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAA  120

Query  570   GGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTT  629
             ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  121   GGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTT  180

Query  630   GGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTT  689
             ||||| ||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   GGTGATCTGGTTAAAAA-CGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTT  239

Query  690   TATTTTATCAAT  701
             ||||||||||||
Sbjct  240   TATTTTATCAAT  251
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 Score = 316 bits (171),  Expect = 6e-82
 Identities = 227/254 (89%), Gaps = 3/254 (1%)
 Strand=Plus/Minus

Query  564  CCAGAAGGTACCCATAGGTAACAAG-TGACACTATGGATCTGATCTGGGGCCAGGTACCT  622
            ||||||||   ||||  ||||||||  | |  ||| ||||||   ||||| ||||| |||
Sbjct  499  CCAGAAGGGCACCATGAGTAACAAGCCGCCCTTAT-GATCTGGGTTGGGGTCAGGTTCCT  441

Query  623  CTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGT  682
             ||||||||||| ||||||||||| ||| |||||||||||||||||||||||||||||||
Sbjct  440  TTATCTTGGTGATCTGGTTAAAAA-CGTTTAGTGGGCCAAACCCGGGGGGGATCCCCGGT  382

Query  683  TTCCTTTTATTTTATCAATGCTACAATGGAGACAATTAAAAGTATTGCAGATATGGCGAC  742
            ||||||||||||||||||||| || |||||||||||||| ||||||||||||||||||||
Sbjct  381  TTCCTTTTATTTTATCAATGCCACTATGGAGACAATTAAGAGTATTGCAGATATGGCGAC  322

Query  743  CGGAGTGGTCAGTTCAGTTGATTCCACTATCAATGCAGTTAATGAGAGAGTAGAAAATGT  802
            ||||||||||||||||||||||||||||||||||| ||||||||||||||| ||||||||
Sbjct  321  CGGAGTGGTCAGTTCAGTTGATTCCACTATCAATGTAGTTAATGAGAGAGTGGAAAATGT  262

Query  803  GGGCAATGAAATTG  816
             || ||||||||||
Sbjct  261  AGGTAATGAAATTG  248


>SRR2298546.866875 866875 length=501
Length=501

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  1276  AACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCATTTACCAATTTACCACATG  1335
             |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  501   AACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCGTTTACCAATTTACCACATG  442

Query  1336  TATTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACA  1395
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  441   TGTTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACA  382

Query  1396  CAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACAC  1455
             |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  381   CAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACAC  322

Query  1456  CTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGATGTAACCATATTGGGTAGTTTAT  1515
             ||||||| ||||||||||||||||| |||||||||||||| |||||||||||||||||||
Sbjct  321   CTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGATGTTACCATATTGGGTAGTTTAT  262

Query  1516  TGCAATTGGAC  1526
             |||||||||||
Sbjct  261   TGCAATTGGAC  251


 Score = 429 bits (232),  Expect = 7e-116
 Identities = 242/247 (98%), Gaps = 0/247 (0%)
 Strand=Plus/Plus

Query  1249  GTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAAT  1308
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1      GTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAAT  60

Query  1309   TTGGAGCATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTG  1368
              ||||||| |||||||||||||||||||| |||||||||||||||||||||||||||||||
Sbjct  61     TTGGAGCGTTTACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTG  120

Query  1369   ATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAG  1428
              ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct  121    ATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAG  180

Query  1429   GGCAACTAAAAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAG  1488
              |||||||||||||||||||||||||||||||||| ||||||||||||||||| |||||||
Sbjct  181    GGCAACTAAAAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAG  240

Query  1489   TTGATGT  1495
              |||||||
Sbjct  241    TTGATGT  247


>SRR2298546.783224 783224 length=502
Length=502

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  1259   GGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCATT  1318
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  252    GGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCGTT  311

Query  1319   TACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTAT  1378
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  312    TACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTAT  371

Query  1379   CCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACTAAA  1438
              ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  372    CCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAACTAAA  431

Query  1439   AGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGATGTAAC  1498
              |||||||||||||||||||||||| ||||||||||||||||| |||||||||||||| ||
Sbjct  432    AGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGATGTTAC  491

Query  1499   CATATTGGGTA  1509
              |||||||||||
Sbjct  492    CATATTGGGTA  502


 Score = 409 bits (221),  Expect = 9e-110
 Identities = 241/251 (96%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  1319   TACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTAT  1378
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  251    TACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTAT  192

Query  1379   CCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACTAAA  1438
              ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  191    CCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAACTAAA  132
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Query  1439  AGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGATGTAAC  1498
             |||||||||||||||||||||||| ||||||||||||||||| |||||||||||||| ||
Sbjct  131   AGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGATGTTAC  72

Query  1499  CATATTGGGTAGTTTATTGCAATTGGACTTCCAAAATCCTAGGGTGTTTGGCCAAGACGT  1558
             |||||||||||| |||||||||||||||||||||||||||||||| || || ||||||||
Sbjct  71    CATATTGGGTAGCTTATTGCAATTGGACTTCCAAAATCCTAGGGTATTCGGTCAAGACGT  12

Query  1559  TGGTATCTATG  1569
             |||||| ||||
Sbjct  11    TGGTATTTATG  1


>SRR2298546.762882 762882 length=502
Length=502

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  1258  TGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCAT  1317
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  502   TGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCGT  443

Query  1318  TTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTA  1377
             ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  442   TTACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTA  383

Query  1378  TCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACTAA  1437
             |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  382   TCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAACTAA  323

Query  1438  AAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGATGTAA  1497
             ||||||||||||||||||||||||| ||||||||||||||||| |||||||||||||| |
Sbjct  322   AAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGATGTTA  263

Query  1498  CCATATTGGGT  1508
             |||||||||||
Sbjct  262   CCATATTGGGT  252


 Score = 422 bits (228),  Expect = 1e-113
 Identities = 242/249 (97%), Gaps = 0/249 (0%)
 Strand=Plus/Plus

Query  1218  GTGCAAGTGAATGTTAACCAAGGAACAGCTGGTAGTGCATTGGTGGTGTATGAACCCAAA  1277
             || |||||||||||||| ||||||||||| ||||||||||||||||||||||||||||||
Sbjct  3     GTACAAGTGAATGTTAATCAAGGAACAGCCGGTAGTGCATTGGTGGTGTATGAACCCAAA  62

Query  1278  CCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCATTTACCAATTTACCACATGTA  1337
             |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  63    CCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCGTTTACCAATTTACCACATGTG  122

Query  1338  TTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACA  1397
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  123   TTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACA  182

Query  1398  AACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCT  1457
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             |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  183   AACTATGTTAAAACAGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCT  242

Query  1458  TTATCTATA  1466
             ||||| |||
Sbjct  243   TTATCCATA  251


>SRR2298546.676879 676879 length=502
Length=502

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 247/254 (97%), Gaps = 0/254 (0%)
 Strand=Plus/Plus

Query  1291  ATGACTCAAAGTTAGAATTTGGAGCATTTACCAATTTACCACATGTATTGATGAATTTGG  1350
             ||||||||||||||||||||||||| |||||||||||||||||||| |||||||||||||
Sbjct  1     ATGACTCAAAGTTAGAATTTGGAGCGTTTACCAATTTACCACATGTGTTGATGAATTTGG  60

Query  1351  CTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAA  1410
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    CTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAA  120

Query  1411  CGGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCTATACCTT  1470
             | |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  121   CAGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCCATACCTT  180

Query  1471  CAGGTTCTGCGACACAAGTTGATGTAACCATATTGGGTAGTTTATTGCAATTGGACTTCC  1530
             |||||||||| |||||||||||||| |||||||||||||| |||||||||||||||||||
Sbjct  181   CAGGTTCTGCTACACAAGTTGATGTTACCATATTGGGTAGCTTATTGCAATTGGACTTCC  240

Query  1531  AAAATCCTAGGGTG  1544
             ||||||||||||||
Sbjct  241   AAAATCCTAGGGTG  254


 Score = 387 bits (209),  Expect = 4e-103
 Identities = 237/251 (94%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  1371  TTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGG  1430
             |||||||||||||||||||||||||||| |||||||||||| ||||||||||||||||||
Sbjct  502   TTATGTATCCCCTATGTTGCTGACACAATCTATGTTAAAACAGATTCGTCAGACTTAGGG  443

Query  1431  CAACTAAAAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTT  1490
             |||||||||||||||||||||||||||||||| ||||||||||||||||| |||||||||
Sbjct  442   CAACTAAAAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTT  383

Query  1491  GATGTAACCATATTGGGTAGTTTATTGCAATTGGACTTCCAAAATCCTAGGGTGTTTGGC  1550
             ||||| |||||||||||||| |||||||||||||||||||||||||||||||| || || 
Sbjct  382   GATGTTACCATATTGGGTAGCTTATTGCAATTGGACTTCCAAAATCCTAGGGTATTCGGT  323

Query  1551  CAAGACGTTGGTATCTATGATAATGCACCAACGCGGAAACAAAATCTTAAAAAGATTCTT  1610
             |||||||||||||| ||||| ||||||||||||||||| ||||||||||| || ||||||
Sbjct  322   CAAGACGTTGGTATTTATGACAATGCACCAACGCGGAAGCAAAATCTTAAGAAAATTCTT  263

Query  1611  ACAATGAGCAC  1621
             |||||||||||
Sbjct  262   ACAATGAGCAC  252
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>SRR2298546.661134 661134 length=501
Length=501

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  1249  GTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAAT  1308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAAT  60

Query  1309  TTGGAGCATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTG  1368
              ||||||| |||||||||||||||||||| |||||||||||||||||||||||||||||||
Sbjct  61    TTGGAGCGTTTACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTG  120

Query  1369  ATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAG  1428
              ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct  121   ATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAG  180

Query  1429  GGCAACTAAAAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAG  1488
              |||||||||||||||||||||||||||||||||| ||||||||||||||||| |||||||
Sbjct  181   GGCAACTAAAAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAG  240

Query  1489  TTGATGTAACC  1499
              ||||||| |||
Sbjct  241   TTGATGTTACC  251


 Score = 425 bits (230),  Expect = 9e-115
 Identities = 244/251 (97%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  1292  TGACTCAAAGTTAGAATTTGGAGCATTTACCAATTTACCACATGTATTGATGAATTTGGC  1351
              |||||||||||||||||||||||| |||||||||||||||||||| ||||||||||||||
Sbjct  501   TGACTCAAAGTTAGAATTTGGAGCGTTTACCAATTTACCACATGTGTTGATGAATTTGGC  442

Query  1352  TGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAAC  1411
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  441   TGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAAC  382

Query  1412  GGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCTATACCTTC  1471
               |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  381   AGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCCATACCTTC  322

Query  1472  AGGTTCTGCGACACAAGTTGATGTAACCATATTGGGTAGTTTATTGCAATTGGACTTCCA  1531
              ||||||||| |||||||||||||| ||||||||||||| |||||||||||||||||||||
Sbjct  321   AGGTTCTGCTACACAAGTTGATGTTACCATATTGGGTAGCTTATTGCAATTGGACTTCCA  262

Query  1532  AAATCCTAGGG  1542
              |||||||||||
Sbjct  261   AAATCCTAGGG  251


>SRR2298546.580465 580465 length=501
Length=501

 Score = 431 bits (233),  Expect = 2e-116
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 Identities = 243/248 (98%), Gaps = 0/248 (0%)
 Strand=Plus/Plus

Query  1248  GGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAA  1307
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  251   GGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAA  310

Query  1308  TTTGGAGCATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCT  1367
             |||||||| |||||||||||||||||||| ||||||||||||||||||||||||||||||
Sbjct  311   TTTGGAGCGTTTACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCT  370

Query  1368  GATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTA  1427
             |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Sbjct  371   GATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTA  430

Query  1428  GGGCAACTAAAAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAA  1487
             |||||||||||||||||||||||||||||||||| |||||||||||||||||| ||||||
Sbjct  431   GGGCAACTAAAAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAA  490

Query  1488  GTTGATGT  1495
             ||||||||
Sbjct  491   GTTGATGT  498


 Score = 403 bits (218),  Expect = 4e-108
 Identities = 240/251 (96%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  1329  CCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTT  1388
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  251   CCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTT  192

Query  1389  GCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTT  1448
             ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  191   GCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTT  132

Query  1449  TGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGATGTAACCATATTGGGT  1508
             |||||||||||||| ||||||||||||||||| |||||||||||||| ||||||||||||
Sbjct  131   TGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGATGTTACCATATTGGGT  72

Query  1509  AGTTTATTGCAATTGGACTTCCAAAATCCTAGGGTGTTTGGCCAAGACGTTGGTATCTAT  1568
             || |||||||||||||||||||||||||||||||| || || |||||||||||||| |||
Sbjct  71    AGCTTATTGCAATTGGACTTCCAAAATCCTAGGGTATTCGGTCAAGACGTTGGTATTTAT  12

Query  1569  GATAATGCACC  1579
             || ||||||||
Sbjct  11    GACAATGCACC  1


>SRR2298546.555649 555649 length=502
Length=502

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  1254  GCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGA  1313
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGA  60
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Query  1314  GCATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTTA  1373
             || |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  61    GCGTTTACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATTTA  120

Query  1374  TGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAA  1433
             |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Sbjct  121   TGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAA  180

Query  1434  CTAAAAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGAT  1493
             ||||||||||||||||||||||||||||| ||||||||||||||||| ||||||||||||
Sbjct  181   CTAAAAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGAT  240

Query  1494  GTAACCATATT  1504
             || ||||||||
Sbjct  241   GTTACCATATT  251


 Score = 387 bits (209),  Expect = 4e-103
 Identities = 238/252 (94%), Gaps = 1/252 (0%)
 Strand=Plus/Minus

Query  1382  CTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACTAAAAGT  1441
             |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Sbjct  502   CTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAACTAAAAGT  443

Query  1442  CTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGATGTAACCAT  1501
             ||||||||||||||||||||| ||||||||||||||||| |||||||||||||| |||||
Sbjct  442   CTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGATGTTACCAT  383

Query  1502  ATTGGGTAGTTTATTGCAATTGGACTTCCAAAATCCTAGGGTGTTTGGCCAAGACGTTGG  1561
             ||||||||| |||||||||||||||||||||||||||||||| || || |||||||||||
Sbjct  382   ATTGGGTAGCTTATTGCAATTGGACTTCCAAAATCCTAGGGTATTCGGTCAAGACGTTGG  323

Query  1562  TATCTATGATAATGCACCAACGCGGAAACAAAATCTTAAAAAGATTCTTACAATGAGCAC  1621
             ||| ||||| ||||||||||||||||| ||||||||||| || |||||||||||||||||
Sbjct  322   TATTTATGACAATGCACCAACGCGGAAGCAAAATCTTAAGAAAATTCTTACAATGAGCAC  263

Query  1622  TAAATACAAGTG  1633
             ||| ||||||||
Sbjct  262   TAA-TACAAGTG  252


>SRR2298546.529810 529810 length=502
Length=502

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  1257  TTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCA  1316
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     TTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCG  60

Query  1317  TTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGT  1376
             |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct  61    TTTACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGT  120

Query  1377  ATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACTA  1436
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             ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  121   ATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAACTA  180

Query  1437  AAAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGATGTA  1496
             |||||||||||||||||||||||||| ||||||||||||||||| ||||||||||||||
Sbjct  181   AAAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGATGTT  240

Query  1497  ACCATATTGGG  1507
             |||||||||||
Sbjct  241   ACCATATTGGG  251


 Score = 425 bits (230),  Expect = 9e-115
 Identities = 244/251 (97%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  1292  TGACTCAAAGTTAGAATTTGGAGCATTTACCAATTTACCACATGTATTGATGAATTTGGC  1351
             |||||||||||||||||||||||| |||||||||||||||||||| ||||||||||||||
Sbjct  502   TGACTCAAAGTTAGAATTTGGAGCGTTTACCAATTTACCACATGTGTTGATGAATTTGGC  443

Query  1352  TGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAAC  1411
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  442   TGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAAC  383

Query  1412  GGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCTATACCTTC  1471
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  382   AGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCCATACCTTC  323

Query  1472  AGGTTCTGCGACACAAGTTGATGTAACCATATTGGGTAGTTTATTGCAATTGGACTTCCA  1531
             ||||||||| |||||||||||||| |||||||||||||| ||||||||||||||||||||
Sbjct  322   AGGTTCTGCTACACAAGTTGATGTTACCATATTGGGTAGCTTATTGCAATTGGACTTCCA  263

Query  1532  AAATCCTAGGG  1542
             |||||||||||
Sbjct  262   AAATCCTAGGG  252


>SRR2298546.521679 521679 length=502
Length=502

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  1254  GCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGA  1313
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  252   GCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGA  311

Query  1314  GCATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTTA  1373
             || |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  312   GCGTTTACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATTTA  371

Query  1374  TGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAA  1433
             |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Sbjct  372   TGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAA  431

Query  1434  CTAAAAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGAT  1493
             ||||||||||||||||||||||||||||| ||||||||||||||||| ||||||||||||
Sbjct  432   CTAAAAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGAT  491
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Query  1494  GTAACCATATT  1504
             || ||||||||
Sbjct  492   GTTACCATATT  502


 Score = 403 bits (218),  Expect = 4e-108
 Identities = 240/251 (96%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  1329  CCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTT  1388
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  251   CCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTT  192

Query  1389  GCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTT  1448
             ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  191   GCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTT  132

Query  1449  TGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGATGTAACCATATTGGGT  1508
             |||||||||||||| ||||||||||||||||| |||||||||||||| ||||||||||||
Sbjct  131   TGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGATGTTACCATATTGGGT  72

Query  1509  AGTTTATTGCAATTGGACTTCCAAAATCCTAGGGTGTTTGGCCAAGACGTTGGTATCTAT  1568
             || |||||||||||||||||||||||||||||||| || || |||||||||||||| |||
Sbjct  71    AGCTTATTGCAATTGGACTTCCAAAATCCTAGGGTATTCGGTCAAGACGTTGGTATTTAT  12

Query  1569  GATAATGCACC  1579
             || ||||||||
Sbjct  11    GACAATGCACC  1


>SRR2298546.519576 519576 length=502
Length=502

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  1258  TGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCAT  1317
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  502   TGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCGT  443

Query  1318  TTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTA  1377
             ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  442   TTACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTA  383

Query  1378  TCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACTAA  1437
             |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  382   TCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAACTAA  323

Query  1438  AAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGATGTAA  1497
             ||||||||||||||||||||||||| ||||||||||||||||| |||||||||||||| |
Sbjct  322   AAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGATGTTA  263

Query  1498  CCATATTGGGT  1508
             |||||||||||
Sbjct  262   CCATATTGGGT  252
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 Score = 407 bits (220),  Expect = 3e-109
 Identities = 230/235 (98%), Gaps = 0/235 (0%)
 Strand=Plus/Plus

Query  1258  TGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCAT  1317
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  17    TGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCGT  76

Query  1318  TTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTA  1377
             ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  77    TTACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTA  136

Query  1378  TCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACTAA  1437
             |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  137   TCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAACTAA  196

Query  1438  AAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGA  1492
             ||||||||||||||||||||||||| ||||||||||||||||| |||||||||||
Sbjct  197   AAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGA  251


>SRR2298546.505689 505689 length=502
Length=502

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  1259  GGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCATT  1318
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  252   GGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCGTT  311

Query  1319  TACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTAT  1378
             |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  312   TACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTAT  371

Query  1379  CCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACTAAA  1438
             ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  372   CCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAACTAAA  431

Query  1439  AGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGATGTAAC  1498
             |||||||||||||||||||||||| ||||||||||||||||| |||||||||||||| ||
Sbjct  432   AGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGATGTTAC  491

Query  1499  CATATTGGGTA  1509
             |||||||||||
Sbjct  492   CATATTGGGTA  502


 Score = 398 bits (215),  Expect = 2e-106
 Identities = 239/251 (95%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  1508  TAGTTTATTGCAATTGGACTTCCAAAATCCTAGGGTGTTTGGCCAAGACGTTGGTATCTA  1567
             ||| |||||||||||||||||||||||||||||||| || || |||||||||||||| ||
Sbjct  251   TAGCTTATTGCAATTGGACTTCCAAAATCCTAGGGTATTCGGTCAAGACGTTGGTATTTA  192

Query  1568  TGATAATGCACCAACGCGGAAACAAAATCTTAAAAAGATTCTTACAATGAGCACTAAATA  1627
             ||| ||||||||||||||||| ||||||||||| || |||||||||||||||||||||||
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Sbjct  191   TGACAATGCACCAACGCGGAAGCAAAATCTTAAGAAAATTCTTACAATGAGCACTAAATA  132

Query  1628  CAAGTGGACTAGGGGAAAAATTGACATTGCAGAAGGGCCAGGTTCTATGAACATGGCGAA  1687
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  131   CAAGTGGACTAGGGGAAAAATTGACATTGCAGAAGGGCCAGGTTCTATGAACATGGCGAA  72

Query  1688  CGTATTGAGTACCACTGCAGCGCAATCAATTGCTTTGGTTGGAGAAAGAGCATTCTATGA  1747
             |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  71    CGTATTGAGTACCACTGCAGCGCAATCAATTGCTTTGGTTGGAGAAAGGGCATTCTATGA  12

Query  1748  TCCAAGAACAG  1758
              ||||| ||||
Sbjct  11    CCCAAGGACAG  1




>SRR2298546.478474 478474 length=501
Length=501

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  1252  GTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTG  1311
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTG  60

Query  1312  GAGCATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATT  1371
             |||| |||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  61    GAGCGTTTACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATT  120

Query  1372  TATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGC  1431
             |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  121   TATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGC  180

Query  1432  AACTAAAAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTG  1491
             ||||||||||||||||||||||||||||||| ||||||||||||||||| ||||||||||
Sbjct  181   AACTAAAAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTG  240

Query  1492  ATGTAACCATA  1502
             |||| ||||||
Sbjct  241   ATGTTACCATA  251



 Score = 390 bits (211),  Expect = 3e-104
 Identities = 237/250 (95%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  1393  ACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGA  1452
             ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  501   ACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGA  442

Query  1453  CACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGATGTAACCATATTGGGTAGTT  1512
             |||||||||| ||||||||||||||||| |||||||||||||| |||||||||||||| |
Sbjct  441   CACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGATGTTACCATATTGGGTAGCT  382

Query  1513  TATTGCAATTGGACTTCCAAAATCCTAGGGTGTTTGGCCAAGACGTTGGTATCTATGATA  1572
             ||||||||||||||||||||||||||||||| || || |||||||||||||| ||||| |
Sbjct  381   TATTGCAATTGGACTTCCAAAATCCTAGGGTATTCGGTCAAGACGTTGGTATTTATGACA  322
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Query  1573  ATGCACCAACGCGGAAACAAAATCTTAAAAAGATTCTTACAATGAGCACTAAATACAAGT  1632
             |||||||||||||||| ||||||||||| || ||||||||||||||||||||||||||||
Sbjct  321   ATGCACCAACGCGGAAGCAAAATCTTAAGAAAATTCTTACAATGAGCACTAAATACAAGT  262

Query  1633  GGACTAGGGG  1642
             ||||||||||
Sbjct  261   GGACTAGGGG  252


>SRR2298546.429699 429699 length=502
Length=502

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  1223  AGTGAATGTTAACCAAGGAACAGCTGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGT  1282
             |||||||||||| ||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  252   AGTGAATGTTAATCAAGGAACAGCCGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGT  311

Query  1283  TGTGACATATGACTCAAAGTTAGAATTTGGAGCATTTACCAATTTACCACATGTATTGAT  1342
             ||||||||||||||||||||||||||||||||| |||||||||||||||||||| |||||
Sbjct  312   TGTGACATATGACTCAAAGTTAGAATTTGGAGCGTTTACCAATTTACCACATGTGTTGAT  371

Query  1343  GAATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTA  1402
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  372   GAATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTA  431

Query  1403  TGTTAAAACGGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATC  1462
             ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  432   TGTTAAAACAGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATC  491

Query  1463  TATACCTTCAG  1473
              ||||||||||
Sbjct  492   CATACCTTCAG  502


 Score = 414 bits (224),  Expect = 2e-111
 Identities = 243/252 (96%), Gaps = 1/252 (0%)
 Strand=Plus/Minus

Query  1601  AAAGATTCTTACAATGAGCACTAAATACAAGTGGACTAGGGGAAAAATTGACATTGCAGA  1660
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  251   AAA-ATTCTTACAATGAGCACTAAATACAAGTGGACTAGGGGAAAAATTGACATTGCAGA  193

Query  1661  AGGGCCAGGTTCTATGAACATGGCGAACGTATTGAGTACCACTGCAGCGCAATCAATTGC  1720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  192   AGGGCCAGGTTCTATGAACATGGCGAACGTATTGAGTACCACTGCAGCGCAATCAATTGC  133

Query  1721  TTTGGTTGGAGAAAGAGCATTCTATGATCCAAGAACAGCAGGAAGCAAGAGTAGGTTTGA  1780
             ||||||||||||||| ||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  132   TTTGGTTGGAGAAAGGGCATTCTATGACCCAAGAACAGCAGGAAGCAAGAGTAGGTTTGA  73

Query  1781  TGATTTAGTGAAAATATCCCAACTTTTTTCTGTGATGAGTGACTCCACAACTCCCTCAGC  1840
             ||||||||| |||||||| |||||||||||||| ||||||||||||||||| || |||||
Sbjct  72    TGATTTAGTAAAAATATCTCAACTTTTTTCTGTAATGAGTGACTCCACAACCCCTTCAGC  13

Query  1841  CAACCATGGTAT  1852
             ||||||||| ||
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Sbjct  12    CAACCATGGCAT  1


>SRR2298546.417769 417769 length=502
Length=502

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  1225  TGAATGTTAACCAAGGAACAGCTGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTG  1284
             |||||||||| ||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  251   TGAATGTTAATCAAGGAACAGCCGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTG  192

Query  1285  TGACATATGACTCAAAGTTAGAATTTGGAGCATTTACCAATTTACCACATGTATTGATGA  1344
             |||||||||||||||||||||||||||||| ||||||||||||||||||||| |||||||
Sbjct  191   TGACATATGACTCAAAGTTAGAATTTGGAGCGTTTACCAATTTACCACATGTGTTGATGA  132

Query  1345  ATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATG  1404
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  131   ATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATG  72

Query  1405  TTAAAACGGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCTA  1464
             ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  71    TTAAAACAGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCCA  12

Query  1465  TACCTTCAGGT  1475
             |||||||||||
Sbjct  11    TACCTTCAGGT  1


 Score = 411 bits (222),  Expect = 3e-110
 Identities = 242/252 (96%), Gaps = 0/252 (0%)
 Strand=Plus/Plus

Query  1103  AGGACATCAGATAACCCATGTGGAATTGCCAAAAGTCTTTTGGGACAAAAACAGTAAGCC  1162
             ||||||||||||||||||||||||| | |||||||||||||||||||||||||| |||||
Sbjct  251   AGGACATCAGATAACCCATGTGGAACTACCAAAAGTCTTTTGGGACAAAAACAGCAAGCC  310

Query  1163  AGCCTATGGCCAATCAAGATACTTTGCAGCAGTACGGTGTGGCTTTCATTTTCAGGTGCA  1222
             |||||||||||||||||||||||||||||||||||||||||| ||||||||||| || ||
Sbjct  311   AGCCTATGGCCAATCAAGATACTTTGCAGCAGTACGGTGTGGTTTTCATTTTCAAGTACA  370

Query  1223  AGTGAATGTTAACCAAGGAACAGCTGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGT  1282
             |||||||||||| ||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  371   AGTGAATGTTAATCAAGGAACAGCCGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGT  430

Query  1283  TGTGACATATGACTCAAAGTTAGAATTTGGAGCATTTACCAATTTACCACATGTATTGAT  1342
             |||||||||||||||||||||||||||||||| ||||||||||||||||||||| |||||
Sbjct  431   TGTGACATATGACTCAAAGTTAGAATTTGGAGCGTTTACCAATTTACCACATGTGTTGAT  490

Query  1343  GAATTTGGCTGA  1354
             ||||||||||||
Sbjct  491   GAATTTGGCTGA  502


>SRR2298546.405018 405018 length=502
Length=502
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 Score = 431 bits (233),  Expect = 2e-116
 Identities = 243/248 (98%), Gaps = 0/248 (0%)
 Strand=Plus/Plus

Query  1248  GGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAA  1307
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  252   GGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAA  311

Query  1308  TTTGGAGCATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCT  1367
             |||||||| |||||||||||||||||||| ||||||||||||||||||||||||||||||
Sbjct  312   TTTGGAGCGTTTACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCT  371

Query  1368  GATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTA  1427
             |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Sbjct  372   GATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTA  431

Query  1428  GGGCAACTAAAAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAA  1487
             ||||||||||||||||||||||||||||||||||| ||||||||||||||||| ||||||
Sbjct  432   GGGCAACTAAAAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAA  491

Query  1488  GTTGATGT  1495
             ||||||||
Sbjct  492   GTTGATGT  499


 Score = 425 bits (230),  Expect = 9e-115
 Identities = 244/251 (97%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  1268  TGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCATTTACCAATTT  1327
             |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  251   TGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCGTTTACCAATTT  192

Query  1328  ACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGT  1387
             ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  191   ACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGT  132

Query  1388  TGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGT  1447
             |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  131   TGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGT  72

Query  1448  TTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGATGTAACCATATTGGG  1507
             ||||||||||||||| ||||||||||||||||| |||||||||||||| |||||||||||
Sbjct  71    TTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGATGTTACCATATTGGG  12

Query  1508  TAGTTTATTGC  1518
             ||| |||||||
Sbjct  11    TAGCTTATTGC  1


>SRR2298546.355837 355837 length=502
Length=502

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  1255  CATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAG  1314
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  1     CATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAG  60

Query  1315  CATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTTAT  1374
             | |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  61    CGTTTACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATTTAT  120

Query  1375  GTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAAC  1434
             ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct  121   GTATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAAC  180

Query  1435  TAAAAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGATG  1494
             |||||||||||||||||||||||||||| ||||||||||||||||| |||||||||||||
Sbjct  181   TAAAAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGATG  240

Query  1495  TAACCATATTG  1505
             | |||||||||
Sbjct  241   TTACCATATTG  251


 Score = 409 bits (221),  Expect = 9e-110
 Identities = 241/251 (96%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  1319  TACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTAT  1378
             |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  502   TACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTAT  443

Query  1379  CCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACTAAA  1438
             ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  442   CCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAACTAAA  383

Query  1439  AGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGATGTAAC  1498
             |||||||||||||||||||||||| ||||||||||||||||| |||||||||||||| ||
Sbjct  382   AGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGATGTTAC  323

Query  1499  CATATTGGGTAGTTTATTGCAATTGGACTTCCAAAATCCTAGGGTGTTTGGCCAAGACGT  1558
             |||||||||||| |||||||||||||||||||||||||||||||| || || ||||||||
Sbjct  322   CATATTGGGTAGCTTATTGCAATTGGACTTCCAAAATCCTAGGGTATTCGGTCAAGACGT  263

Query  1559  TGGTATCTATG  1569
             |||||| ||||
Sbjct  262   TGGTATTTATG  252


>SRR2298546.310301 310301 length=501
Length=501

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  1223  AGTGAATGTTAACCAAGGAACAGCTGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGT  1282
             |||||||||||| ||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  251   AGTGAATGTTAATCAAGGAACAGCCGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGT  310

Query  1283  TGTGACATATGACTCAAAGTTAGAATTTGGAGCATTTACCAATTTACCACATGTATTGAT  1342
             ||||||||||||||||||||||||||||||||| |||||||||||||||||||| |||||
Sbjct  311   TGTGACATATGACTCAAAGTTAGAATTTGGAGCGTTTACCAATTTACCACATGTGTTGAT  370
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Query  1343  GAATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTA  1402
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  371   GAATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTA  430

Query  1403  TGTTAAAACGGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATC  1462
             ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  431   TGTTAAAACAGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATC  490

Query  1463  TATACCTTCAG  1473
              ||||||||||
Sbjct  491   CATACCTTCAG  501


 Score = 407 bits (220),  Expect = 3e-109
 Identities = 240/250 (96%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  1312  GAGCATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATT  1371
             |||| |||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  250   GAGCGTTTACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATT  191

Query  1372  TATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGC  1431
             |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  190   TATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGC  131

Query  1432  AACTAAAAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTG  1491
             ||||||||||||||||||||||||||||||| ||||||||||||||||| ||||||||||
Sbjct  130   AACTAAAAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTG  71

Query  1492  ATGTAACCATATTGGGTAGTTTATTGCAATTGGACTTCCAAAATCCTAGGGTGTTTGGCC  1551
             |||| |||||||||||||| |||||||||||||||||||||||||||||||| || || |
Sbjct  70    ATGTTACCATATTGGGTAGCTTATTGCAATTGGACTTCCAAAATCCTAGGGTATTCGGTC  11

Query  1552  AAGACGTTGG  1561
             ||||||||||
Sbjct  10    AAGACGTTGG  1


>SRR2298546.275254 275254 length=502
Length=502

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  1252  GTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTG  1311
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  252   GTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTG  311

Query  1312  GAGCATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATT  1371
             |||| |||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  312   GAGCGTTTACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATT  371

Query  1372  TATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGC  1431
             |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  372   TATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGC  431

Query  1432  AACTAAAAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTG  1491
             ||||||||||||||||||||||||||||||| ||||||||||||||||| ||||||||||
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Sbjct  432   AACTAAAAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTG  491

Query  1492  ATGTAACCATA  1502
             |||| ||||||
Sbjct  492   ATGTTACCATA  502


 Score = 383 bits (207),  Expect = 6e-102
 Identities = 238/253 (94%), Gaps = 1/253 (0%)
 Strand=Plus/Minus

Query  1379  CCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACTAAA  1438
             ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  252   CCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAACTAAA  193

Query  1439  AGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGATGTAAC  1498
             |||||||||||||||||||||||| ||||||||||||||||| |||||||||||||| ||
Sbjct  192   AGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGATGTTAC  133

Query  1499  CATATTGGGTAGTTTATTGCAATTGGACTTCCAAAATCCTAGGGTGTTTGGCCAAGACGT  1558
             |||||||||||| ||||||||||||| |||||||||||||||||| || || ||||||||
Sbjct  132   CATATTGGGTAGCTTATTGCAATTGGGCTTCCAAAATCCTAGGGTATTCGGTCAAGACGT  73

Query  1559  TGGTATCTATGATAATGCACCAACGCGGAAACAAAATCTTAAAAAGATTCTTACAATGAG  1618
             ||| || ||||| ||||||||||||||||| ||||||||||| || ||||||||||||||
Sbjct  72    TGG-ATTTATGACAATGCACCAACGCGGAAGCAAAATCTTAAGAAAATTCTTACAATGAG  14

Query  1619  CACTAAATACAAG  1631
             |||||||||||||
Sbjct  13    CACTAAATACAAG  1


>SRR2298546.252499 252499 length=501
Length=501

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  1249  GTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAAT  1308
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAAT  60

Query  1309  TTGGAGCATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTG  1368
             ||||||| |||||||||||||||||||| |||||||||||||||||||||||||||||||
Sbjct  61    TTGGAGCGTTTACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTG  120

Query  1369  ATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAG  1428
             ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct  121   ATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAG  180

Query  1429  GGCAACTAAAAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAG  1488
             |||||||||||||||||||||||||||||||||| ||||||||||||||||| |||||||
Sbjct  181   GGCAACTAAAAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAG  240

Query  1489  TTGATGTAACC  1499
             ||||||| |||
Sbjct  241   TTGATGTTACC  251
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 Score = 425 bits (230),  Expect = 9e-115
 Identities = 244/251 (97%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  1292  TGACTCAAAGTTAGAATTTGGAGCATTTACCAATTTACCACATGTATTGATGAATTTGGC  1351
             |||||||||||||||||||||||| |||||||||||||||||||| ||||||||||||||
Sbjct  501   TGACTCAAAGTTAGAATTTGGAGCGTTTACCAATTTACCACATGTGTTGATGAATTTGGC  442

Query  1352  TGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAAC  1411
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  441   TGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAAC  382

Query  1412  GGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCTATACCTTC  1471
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  381   AGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCCATACCTTC  322

Query  1472  AGGTTCTGCGACACAAGTTGATGTAACCATATTGGGTAGTTTATTGCAATTGGACTTCCA  1531
             ||||||||| |||||||||||||| |||||||||||||| ||||||||||||||||||||
Sbjct  321   AGGTTCTGCTACACAAGTTGATGTTACCATATTGGGTAGCTTATTGCAATTGGACTTCCA  262

Query  1532  AAATCCTAGGG  1542
             |||||||||||
Sbjct  261   AAATCCTAGGG  251


>SRR2298546.193011 193011 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  1228  ATGTTAACCAAGGAACAGCTGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGA  1287
             ||||||| ||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  1     ATGTTAATCAAGGAACAGCCGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGA  60

Query  1288  CATATGACTCAAAGTTAGAATTTGGAGCATTTACCAATTTACCACATGTATTGATGAATT  1347
             |||||||||||||||||||||||||||| |||||||||||||||||||| ||||||||||
Sbjct  61    CATATGACTCAAAGTTAGAATTTGGAGCGTTTACCAATTTACCACATGTGTTGATGAATT  120

Query  1348  TGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTA  1407
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   TGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTA  180

Query  1408  AAACGGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCTATAC  1467
             |||| |||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  181   AAACAGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCCATAC  240

Query  1468  CTTCAGGTTCT  1478
             |||||||||||
Sbjct  241   CTTCAGGTTCT  251


 Score = 392 bits (212),  Expect = 9e-105
 Identities = 238/251 (95%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  1381  CCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACTAAAAG  1440
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             ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  500   CCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAACTAAAAG  441

Query  1441  TCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGATGTAACCA  1500
             |||||||||||||||||||||| ||||||||||||||||| |||||||||||||| ||||
Sbjct  440   TCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGATGTTACCA  381

Query  1501  TATTGGGTAGTTTATTGCAATTGGACTTCCAAAATCCTAGGGTGTTTGGCCAAGACGTTG  1560
             ||||||||||||||||||||||||||||||||||||||||||| || || ||||||||||
Sbjct  380   TATTGGGTAGTTTATTGCAATTGGACTTCCAAAATCCTAGGGTATTCGGTCAAGACGTTG  321

Query  1561  GTATCTATGATAATGCACCAACGCGGAAACAAAATCTTAAAAAGATTCTTACAATGAGCA  1620
             |||| ||||| ||||||||||||||||| ||||||||||| || ||||||||||||||||
Sbjct  320   GTATTTATGACAATGCACCAACGCGGAAGCAAAATCTTAAGAAAATTCTTACAATGAGCA  261

Query  1621  CTAAATACAAG  1631
             ||||| |||||
Sbjct  260   CTAAACACAAG  250


>SRR2298546.191934 191934 length=501
Length=501

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 243/248 (98%), Gaps = 0/248 (0%)
 Strand=Plus/Plus

Query  1248  GGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAA  1307
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAA  60

Query  1308  TTTGGAGCATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCT  1367
             |||||||| |||||||||||||||||||| ||||||||||||||||||||||||||||||
Sbjct  61    TTTGGAGCGTTTACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCT  120

Query  1368  GATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTA  1427
             |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Sbjct  121   GATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTA  180

Query  1428  GGGCAACTAAAAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAA  1487
             |||||||||||||||||||||||||||||||||| ||||||||||||||||| |||||||
Sbjct  181   GGGCAACTAAAAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAA  240

Query  1488  GTTGATGT  1495
             ||||||||
Sbjct  241   GTTGATGT  248


 Score = 401 bits (217),  Expect = 2e-107
 Identities = 239/250 (96%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  1465  TACCTTCAGGTTCTGCGACACAAGTTGATGTAACCATATTGGGTAGTTTATTGCAATTGG  1524
             |||||||||||||||| |||||||||||||| |||||||||||||| |||||||||||||
Sbjct  500   TACCTTCAGGTTCTGCTACACAAGTTGATGTTACCATATTGGGTAGCTTATTGCAATTGG  441

Query  1525  ACTTCCAAAATCCTAGGGTGTTTGGCCAAGACGTTGGTATCTATGATAATGCACCAACGC  1584
             ||||||||||||||||||| || || |||||||||||||| ||||| |||||||||||||
Sbjct  440   ACTTCCAAAATCCTAGGGTATTCGGTCAAGACGTTGGTATTTATGACAATGCACCAACGC  381
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Query  1585  GGAAACAAAATCTTAAAAAGATTCTTACAATGAGCACTAAATACAAGTGGACTAGGGGAA  1644
             |||| ||||||||||| || ||||||||||||||||||||||||||||||||||||||||
Sbjct  380   GGAAGCAAAATCTTAAGAAAATTCTTACAATGAGCACTAAATACAAGTGGACTAGGGGAA  321

Query  1645  AAATTGACATTGCAGAAGGGCCAGGTTCTATGAACATGGCGAACGTATTGAGTACCACTG  1704
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  320   AAATTGACATTGCAGAAGGGCCAGGTTCTATGAACATGGCGAACGTATTGAGTACCACTG  261

Query  1705  CAGCGCAATC  1714
             ||||||||||
Sbjct  260   CAGCGCAATC  251


>SRR2298546.179038 179038 length=501
Length=501

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  1230  GTTAACCAAGGAACAGCTGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACA  1289
             ||||| ||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  251   GTTAATCAAGGAACAGCCGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACA  192

Query  1290  TATGACTCAAAGTTAGAATTTGGAGCATTTACCAATTTACCACATGTATTGATGAATTTG  1349
             |||||||||||||||||||||||||| |||||||||||||||||||| ||||||||||||
Sbjct  191   TATGACTCAAAGTTAGAATTTGGAGCGTTTACCAATTTACCACATGTGTTGATGAATTTG  132

Query  1350  GCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAA  1409
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  131   GCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAA  72

Query  1410  ACGGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCTATACCT  1469
             || |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  71    ACAGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCCATACCT  12

Query  1470  TCAGGTTCTGC  1480
             |||||||||||
Sbjct  11    TCAGGTTCTGC  1


 Score = 420 bits (227),  Expect = 4e-113
 Identities = 243/251 (97%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  1183  ACTTTGCAGCAGTACGGTGTGGCTTTCATTTTCAGGTGCAAGTGAATGTTAACCAAGGAA  1242
             |||||||||||||||||||||| ||||||||||| || |||||||||||||| |||||||
Sbjct  250   ACTTTGCAGCAGTACGGTGTGGTTTTCATTTTCAAGTACAAGTGAATGTTAATCAAGGAA  309

Query  1243  CAGCTGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGT  1302
             |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  310   CAGCCGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGT  369

Query  1303  TAGAATTTGGAGCATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACAC  1362
             ||||||||||||| |||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  370   TAGAATTTGGAGCGTTTACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACAC  429

Query  1363  AGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAG  1422
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                 ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  430   AGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAG  489

Query  1423  ACTTAGGGCAA  1433
             |||||||||||
Sbjct  490   ACTTAGGGCAA  500


>SRR2298546.106566 106566 length=502
Length=502

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  1258  TGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCAT  1317
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  502   TGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCGT  443

Query  1318  TTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTA  1377
             ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  442   TTACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTA  383

Query  1378  TCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACTAA  1437
             |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  382   TCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAACTAA  323

Query  1438  AAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGATGTAA  1497
             ||||||||||||||||||||||||| ||||||||||||||||| |||||||||||||| |
Sbjct  322   AAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGATGTTA  263

Query  1498  CCATATTGGGT  1508
             |||||||||||
Sbjct  262   CCATATTGGGT  252


 Score = 414 bits (224),  Expect = 2e-111
 Identities = 244/254 (96%), Gaps = 0/254 (0%)
 Strand=Plus/Plus

Query  1105  GACATCAGATAACCCATGTGGAATTGCCAAAAGTCTTTTGGGACAAAAACAGTAAGCCAG  1164
             ||||||||||||||||||||||| | |||||||||||||||||||||||||| |||||||
Sbjct  1     GACATCAGATAACCCATGTGGAACTACCAAAAGTCTTTTGGGACAAAAACAGCAAGCCAG  60

Query  1165  CCTATGGCCAATCAAGATACTTTGCAGCAGTACGGTGTGGCTTTCATTTTCAGGTGCAAG  1224
             |||||||||||||||||||||||||||||||||||||||| ||||||||||| || ||||
Sbjct  61    CCTATGGCCAATCAAGATACTTTGCAGCAGTACGGTGTGGTTTTCATTTTCAAGTACAAG  120

Query  1225  TGAATGTTAACCAAGGAACAGCTGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTG  1284
             |||||||||| ||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  121   TGAATGTTAATCAAGGAACAGCCGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTG  180

Query  1285  TGACATATGACTCAAAGTTAGAATTTGGAGCATTTACCAATTTACCACATGTATTGATGA  1344
             ||||||||||||||||||||||||||||||| |||||||||||||||||||| |||||||
Sbjct  181   TGACATATGACTCAAAGTTAGAATTTGGAGCGTTTACCAATTTACCACATGTGTTGATGA  240

Query  1345  ATTTGGCTGAGACC  1358
             ||||||||||||||
Sbjct  241   ATTTGGCTGAGACC  254
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>SRR2298382.118509 118509 length=500
Length=500

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 248/255 (97%), Gaps = 1/255 (0%)
 Strand=Plus/Plus

Query  433  TCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGT  492
            ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGT  60

Query  493  TGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCC  552
            ||||||||||||||||||||| |||||||||||||| |||||||||||||||||||||||
Sbjct  61   TGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCC  120

Query  553  ACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGG  612
            |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct  121  ACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGG  180

Query  613  CCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggg  672
            |||||||||||||||||||||| ||||||||||| |||||||||||||||||||||||||
Sbjct  181  CCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGG  240

Query  673  gATCCCCGG-TTTCC  686
            ||||||||| |||||
Sbjct  241  GATCCCCGGATTTCC  255


 Score = 418 bits (226),  Expect = 2e-112
 Identities = 242/250 (97%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  549  GCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCT  608
            |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  500  GCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCT  441

Query  609  GGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgg  668
            |||||||||||||||||||||||||| ||||||||||| |||||||||||||||||||||
Sbjct  440  GGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGG  381

Query  669  ggggATCCCCGGTTTCCTTTTATTTTATCAATGCTACAATGGAGACAATTAAAAGTATT  728
            ||||||||||||||||||||||||||||||||||| || |||||||||||||| ||||||
Sbjct  380  GGGGGATCCCCGGTTTCCTTTTATTTTATCAATGCCACTATGGAGACAATTAAGAGTATT  321

Query  729  GCAGATATGGCGACCGGAGTGGTCAGTTCAGTTGATTCCACTATCAATGCAGTTAATGAG  788
            ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  320  GCAGATATGGCGACCGGAGTGGTCAGTTCAGTTGATTCCACTATCAATGTAGTTAATGAG  261

Query  789  AGAGTAGAAA  798
            ||||| ||||
Sbjct  260  AGAGTGGAAA  251


>SRR2298382.107523 107523 length=502
Length=502

 Score = 431 bits (233),  Expect = 2e-116
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 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  417  CCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGT  476
            ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct  1    CCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGT  60

Query  477  TCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAAC  536
            ||||||||||||||||||||||||||||||||||||| |||||||||||||| |||||||
Sbjct  61   TCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAAC  120

Query  537  ACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTA  596
            |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  121  ACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTA  180

Query  597  TGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTG  656
            |||||||||||||||||||||||||||||||||||||| ||||||||||| |||||||||
Sbjct  181  TGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTG  240

Query  657  GGCCAAACCCg  667
            |||||||||||
Sbjct  241  GGCCAAACCCG  251


 Score = 414 bits (224),  Expect = 2e-111
 Identities = 242/251 (96%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  538  CTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTAT  597
            ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  502  CTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTAT  443

Query  598  GGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGG  657
            ||||||||||||||||||||||||||||||||||||| ||||||||||| ||||||||||
Sbjct  442  GGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGG  383

Query  658  GCCAAACCCggggggATCCCCGGTTTCCTTTTATTTTATCAATGCTACAATGGAGACAA  717
            |||||||||||||||||||||||||||||| ||||||||||||||| || ||||||||||
Sbjct  382  GCCAAACCCGGGGGGGATCCCCGGTTTCCTGTTATTTTATCAATGCCACTATGGAGACAA  323

Query  718  TTAAAAGTATTGCAGATATGGCGACCGGAGTGGTCAGTTCAGTTGATTCCACTATCAATG  777
            |||| |||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  322  TTAAGAGTATTGCAGATATGGCGACCGGAGTGGTCAGTTCAGTTGATTCCAATATCAATG  263

Query  778  CAGTTAATGAG  788
             ||||||||||
Sbjct  262  TAGTTAATGAG  252


>SRR2298382.63975 63975 length=502
Length=502

 Score = 431 bits (233),  Expect = 2e-116
 Identities = 245/251 (98%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  327  CTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCT  386
            ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  1    CTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCT  60
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Query  387  GCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAG  446
            | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAG  120

Query  447  CCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTT  506
            ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTT  180

Query  507  AGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCA  566
            ||||||| |||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  181  AGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCA  240

Query  567  GAAGGTACCCA  577
            ||||| |||||
Sbjct  241  GAAGGAACCCA  251


 Score = 420 bits (227),  Expect = 4e-113
 Identities = 245/254 (96%), Gaps = 0/254 (0%)
 Strand=Plus/Minus

Query  458  CAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCG  517
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  502  CAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCG  443

Query  518  ATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCA  577
            ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  442  ATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCA  383

Query  578  TAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCT  637
            ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  382  TAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCT  323

Query  638  GGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTTTAT  697
            ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  322  GGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTAT  263

Query  698  CAATGCTACAATGG  711
            || | | ||| |||
Sbjct  262  CACTACCACAGTGG  249


>SRR2298578.700636 700636 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  1247  TGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGA  1306
             ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  1     TGGTAGTGCATTGGTGGTGTATGAACCCAAACCCGTTGTGACATATGACTCAAAGTTAGA  60

Query  1307  ATTTGGAGCATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGC  1366
             ||||||||||||||||||| |||||||||| |||||||||||||||||||||||||||||
Sbjct  61    ATTTGGAGCATTTACCAATCTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGC  120

Query  1367  TGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTT  1426
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             ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  121   TGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTT  180

Query  1427  AGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACA  1486
             ||||||||||||||||||||||||||||||||||| ||||||||||||||||||| |||||
Sbjct  181   AGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACA  240

Query  1487  AGTTGATGTA  1496
             ||||||||||
Sbjct  241   AGTTGATGTA  250


 Score = 353 bits (191),  Expect = 4e-93
 Identities = 231/251 (92%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  1382  CTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACTAAAAGT  1441
             ||||||| ||||| |||| | ||||||||| | ||| |||||||||||||||||||||||
Sbjct  500   CTATGTTTCTGACCCAAATTTTGTTAAAACCGTTTCCTCAGACTTAGGGCAACTAAAAGT  441

Query  1442  CTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGATGTAACCAT  1501
              ||||||||||||||||||| |||||||||||||||||| ||||||||||||||||||||
Sbjct  440   TTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGATGTAACCAT  381

Query  1502  ATTGGGTAGTTTATTGCAATTGGACTTCCAAAATCCTAGGGTGTTTGGCCAAGACGTTGG  1561
             ||||||||| ||||||||||||||||||||||| |||||||| || ||||| ||||||||
Sbjct  380   ATTGGGTAGCTTATTGCAATTGGACTTCCAAAACCCTAGGGTATTCGGCCAGGACGTTGG  321

Query  1562  TATCTATGATAATGCACCAACGCGGAAACAAAATCTTAAAAAGATTCTTACAATGAGCAC  1621
             ||| ||||| ||||||||||||||||| |||||||| ||||| |||||||||||||||||
Sbjct  320   TATTTATGACAATGCACCAACGCGGAAGCAAAATCTAAAAAAAATTCTTACAATGAGCAC  261

Query  1622  TAAATACAAGT  1632
             |||||||||||
Sbjct  260   TAAATACAAGT  250


>SRR2298578.248012 248012 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 255/266 (96%), Gaps = 2/266 (1%)
 Strand=Plus/Plus

Query  1284  GTGACATATGACTCAAAGTTAGAATTTGGAGCATTTACCAATTTACCACATGTATTGATG  1343
             |||||||||||||||||||||||||||||||||||||||||| |||||||||| ||||||
Sbjct  1     GTGACATATGACTCAAAGTTAGAATTTGGAGCATTTACCAATCTACCACATGTGTTGATG  60

Query  1344  AATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTAT  1403
             |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Sbjct  61    AATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGTTGACACAAACTAT  120

Query  1404  GTTAAAACGGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCT  1463
             |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   GTTAAAACAGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCC  180

Query  1464  ATACCTTCAGGTTCTGCGACACAAGTTGATGTAACCATATTGGGTAGTTTATTGCAATTG  1523
             ||||||||||||||||| ||||||||||||||||||| ||||||||| ||||||||||||
Sbjct  181   ATACCTTCAGGTTCTGCTACACAAGTTGATGTAACCAAATTGGGTAGCTTATTGCAATTG  240
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Query  1524  GACTTCCAAAATCCTAGGGTGTTTGG  1549
             ||||||||||  |||||||| |||||
Sbjct  241   GACTTCCAAAC-CCTAGGGT-TTTGG  264


 Score = 407 bits (220),  Expect = 3e-109
 Identities = 240/250 (96%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  1294  ACTCAAAGTTAGAATTTGGAGCATTTACCAATTTACCACATGTATTGATGAATTTGGCTG  1353
             |||||||||||||||||||| ||||||||||| |||||||||| ||||||||||||||||
Sbjct  499   ACTCAAAGTTAGAATTTGGACCATTTACCAATCTACCACATGTTTTGATGAATTTGGCTG  440

Query  1354  AGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGG  1413
             |||||||||||||||||||||||||||||||||||  ||||||||||||||||||||| |
Sbjct  439   AGACCACACAGGCTGATTTATGTATCCCCTATGTTTTTGACACAAACTATGTTAAAACAG  380

Query  1414  ATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCTATACCTTCAG  1473
             ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  379   ATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCCATACCTTCAG  320

Query  1474  GTTCTGCGACACAAGTTGATGTAACCATATTGGGTAGTTTATTGCAATTGGACTTCCAAA  1533
             ||||||| ||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct  319   GTTCTGCTACACAAGTTGATGTAACCATATTGGGTAGCTTATTGCAATTGGACTTCCAAA  260

Query  1534  ATCCTAGGGT  1543
             | ||||||||
Sbjct  259   ACCCTAGGGT  250


>SRR2298573.878601 878601 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  348   TGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGC  407
             |||||||||||||||||||||||||| ||||||||||||| |||||||||||||||||||
Sbjct  500   TGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGC  441

Query  408   GGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTT  467
             |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Sbjct  440   GGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTT  381

Query  468   AGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGT  527
             |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Sbjct  380   AGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGT  321

Query  528   ACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAA  587
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  320   AGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAA  261

Query  588   GTGACACTAT  597
             | ||||||||
Sbjct  260   GCGACACTAT  251
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 Score = 387 bits (209),  Expect = 4e-103
 Identities = 223/230 (97%), Gaps = 0/230 (0%)
 Strand=Plus/Plus

Query  276  TCTACTAGTGAGATACCACGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGT  335
            |||| ||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  2    TCTATTAGTGAGATACCATGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGT  61

Query  336  TTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCAT  395
            |||||||||||||||||||||||||||||||||||||| ||||||||||||| |||||||
Sbjct  62   TTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCAT  121

Query  396  CCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCT  455
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  122  CCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTT  181

Query  456  AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACT  505
            |||||||||||||||||||||||||||||| ||||||||||||||| |||
Sbjct  182  AACAAACCCTTTAGGATTGGTTCTAAACCTTAGATGTTGTGGAAGAAACT  231


>SRR2298573.877679 877679 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  462  CCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCT  521
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCT  60

Query  522  GGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGG  581
            ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGG  120

Query  582  TAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTT  641
            ||||||| ||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  121  TAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTT  180

Query  642  AAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTTTATCAAT  701
            ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTATCAAT  240

Query  702  GCTACAATGG  711
            || || ||||
Sbjct  241  GCCACTATGG  250


 Score = 370 bits (200),  Expect = 4e-98
 Identities = 230/245 (94%), Gaps = 0/245 (0%)
 Strand=Plus/Minus

Query  480  AAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACT  539
            ||||||| | ||||  ||||| |||||||||||| |||||||||||||| ||||||| ||
Sbjct  495  AAACCTGGGGTGTTTGGGAAGGTACTTAGTACCTTCCGATCTGGTAGTAGTGCAAACCCT  436

Query  540  AGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGG  599
            ||||||||||||||||||||||||||||||||||||||||||||||||| ||| ||||||
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Sbjct  435   AGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACCCTATGG  376

Query  600   ATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGC  659
             ||||||||||||||||||||||||||||||||||| ||||||||||| ||||||||||||
Sbjct  375   ATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGC  316

Query  660   CAAACCCggggggATCCCCGGTTTCCTTTTATTTTATCAATGCTACAATGGAGACAATT  719
             |||||||||||||||||||||||||||||||||||||||||||| || ||||||||||||
Sbjct  315   CAAACCCGGGGGGATCCCCGGTTTCCTTTTATTTTATCAATGCCACTATGGAGACAATT  256

Query  720   AAAAG  724
             || ||
Sbjct  255   AAGAG  251


>SRR2298573.870403 870403 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  397   CTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTA  456
             ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||| ||
Sbjct  500   CTATTGCCAGCGGAACAACCCCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTA  441

Query  457   ACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCC  516
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  440   ACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACC  381

Query  517   GATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCC  576
             |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  380   GATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCC  321

Query  577   ATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACC  636
             |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  320   ATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATC  261

Query  637   TGGTTAAAAA  646
             ||||||||||
Sbjct  260   TGGTTAAAAA  251


 Score = 425 bits (230),  Expect = 9e-115
 Identities = 240/245 (98%), Gaps = 0/245 (0%)
 Strand=Plus/Plus

Query  344   CGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGC  403
             |||||||||||||||||||||||||||||| ||||||||||||| |||||||||||||||
Sbjct  1     CGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGC  60

Query  404   CAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACC  463
             |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct  61    CAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACC  120

Query  464   CTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGG  523
             |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct  121   CTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGG  180
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Query  524  TAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTA  583
            ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTA  240

Query  584  ACAAG  588
            |||||
Sbjct  241  ACAAG  245


>SRR2298573.865355 865355 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  332  AAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAA  391
            |||||||||||||||||||||||||||||||||||||||||| ||||||||||||| |||
Sbjct  251  AAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAA  310

Query  392  GCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAG  451
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  311  GCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAG  370

Query  452  GTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTAC  511
            || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  371  GTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTAC  430

Query  512  CTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGG  571
            || |||||||||||||| |||||||||||||||||||||||||||||||||||| |||||
Sbjct  431  CTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCCGAAGG  490

Query  572  TACCCATAGG  581
            ||||||||||
Sbjct  491  TACCCATAGG  500


 Score = 374 bits (202),  Expect = 3e-99
 Identities = 228/241 (95%), Gaps = 0/241 (0%)
 Strand=Plus/Minus

Query  475  GTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAA  534
            |||| |||||||| || ||| ||||||| |||||||||| |||||||||||||| |||||
Sbjct  249  GTTCCAAACCTGAAATTTTGGGGAAGATTCTTAGTACCTACCGATCTGGTAGTAATGCAA  190

Query  535  ACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACAC  594
            || ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  189  ACTCTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACAC  130

Query  595  TATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAG  654
            |||||||||||||||||||||||||||||||||||||||| ||||||||||| |||||||
Sbjct  129  TATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAG  70

Query  655  TGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTTTATCAATGCTACAATGGAGA  714
            ||||||||||||||||||||||||||||||||||||||||||||||||| || |||||||
Sbjct  69   TGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTATCAATGCCACTATGGAGA  10

Query  715  C  715
            |
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Sbjct  9    C  9


>SRR2298573.855147 855147 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  412  CAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGA  471
            |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Sbjct  1    CAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGA  60

Query  472  TTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTG  531
            |||||||||||||||||||||||||||||||||||||||||| |||||||||||||| ||
Sbjct  61   TTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTG  120

Query  532  CAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGA  591
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  121  CAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGA  180

Query  592  CACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTC  651
            ||||||||||||||||||||||||||||||||||||||||||| ||||||||||| ||||
Sbjct  181  CACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTC  240

Query  652  TAGTGGGCCA  661
            ||||||||||
Sbjct  241  TAGTGGGCCA  250


 Score = 405 bits (219),  Expect = 1e-108
 Identities = 239/249 (96%), Gaps = 0/249 (0%)
 Strand=Plus/Minus

Query  462  CCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCT  521
            |||||||||||||||||||||||||||||||||||||||||||||||| ||| |||||||
Sbjct  499  CCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTTCCTACCGATCT  440

Query  522  GGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGG  581
            ||| ||| ||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  439  GGTTGTAGTGCAAACCCTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGG  380

Query  582  TAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTT  641
            ||||||| ||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  379  TAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTT  320

Query  642  AAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTTTATCAAT  701
            ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  319  AAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTATCAAT  260

Query  702  GCTACAATG  710
            || || |||
Sbjct  259  GCCACTATG  251


>SRR2298573.849493 849493 length=500
Length=500
```

```
 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  462   CCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCT  521
             |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  1     CCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCT  60

Query  522   GGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGG  581
             ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    GGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGG  120

Query  582   TAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTT  641
             ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  121   TAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTT  180

Query  642   AAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTTTATCAAT  701
             ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   AAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTATCAAT  240

Query  702   GCTACAATGG  711
             || || ||||
Sbjct  241   GCCACTATGG  250


 Score = 416 bits (225),  Expect = 6e-112
 Identities = 241/249 (97%), Gaps = 0/249 (0%)
 Strand=Plus/Minus

Query  473   TGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGC  532
             |||||||||||| | |||||||||||||||||||||||||| |||||||||||||| |||
Sbjct  500   TGGTTCTAAACCGGGGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGC  441

Query  533   AAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGAC  592
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  440   AAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGAC  381

Query  593   ACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCT  652
             |||||||||||||||||||||||||||||||||||||||||| ||||||||||| |||||
Sbjct  380   ACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCT  321

Query  653   AGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTTTATCAATGCTACAATGGA  712
             ||||||||||||||||||||||||||||||||||||||||||||||||||| || |||||
Sbjct  320   AGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTATCAATGCCACTATGGA  261

Query  713   GACAATTAA  721
             |||||||||
Sbjct  260   GACAATTAA  252


>SRR2298573.839628 839628 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  452   GTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTAC  511
             || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

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Sbjct  1    GTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTAC  60

Query  512  CTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGG  571
            || |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGG  120

Query  572  TACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGG  631
            ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGG  180

Query  632  TGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTA  691
            ||| ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTA  240

Query  692  TTTTATCAAT  701
            ||||||||||
Sbjct  241  TTTTATCAAT  250


 Score = 409 bits (221),  Expect = 9e-110
 Identities = 243/254 (96%), Gaps = 0/254 (0%)
 Strand=Plus/Minus

Query  476  TTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAA  535
            ||||||||||| ||||||||||||| | |||||||||| |||||||||||||| ||||||
Sbjct  500  TTCTAAACCTGGGATGTTGTGGAAGTTTCTTAGTACCTACCGATCTGGTAGTAGTGCAAA  441

Query  536  CACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACT  595
            ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  440  CACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGGGACACT  381

Query  596  ATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGT  655
            ||||||||||||||||||||||||||||||||||||||| ||||||||||| ||||||||
Sbjct  380  ATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGT  321

Query  656  GGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTTTATCAATGCTACAATGGAGAC  715
            |||||||||||||||||||||||||||||||||||||||||||||||| || ||||||||
Sbjct  320  GGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTATCAATGCCACTATGGAGAC  261

Query  716  AATTAAAAGTATTG  729
            |||||| |||||||
Sbjct  260  AATTAAGAGTATTG  247


>SRR2298573.835256 835256 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  326  TCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGC  385
            |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  1    TCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGC  60

Query  386  TGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAA  445
            || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAA  120
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Query  446   GCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACT  505
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   GCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACT  180

Query  506   TAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCC  565
             |||||||| |||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  181   TAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCC  240

Query  566   AGAAGGTACC  575
             |||||| |||
Sbjct  241   AGAAGGAACC  250


 Score = 388 bits (210),  Expect = 1e-103
 Identities = 230/240 (96%), Gaps = 0/240 (0%)
 Strand=Plus/Minus

Query  420   GGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCT  479
             |||||| || |||  ||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  490   GGTAACCGGGGCCCTTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCT  431

Query  480   AAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACT  539
             |||||||||||||||||||||||||||||||||| |||||||||||||| ||||||||||
Sbjct  430   AAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACT  371

Query  540   AGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGG  599
             ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  370   AGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGG  311

Query  600   ATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGC  659
             ||||||||||||||||||||||||||||||||||| ||||||||||| ||||||||||||
Sbjct  310   ATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGC  251


>SRR2298573.819549 819549 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  339   TGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCT  398
             |||||||||||||||||||||||||||| |||||| ||||||||||||| ||||||||||
Sbjct  250   TGAGACGTCTGGTGACGTGTGGGAACTTTTTGGAAACAACATTTTGCTGTAAAGCATCCT  191

Query  399   ATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAAC  458
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  190   ATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAAC  131

Query  459   AAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGA  518
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  130   AAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGA  71

Query  519   TCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCAT  578
             |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  70    TCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCAT  11

Query  579   AGGTAACAAG  588
             ||||||||||
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Sbjct  10   AGGTAACAAG  1


 Score = 353 bits (191),  Expect = 4e-93
 Identities = 225/242 (93%), Gaps = 0/242 (0%)
 Strand=Plus/Plus

Query  247  GTGTGGGGTGGCAGATGGCGTGCCATAATTCTACTAGTGAGATACCACGCTTGTGGACCT  306
            |||||||||||||||||||||||||||  |||| ||||||||||||| ||||||||||||
Sbjct  256  GTGTGGGGTGGCAGATGGCGTGCCATAGCTCTATTAGTGAGATACCATGCTTGTGGACCT  315

Query  307  TATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTT  366
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  316  TATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTT  375

Query  367  ATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACA  426
            ||||||| ||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  376  ATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACA  435

Query  427  GGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTG  486
            |  |||||||||||||||||||||||| ||| ||| ||||| || | || | |||||| |
Sbjct  436  GTGGCCTCTGGGGCCAAAAGCCAAGGTTTAAAAAAACCTTTGGGGTGGGGTTTAAACCCG  495

Query  487  AG  488
            ||
Sbjct  496  AG  497


>SRR2298573.806866 806866 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 259/272 (95%), Gaps = 2/272 (1%)
 Strand=Plus/Minus

Query  415  CACCTGGTAACAGGTG--CCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGAT  472
            |||||| || ||||||    || |||||||||||||||||| ||||||||||||||||||
Sbjct  272  CACCTGTTACCAGGTGTTGTTCCGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGAT  213

Query  473  TGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGC  532
            ||||||||||||||||||||||||||||||||||||||||| |||||||||||||| |||
Sbjct  212  TGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGC  153

Query  533  AAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGAC  592
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  152  AAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGAC  93

Query  593  ACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCT  652
            |||||||||||||||||||||||||||||||||||||||||| ||||||||||| |||||
Sbjct  92   ACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCT  33

Query  653  AGTGGGCCAAACCCgggggggATCCCCGGTTT  684
            ||||||||||||||||||||||||||||||||
Sbjct  32   AGTGGGCCAAACCCGGGGGGGATCCCCGGTTT  1


 Score = 411 bits (222),  Expect = 3e-110
 Identities = 242/252 (96%), Gaps = 0/252 (0%)
 Strand=Plus/Plus
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Query  407  CGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTT  466
            ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  249  CGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTT  308

Query  467  TAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAG  526
            ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  309  TAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAG  368

Query  527  TACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACA  586
            || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  369  TAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACA  428

Query  587  AGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAA  646
            || |||||||||||||||| ||||||||||||||||||||||||| || |||||||||||
Sbjct  429  AGCGACACTATGGATCTGAACTGGGGCCAGGTACCTCTATCTTGGGGATCTGGTTAAAAA  488

Query  647  GCGTCTAGTGGG  658
              | ||||||||
Sbjct  489  CAGCCTAGTGGG  500


>SRR2298573.801823 801823 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 248/256 (97%), Gaps = 0/256 (0%)
 Strand=Plus/Minus

Query  328  TAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTG  387
            ||||||||||| ||| |||||||||||||||||||||||||||||| |||||||||||||
Sbjct  500  TAGTAAGTTTGGGAGCCGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTG  441

Query  388  CAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGC  447
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  440  TAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGC  381

Query  448  CAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTA  507
            |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  380  CAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTA  321

Query  508  GTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAG  567
            |||||| |||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  320  GTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAG  261

Query  568  AAGGTACCCATAGGTA  583
            ||||||||||| ||||
Sbjct  260  AAGGTACCCATCGGTA  245


 Score = 420 bits (227),  Expect = 4e-113
 Identities = 243/251 (97%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  269  CCATAATTCTACTAGTGAGATACCACGCTTGTGGACCTTATGCTCACACAGCCATCCTCT  328
            |||||  |||| ||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  1    CCATAGCTCTATTAGTGAGATACCATGCTTGTGGACCTTATGCTCACACAGCCATCCTCT  60

Query  329  AGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGC  388
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            ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||| 
Sbjct  61   AGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGT  120

Query  389  AAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCC  448
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCC  180

Query  449  AAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAG  508
            ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAG  240

Query  509  TACCTGCCGAT  519
            ||||| |||||
Sbjct  241  TACCTACCGAT  251


>SRR2298573.786859 786859 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  358  TGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACAC  417
            |||||||||||||||| ||||||||||||| |||||||||||||||||||||||||||||
Sbjct  500  TGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACAC  441

Query  418  CTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTT  477
            |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct  440  CTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTT  381

Query  478  CTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACA  537
            |||||||||||||||||||||||||||||||||||| |||||||||||||| ||||||||
Sbjct  380  CTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACA  321

Query  538  CTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTAT  597
            ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  320  CTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTAT  261

Query  598  GGATCTGATC  607
            ||||||||||
Sbjct  260  GGATCTGATC  251


 Score = 418 bits (226),  Expect = 2e-112
 Identities = 242/250 (97%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  326  TCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGC  385
            |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  1    TCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGC  60

Query  386  TGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAA  445
            || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAA  120

Query  446  GCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACT  505
            |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACT  180
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Query  506   TAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCC  565
             |||||||| |||||||||||||| |||||| |||||||| ||||||||||||||||||||
Sbjct  181   TAGTACCTACCGATCTGGTAGTAGTGCAAAAACTAGTTGAAAGGCCCACGAAGGATGCCC  240

Query  566   AGAAGGTACC  575
             |||||| |||
Sbjct  241   AGAAGGGACC  250


>SRR2298573.768862 768862 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 242/247 (98%), Gaps = 0/247 (0%)
 Strand=Plus/Plus

Query  375   CAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTC  434
             ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     CAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTC  60

Query  435   TGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTG  494
             ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  61    TGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTG  120

Query  495   TGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCAC  554
             ||||||||||||||||||| |||||||||||||| |||||||||||||||||||||||||
Sbjct  121   TGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCAC  180

Query  555   GAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCC  614
             |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  181   GAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCC  240

Query  615   AGGTACC  621
             |||||||
Sbjct  241   AGGTACC  247


 Score = 355 bits (192),  Expect = 1e-93
 Identities = 230/249 (92%), Gaps = 0/249 (0%)
 Strand=Plus/Minus

Query  490   TGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGG  549
             |||||||||||||  || |||||| ||| | |||| ||  ||||||  || |||||||||
Sbjct  499   TGTTGTGGAAGATCGTTGGTACCTACCGGTTTGGTTGTTGTGCAAAACCTTGTTGTAAGG  440

Query  550   CCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTG  609
             |||||||||||| |||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  439   CCCACGAAGGATTCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTG  380

Query  610   GGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCggg  669
             ||||||||||||||||||||||||| ||||||||||| ||||||||||||||||||||||
Sbjct  379   GGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGG  320

Query  670   ggggATCCCCGGTTTCCTTTTATTTTATCAATGCTACAATGGAGACAATTAAAAGTATTG  729
             |||||||||||||||||||||||||||||||||| || |||||||||||||| |||||||
Sbjct  319   GGGGATCCCCGGTTTCCTTTTATTTTATCAATGCCACTATGGAGACAATTAAGAGTATTG  260

Query  730   CAGATATGG  738
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            |||||||||
Sbjct  259  CAGATATGG  251


>SRR2298573.759611 759611 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  450  AGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGT  509
            |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  251  AGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGT  310

Query  510  ACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAA  569
            |||| |||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  311  ACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAA  370

Query  570  GGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTT  629
            ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  371  GGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTT  430

Query  630  GGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTT  689
            ||||| ||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  431  GGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTT  490

Query  690  TATTTTATCA  699
            ||||||||||
Sbjct  491  TATTTTATCA  500


 Score = 399 bits (216),  Expect = 6e-107
 Identities = 246/260 (95%), Gaps = 3/260 (1%)
 Strand=Plus/Minus

Query  479  TAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACAC  538
            |||||||  | ||||||||||||| |||||||||||||||| |||||||| |||||||||
Sbjct  257  TAAACCT--G-TGTTGTGGAAGATCCTTAGTACCTGCCGATTTGGTAGTAGTGCAAACAC  201

Query  539  TAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATG  598
            |||||  ||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct  200  TAGTTTGAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATG  141

Query  599  GATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGG  658
            ||||||||||||||||||||||||||||||||||| |||||||||||| |||||||||||
Sbjct  140  GATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGG  81

Query  659  CCAAACCCgggggggATCCCCGGTTTCCTTTTATTTTATCAATGCTACAATGGAGACAAT  718
            ||||||||||||||||||||||||||||||||||||||||||||| || |||||||||||
Sbjct  80   CCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTATCAATGCCACTATGGAGACAAT  21

Query  719  TAAAAGTATTGCAGATATGG  738
            ||| ||||||||||||||||
Sbjct  20   TAAGAGTATTGCAGATATGG  1


>SRR2298573.759443 759443 length=500
Length=500
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 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  382  TTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCC  441
            |||||| ||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  250  TTGCTGTAAAGCATCCTATTGCCAGCGGAACAACCCCTGGTAACAGGTGCCTCTGGGGCC  191

Query  442  AAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGA  501
            |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  190  AAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGA  131

Query  502  TACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGAT  561
            |||||||||||| |||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  130  TACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGAT  71

Query  562  GCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACC  621
            ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  70   GCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACC  11

Query  622  TCTATCTTGG  631
            ||||||||||
Sbjct  10   TCTATCTTGG  1


 Score = 390 bits (211),  Expect = 3e-104
 Identities = 237/250 (95%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  290  ACCACGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTG  349
            |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  250  ACCATGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTG  309

Query  350  GTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGG  409
            |||||||||||||||||||||||| |||||||||||||| ||||||||||||||||||||
Sbjct  310  GTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGG  369

Query  410  AACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAG  469
            |||||||||||||||||||||| ||||||||||||||||||||| |||||||||||||||
Sbjct  370  AACAACACCTGGTAACAGGTGCATCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAG  429

Query  470  GATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTAC  529
            ||||||||||||||||||||  || ||||||| ||| ||||||| |||||||||| ||| 
Sbjct  430  GATTGGTTCTAAACCTGAGAGATTTTGGAAGAAACTAAGTACCTACCGATCTGGTGGTAG  489

Query  530  TGCAAACACT  539
            ||||||||||
Sbjct  490  TGCAAACACT  499


>SRR2298573.756161 756161 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  331  TAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAA  390
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             |||||||||||||||||||||||||||||||| |||||||||| ||||||||||||| ||
Sbjct  500   TAAGTTTGTGAGACGTCTGGTGACGTGTGGGACCTTATTGGAAACAACATTTTGCTGTAA  441

Query  391   AGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAA  450
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  440   AGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAA  381

Query  451   GGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTA  510
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  380   GGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTA  321

Query  511   CCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAG  570
             ||| |||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  320   CCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAG  261

Query  571   GTACCCATAG  580
             ||||||||||
Sbjct  260   GTACCCATAG  251


 Score = 398 bits (215),  Expect = 2e-106
 Identities = 238/249 (96%), Gaps = 2/249 (1%)
 Strand=Plus/Plus

Query  313   CACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGA  372
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     CACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGA  60

Query  373   AGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCC  432
             | ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    AACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCC  120

Query  433   TCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGT  492
             ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  121   TCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGT  180

Query  493   TGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCC  552
             ||||||||||||||||||||| ||||||||| || | |||||| || ||||||||||||
Sbjct  181   TGTGGAAGATACTTAGTACCTACCGATCTGGAAGAAGTGCAAAAACAAGTTGTAAGGCC-  239

Query  553   ACG-AAGGA  560
             ||| |||||
Sbjct  240   ACGGAAGGA  248


>SRR2298573.737432 737432 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  451   GGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTA  510
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  251   GGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTA  310

Query  511   CCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAG  570
             ||| |||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  311   CCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAG  370
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Query  571  GTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTG  630
            |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  371  GTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTG  430

Query  631  GTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTT  690
            |||| ||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  431  GTGATCTGGTTAAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTT  490

Query  691  ATTTTATCAA  700
            ||||||||||
Sbjct  491  ATTTTATCAA  500


 Score = 414 bits (224),  Expect = 2e-111
 Identities = 240/248 (97%), Gaps = 0/248 (0%)
 Strand=Plus/Minus

Query  515  CCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTAC  574
            ||||| |||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  248  CCGATTTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTAC  189

Query  575  CCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGA  634
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  188  CCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGA  129

Query  635  CCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTT  694
             ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  128  TCTGGTTAAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTT  69

Query  695  TATCAATGCTACAATGGAGACAATTAAAAGTATTGCAGATATGGCGACCGGAGTGGTCAG  754
            ||||||||| || |||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  68   TATCAATGCCACTATGGAGACAATTAAGAGTATTGCAGATATGGCGACCGGAGTGGTCAG  9

Query  755  TTCAGTTG  762
            ||||||||
Sbjct  8    TTCAGTTG  1


>SRR2298573.723480 723480 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  444  AAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATA  503
            |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  250  AAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATA  191

Query  504  CTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGC  563
            |||||||||| |||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  190  CTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGC  131

Query  564  CCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTC  623
            ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  130  CCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTC  71

Query  624  TATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTT  683
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           ||||||||||| ||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  70   TATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTT  11

Query  684  TCCTTTTATT  693
            ||||||||||
Sbjct  10   TCCTTTTATT  1


 Score = 418 bits (226),  Expect = 2e-112
 Identities = 242/250 (97%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  317  CAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCA  376
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  251  CAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACA  310

Query  377  ACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTG  436
            ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  311  ACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTG  370

Query  437  GGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTG  496
            ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  371  GGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTG  430

Query  497  GAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGA  556
            ||||||||||||||||| ||||||||||||||  |||||||| ||||| |||||||||||
Sbjct  431  GAAGATACTTAGTACCTACCGATCTGGTAGTAGGGCAAACACAAGTTGGAAGGCCCACGA  490

Query  557  AGGATGCCCA  566
            ||||||||||
Sbjct  491  AGGATGCCCA  500


>SRR2298573.716980 716980 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  319  GCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAAC  378
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  1    GCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAAC  60

Query  379  ATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGG  438
            ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGG  120

Query  439  GCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGA  498
            ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGA  180

Query  499  AGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAG  558
            ||||||||||||||| |||||||||||||| |||||| ||||||||||||||||||||||
Sbjct  181  AGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAAAACTAGTTGTAAGGCCCACGAAG  240

Query  559  GATGCCCAGA  568
            ||||||||||
Sbjct  241  GATGCCCAGA  250
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 Score = 424 bits (229),  Expect = 3e-114
 Identities = 243/250 (97%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  321  CATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACAT  380
            |||||| ||||||||||||| |||||||||||||||||||||||||||||||| ||||||
Sbjct  500  CATCCTTTAGTAAGTTTGTGGGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACAT  441

Query  381  TTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGC  440
            ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  440  TTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGC  381

Query  441  CAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAG  500
            ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  380  CAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAG  321

Query  501  ATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGA  560
            ||||||||||||| |||||||||||||| |||||||||||||||||||||||||||||||
Sbjct  320  ATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGA  261

Query  561  TGCCCAGAAG  570
            ||||||||||
Sbjct  260  TGCCCAGAAG  251


>SRR2298573.711657 711657 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  358  TGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACAC  417
            |||||||||||||||| ||||||||||||| |||||||||||||||||||||||||||||
Sbjct  500  TGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACAC  441

Query  418  CTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTT  477
            |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct  440  CTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTT  381

Query  478  CTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACA  537
            |||||||||||||||||||||||||||||||||||| |||||||||||||| ||||||||
Sbjct  380  CTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACA  321

Query  538  CTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTAT  597
            ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  320  CTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTAT  261

Query  598  GGATCTGATC  607
            ||||||||||
Sbjct  260  GGATCTGATC  251


 Score = 420 bits (227),  Expect = 4e-113
 Identities = 242/249 (97%), Gaps = 1/249 (0%)
 Strand=Plus/Plus
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Query  333  AGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAG  392
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||||| ||||
Sbjct  4    AGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAG  63

Query  393  CATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGG  452
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  64   CATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGG  123

Query  453  TCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACC  512
            | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  124  TTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACC  183

Query  513  TGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGT  572
            | |||||||||||||| ||||||||||||||||||||||| |||||||||||||||||||
Sbjct  184  TACCGATCTGGTAGTATTGCAAACACTAGTTGTAAGGCCCCCGAAGGATGCCCAGAAGGT  243

Query  573  ACCCATAGG  581
            ||||| |||
Sbjct  244  ACCCA-AGG  251


>SRR2298573.701171 701171 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  382  TTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCC  441
            |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  250  TTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCC  191

Query  442  AAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGA  501
            |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  190  AAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGA  131

Query  502  TACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGAT  561
            |||||||||||| |||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  130  TACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGAT  71

Query  562  GCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACC  621
            ||||||||||||||||||| ||||||| ||||||||||||||||||||||||||||||||
Sbjct  70   GCCCAGAAGGTACCCATAGTTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACC  11

Query  622  TCTATCTTGG  631
            ||||||||||
Sbjct  10   TCTATCTTGG  1


 Score = 398 bits (215),  Expect = 2e-106
 Identities = 237/248 (96%), Gaps = 0/248 (0%)
 Strand=Plus/Plus

Query  318  AGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAA  377
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  250  AGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAA  309

Query  378  CATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGG  437
            |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  310  CATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGG  369

Query  438  GGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGG  497
            |||||||||||||||| ||||||||||||||||||||||||||||||||||||| |||||
Sbjct  370  GGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGCTGTGG  429

Query  498  AAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAA  557
            |||||||||||||||| |||||||||||| | ||||||| ||||||| || |||| ||||
Sbjct  430  AAGATACTTAGTACCTACCGATCTGGTAGAAGTGCAAACCCTAGTTGCAAAGCCCCCGAA  489

Query  558  GGATGCCC  565
            ||||||||
Sbjct  490  GGATGCCC  497


>SRR2298573.685469 685469 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  440  CCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAA  499
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  250  CCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAA  191

Query  500  GATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGG  559
            |||||||||||||| |||||||||||||| ||||||||||||||||||||||||||||||
Sbjct  190  GATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGG  131

Query  560  ATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTA  619
            ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Sbjct  130  ATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTA  71

Query  620  CCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCC  679
            ||||||||||||||| ||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  70   CCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCC  11

Query  680  GGTTTCCTTT  689
            ||||||||||
Sbjct  10   GGTTTCCTTT  1


 Score = 329 bits (178),  Expect = 7e-86
 Identities = 218/238 (92%), Gaps = 0/238 (0%)
 Strand=Plus/Plus

Query  384  GCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAA  443
            |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  263  GCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAA  322

Query  444  AAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATA  503
            |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  323  AAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATA  382

Query  504  CTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGC  563
            |||||||||| |||||||||||||| ||||||||||||||||||||||||||||| | ||
Sbjct  383  CTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGAAGGC  442
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Query  564  CCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACC  621
            |||||||| ||||| |||||| ||  ||  | ||||| ||  | ||||||| || |||
Sbjct  443  CCAGAAGGAACCCAAAGGTAAAAAAGGAACCAATGGACCTACTTTGGGGCCGGGAACC  500


>SRR2298573.656085 656085 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  397  CTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTA  456
            |||||||||||||||||||||||||||||||||||||||||||||||||||||| || ||
Sbjct  500  CTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAAGTTTA  441

Query  457  ACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCC  516
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  440  ACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACC  381

Query  517  GATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCC  576
            |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  380  GATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCC  321

Query  577  ATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACC  636
            |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  320  ATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATC  261

Query  637  TGGTTAAAAA  646
            ||||||||||
Sbjct  260  TGGTTAAAAA  251


 Score = 424 bits (229),  Expect = 3e-114
 Identities = 243/250 (97%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  396  CCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCT  455
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||| || |
Sbjct  1    CCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAAGTTT  60

Query  456  AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGC  515
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  61   AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTAC  120

Query  516  CGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACC  575
            ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACC  180

Query  576  CATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGAC  635
            ||||||||||||| |||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  181  CATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCCCTATCTTGGTGAT  240

Query  636  CTGGTTAAAA  645
            ||||||||||
Sbjct  241  CTGGTTAAAA  250


>SRR2298573.648379 648379 length=500
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Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  457  ACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCC  516
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  250  ACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACC  191

Query  517  GATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCC  576
            |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  190  GATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCC  131

Query  577  ATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACC  636
            |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  130  ATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATC  71

Query  637  TGGTTAAAAAGCGTCTAGTGGGCCAAACCCggggggGATCCCCGGTTTCCTTTTATTTTA  696
            |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  70   TGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTA  11

Query  697  TCAATGCTAC  706
            ||||||| ||
Sbjct  10   TCAATGCCAC  1


 Score = 414 bits (224),  Expect = 2e-111
 Identities = 242/251 (96%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  419  TGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTC  478
            ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  250  TGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTC  309

Query  479  TAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACAC  538
            ||||||||||||||||||||||||||||||||||| |||||||||||||| |||||||||
Sbjct  310  TAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACAC  369

Query  539  TAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATG  598
            |||||||||||||||||||||||||||||||||||||||||||||||||  ||| |||||
Sbjct  370  TAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAACGACCCTATG  429

Query  599  GATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGG  658
            |||||||||||||||||||||||||||||||||||| ||||||||||| |||||||||||
Sbjct  430  GATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGAACTGGTTAAAAAACGTCTAGTGGG  489

Query  659  CCAAACCCggg  669
            ||||| |||||
Sbjct  490  CCAAAACCGGG  500


>SRR2298573.641321 641321 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus
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Query  464  CTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGG  523
            |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct  1    CTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGG  60

Query  524  TAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTA  583
            ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTA  120

Query  584  ACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAA  643
            ||||| ||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  121  ACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAA  180

Query  644  AAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTTTATCAATGC  703
            ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTATCAATGC  240

Query  704  TACAATGGAG  713
             |||||||||
Sbjct  241  CACAATGGAG  250


 Score = 412 bits (223),  Expect = 7e-111
 Identities = 241/250 (96%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  464  CTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGG  523
            ||||||||||||||||||||||| ||||||||||||||| |||||||||| |||||||||
Sbjct  500  CTTTAGGATTGGTTCTAAACCTGGGATGTTGTGGAAGATGCTTAGTACCTACCGATCTGG  441

Query  524  TAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTA  583
            ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  440  TAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTA  381

Query  584  ACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAA  643
            ||||| ||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  380  ACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAA  321

Query  644  AAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTTTATCAATGC  703
            ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  320  AAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTATCAATGC  261

Query  704  TACAATGGAG  713
             || ||||||
Sbjct  260  CACTATGGAG  251


>SRR2298573.604233 604233 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  334  GTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGC  393
            |||||||||||||||||||||||||||||||||||||||| ||||||||||||| |||||
Sbjct  1    GTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGC  60

Query  394  ATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGT  453
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  61   ATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGT  120

Query  454  CTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCT  513
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCT  180

Query  514  GCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTA  573
             |||||||||||||| ||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  181  ACCGATCTGGTAGTAGTGCAAACACAAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTA  240

Query  574  CCCATAGGTA  583
            ||||||||||
Sbjct  241  CCCATAGGTA  250


 Score = 388 bits (210),  Expect = 1e-103
 Identities = 238/252 (94%), Gaps = 0/252 (0%)
 Strand=Plus/Minus

Query  475  GTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAA  534
            ||| ||| |||||||||||  ||||||| |||||||||| |||||||||||| | |||||
Sbjct  500  GTTTTAACCCTGAGATGTTTGGGAAGATTCTTAGTACCTACCGATCTGGTAGGAGTGCAA  441

Query  535  ACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACAC  594
            |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  440  ACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACAC  381

Query  595  TATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAG  654
            |||||||||||||||||||||||||||||||||||||||| ||||||||||| |||||||
Sbjct  380  TATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAG  321

Query  655  TGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTTTATCAATGCTACAATGGAGA  714
            ||||||||||||||||||||||||||||||||||||||||||||||||| || |||||||
Sbjct  320  TGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTATCAATGCCACTATGGAGA  261

Query  715  CAATTAAAAGTA  726
            ||||||| ||||
Sbjct  260  CAATTAAGAGTA  249


>SRR2298573.602990 602990 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 251/260 (97%), Gaps = 1/260 (0%)
 Strand=Plus/Minus

Query  373  AGCAACAT-TTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGC  431
            ||||| || ||||||| ||||||||||||||||||||||||| | |||||||||||||||
Sbjct  260  AGCAAAATGTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAGCCCCTGGTAACAGGTGC  201

Query  432  CTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATG  491
            ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  200  CTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATG  141

Query  492  TTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCC  551
            |||||||||||||||||||||| |||||||||||||| ||||||||||||||||||||||
Sbjct  140  TTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCC  81
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Query  552  CACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGG  611
            ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct  80   CACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGG  21

Query  612  GCCAGGTACCTCTATCTTGG  631
            ||||||||||||||||||||
Sbjct  20   GCCAGGTACCTCTATCTTGG  1


 Score = 409 bits (221),  Expect = 9e-110
 Identities = 244/255 (96%), Gaps = 1/255 (0%)
 Strand=Plus/Plus

Query  373  AGC-AACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGC  431
            ||| |||||||||||| ||||||||||||||||||||||||| |||||||||||||||||
Sbjct  246  AGCAAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAGCACCTGGTAACAGGTGC  305

Query  432  CTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATG  491
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  306  CTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATG  365

Query  492  TTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCC  551
            |||||||||||||||||||||| |||||||||||||| ||||||||||||||||||||||
Sbjct  366  TTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCC  425

Query  552  CACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGG  611
            ||||||||||||||||||||||||||||||||||||| |||||  |||||||||||||||
Sbjct  426  CACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACACTGGATCTGATCTGGG  485

Query  612  GCCAGGTACCTCTAT  626
            ||  |||||||||||
Sbjct  486  GCACGGTACCTCTAT  500


>SRR2298573.583035 583035 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  395  TCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTC  454
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  1    TCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTT  60

Query  455  TAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTG  514
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  61   TAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTA  120

Query  515  CCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTAC  574
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTAC  180

Query  575  CCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGA  634
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  181  CCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGGGA  240

Query  635  CCTGGTTAAA  644
             |||||||||
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Sbjct  241  TCTGGTTAAA  250


 Score = 364 bits (197),  Expect = 2e-96
 Identities = 233/251 (93%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  609  GGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgg  668
            |||| ||||||||||||||| || || ||||||||||| ||| |||| ||||||||||||
Sbjct  500  GGGGGCAGGTACCTCTATCTGGGGGATCTGGTTAAAAAACGTTTAGTTGGCCAAACCCGG  441

Query  669  gggggATCCCCGGTTTCCTTTTATTTTATCAATGCTACAATGGAGACAATTAAAAGTATT  728
            |||||||||||||||||||||||||||||||||||  | |||||||||||||| ||||||
Sbjct  440  GGGGGATCCCCGGTTTCCTTTTATTTTATCAATGCCCCTATGGAGACAATTAAGAGTATT  381

Query  729  GCAGATATGGCGACCGGAGTGGTCAGTTCAGTTGATTCCACTATCAATGCAGTTAATGAG  788
            ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  380  GCAGATATGGCGACCGGAGTGGTCAGTTCAGTTGATTCCACTATCAATGTAGTTAATGAG  321

Query  789  AGAGTAGAAAATGTGGGCAATGAAATTGGAGGTAACCTATTAACCAAAGTAGCAGATGAT  848
            ||||| |||||||| || |||||||||||||||||  ||||||||||||| |||||||||
Sbjct  320  AGAGTGGAAAATGTAGGTAATGAAATTGGAGGTAATTTATTAACCAAAGTTGCAGATGAT  261

Query  849  GCTTCTAATGT  859
            |||||||||||
Sbjct  260  GCTTCTAATGT  250


>SRR2298573.575252 575252 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 242/247 (98%), Gaps = 0/247 (0%)
 Strand=Plus/Plus

Query  325  CTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTG  384
            ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  1    CTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTG  60

Query  385  CTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAA  444
            ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAA  120

Query  445  AGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATAC  504
            ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATAC  180

Query  505  TTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCC  564
            ||||||||| |||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  181  TTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCC  240

Query  565  CAGAAGG  571
            |||||||
Sbjct  241  CAGAAGG  247


 Score = 416 bits (225),  Expect = 6e-112
 Identities = 241/249 (97%), Gaps = 0/249 (0%)
 Strand=Plus/Minus
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Query  354   CGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACA  413
             |||||||||| ||||||||| ||||||||||||| |||||||||||||||||||||||||
Sbjct  499   CGTGTGGGAAATTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACA  440

Query  414   ACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATT  473
             || ||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  439   ACCCCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATT  380

Query  474   GGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCA  533
             |||||||||||||||||||||||||||||||||||||||| |||||||||||||| ||||
Sbjct  379   GGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCA  320

Query  534   AACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACA  593
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  319   AACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACA  260

Query  594   CTATGGATC  602
             |||||||||
Sbjct  259   CTATGGATC  251


>SRR2298573.567616 567616 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  362   AACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGG  421
             |||||||||||| ||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  1     AACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGG  60

Query  422   TAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAA  481
             |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Sbjct  61    TAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAA  120

Query  482   ACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAG  541
             |||||||||||||||||||||||||||||||| |||||||||||||| ||||||||||||
Sbjct  121   ACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAG  180

Query  542   TTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGAT  601
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  181   TTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGGGACACTATGGAT  240

Query  602   CTGATCTGGG  611
             ||||||||||
Sbjct  241   CTGATCTGGG  250


 Score = 363 bits (196),  Expect = 7e-96
 Identities = 232/250 (93%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  475   GTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAA  534
             |||||||||||||| |||||||| |||| | | | |||| |||||||||||  | | |||
Sbjct  500   GTTCTAAACCTGAGGTGTTGTGGGAGATTCCTTGGACCTACCGATCTGGTAAGAGTTCAA  441

Query  535   ACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACAC  594
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            |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||| |
Sbjct  440  ACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACCC  381

Query  595  TATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAG  654
            |||||||||||||||||||||||||||||||||||||||| ||||||||||| |||||||
Sbjct  380  TATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAG  321

Query  655  TGGGCCAAACCCggggggGATCCCCGGTTTCCTTTTATTTTATCAATGCTACAATGGAGA  714
            ||||||||||||||||||||||||||||||||||||||||||||||||| || |||||||
Sbjct  320  TGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTATCAATGCCACTATGGAGA  261

Query  715  CAATTAAAAG  724
            ||||||| ||
Sbjct  260  CAATTAAGAG  251


>SRR2298573.566690 566690 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  359  GGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACC  418
            ||||||||||||||| ||||||||||||| ||||||||||||||||||||||||||||||
Sbjct  499  GGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACC  440

Query  419  TGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTC  478
            ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  439  TGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTC  380

Query  479  TAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACAC  538
            ||||||||||||||||||||||||||||||||||| |||||||||||||| |||||||||
Sbjct  379  TAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACAC  320

Query  539  TAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATG  598
            |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct  319  TAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATG  260

Query  599  GATCTGATCT  608
            ||||||||||
Sbjct  259  GATCTGATCT  250


 Score = 425 bits (230),  Expect = 9e-115
 Identities = 242/248 (98%), Gaps = 0/248 (0%)
 Strand=Plus/Plus

Query  347  CTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAG  406
            ||||||||||||||||||||||||||| ||||||||||||| ||||||||||||||||||
Sbjct  1    CTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAG  60

Query  407  CGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTT  466
            ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  61   CGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTT  120

Query  467  TAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAG  526
            ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  121  TAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAG  180
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Query  527  TACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACA  586
            || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACA  240

Query  587  AGTGACAC  594
            || |||||
Sbjct  241  AGCGACAC  248


>SRR2298573.556526 556526 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 257/268 (96%), Gaps = 5/268 (2%)
 Strand=Plus/Minus

Query  517  GATCTGGTA-GTACT---GCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGT  572
            |||| |||| |||||   ||||||||||||||||||||||||||||||||||||||||||
Sbjct  267  GATC-GGTAGGTACTAAGGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGT  209

Query  573  ACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGT  632
            |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  208  ACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGT  149

Query  633  GACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCggggggGATCCCCGGTTTCCTTTTAT  692
            || ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  148  GATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTAT  89

Query  693  TTTATCAATGCTACAATGGAGACAATTAAAAGTATTGCAGATATGGCGACCGGAGTGGTC  752
            ||||||||||| || |||||||||||||| ||||||||||||||||||||||||||||||
Sbjct  88   TTTATCAATGCCACTATGGAGACAATTAAGAGTATTGCAGATATGGCGACCGGAGTGGTC  29

Query  753  AGTTCAGTTGATTCCACTATCAATGCAG  780
            ||||||||||||||||||||||||||||
Sbjct  28   AGTTCAGTTGATTCCACTATCAATGCAG  1


 Score = 381 bits (206),  Expect = 2e-101
 Identities = 230/242 (95%), Gaps = 0/242 (0%)
 Strand=Plus/Plus

Query  504  CTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGC  563
            |||||||||| |||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  251  CTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGC  310

Query  564  CCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTC  623
            ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  311  CCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTC  370

Query  624  TATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCggggggGATCCCCGGTT  683
            ||||||||||| ||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  371  TATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTT  430

Query  684  TCCTTTTATTTTATCAATGCTACAATGGAGACAATTAAAAGTATTGCAGATATGGCGACC  743
            ||||||||||||||||||||  | ||||||||||||||| | |||||||| ||||| |||
Sbjct  431  TCCTTTTATTTTATCAATGCCCCTATGGAGACAATTAAAGGAATTGCAGAAATGGCAACC  490

Query  744  GG  745
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            ||
Sbjct  491  GG  492


>SRR2298573.543314 543314 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  325  CTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTG  384
            ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  1    CTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTG  60

Query  385  CTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAA  444
            ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAA  120

Query  445  AGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATAC  504
            ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATAC  180

Query  505  TTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCC  564
            ||||||||| |||||||||||||| ||||||||||||||||||||||||||| |||||||
Sbjct  181  TTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAGGGATGCC  240

Query  565  CAGAAGGTAC  574
            ||||||||||
Sbjct  241  CAGAAGGTAC  250


 Score = 411 bits (222),  Expect = 3e-110
 Identities = 240/249 (96%), Gaps = 0/249 (0%)
 Strand=Plus/Minus

Query  354  CGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACA  413
            |||| ||||||||||||||| ||||||||||||| |||||||||||||||||||||||||
Sbjct  499  CGTGGGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACA  440

Query  414  ACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATT  473
            |||||||||||||||| ||||||||||||||||||||||| |||||||||||||||||||
Sbjct  439  ACACCTGGTAACAGGTCCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATT  380

Query  474  GGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCA  533
            |||||||||||||||||||||||||||||||||||||||| |||||||||||||| ||||
Sbjct  379  GGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCA  320

Query  534  AACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACA  593
            ||||||||||||||||||||||| ||||||||||||||||||||||||||||||| ||||
Sbjct  319  AACACTAGTTGTAAGGCCCACGAGGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACA  260

Query  594  CTATGGATC  602
            |||||||||
Sbjct  259  CTATGGATC  251


>SRR2298573.528592 528592 length=500
Length=500
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 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  431  CCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGAT  490
            ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  1    CCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGAT  60

Query  491  GTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGC  550
            ||||||||||||||||||||||| |||||||||||||| |||||||||||||||||||||
Sbjct  61   GTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGC  120

Query  551  CCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGG  610
            |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Sbjct  121  CCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGG  180

Query  611  GGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggg  670
            |||||||||||||||||||||||| ||||||||||| |||||||||||||||||||||||
Sbjct  181  GGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGG  240

Query  671  gggATCCCCG  680
            ||||||||||
Sbjct  241  GGGATCCCCG  250


 Score = 401 bits (217),  Expect = 2e-107
 Identities = 239/250 (96%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  511  CCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAG  570
            |||||||||||||||||| ||||| | |||||||||||||||| ||||||||||||||||
Sbjct  500  CCTGCCGATCTGGTAGTAGTGCAACCCCTAGTTGTAAGGCCCATGAAGGATGCCCAGAAG  441

Query  571  GTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTG  630
            |||||||| ||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  440  GTACCCATTGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTG  381

Query  631  GTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTT  690
            |||| ||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  380  GTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTT  321

Query  691  ATTTTATCAATGCTACAATGGAGACAATTAAAAGTATTGCAGATATGGCGACCGGAGTGG  750
            ||||||||||||| || |||||||||||||| ||||||||||||||||||||||||||||
Sbjct  320  ATTTTATCAATGCCACTATGGAGACAATTAAGAGTATTGCAGATATGGCGACCGGAGTGG  261

Query  751  TCAGTTCAGT  760
            ||||||||||
Sbjct  260  TCAGTTCAGT  251


>SRR2298573.525005 525005 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 277/299 (93%), Gaps = 2/299 (1%)
 Strand=Plus/Plus

Query  749   GGTCAGTTCAGTTGATTCCACTATCAATGCAGTTAATGAGAGAGTAGAAAATGTGGGCAA  808
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             || ||||| |||||||||||||||||||| ||||||||||||||| |||||||| || ||
Sbjct  1     GGACAGTTGAGTTGATTCCACTATCAATGTAGTTAATGAGAGAGTGGAAAATGTAGGTAA  60

Query  809   TGAAATTGGAGGTAACCTATTAACCAAAGTAGCAGATGATGCTTCTAATGTGCTTGGACC  868
             |||||||||||||||  ||||||||||||| ||||||||||||||||||||||| |||||
Sbjct  61    TGAAATTGGAGGTAATTTATTAACCAAAGTTGCAGATGATGCTTCTAATGTGCTCGGACC  120

Query  869   AAATTGTTATGCTACAACAGCTGAACCAGAGAACAAAGATGTGGTACAGGCAACCACAAC  928
             |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Sbjct  121   AAATTGTTATGCTACAACAGCTGAACCAGAGAACAAAGATGTAGTACAGGCAACCACAAC  180

Query  929   TGTTAATACAACCAATTTGACACAACATCCCTCAGCACCAACAATGCCCTTCACTCCTGA  988
             |||||| || |||||  |||||||||||||||||||||||| ||||||||||||||| ||
Sbjct  181   TGTTAACACGACCAACCTGACACAACATCCCTCAGCACCAAAAATGCCCTTCACTCCGGA  240

Query  989   TTTCTCCA--ATGTTGATACATTCCACTCAATGGCATATGACATCACCACAGGGGAGAA  1045
             |||||||   ||||||||||||||||||||||||||||||| |||||||| ||||||||
Sbjct  241   TTTCTCCCCGATGTTGATACATTCCACTCAATGGCATATGATATCACCACTGGGGAGAA  299


 Score = 303 bits (164),  Expect = 4e-78
 Identities = 230/261 (88%), Gaps = 8/261 (3%)
 Strand=Plus/Minus

Query  790   GAGTAGAAAATGTGGGCAATGAAATTGGAGGTAACCTATTAACCAAAGTAGCAGATGATG  849
             |||| |||||||| || |||||| ||||||||||  ||||||||||||| ||||||||||
Sbjct  499   GAGTGGAAAATGTAGGTAATGAATTTGGAGGTAATTTATTAACCAAAGTTGCAGATGATG  440

Query  850   CTTCTAATGTGCTTGGACCAAATTGTTATGCTACAACAGCTGAACCAGAGAACAAAGATG  909
             ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  439   CTTCTAATGTGCTCGGACCAAATTGTTATGCTACAACAGCTGAACCAGAGAACAAAGATG  380

Query  910   TGGTACAGGCAACCACAACTGTTAATACAACCAATTTGACACAACATCCCTCAGCACCAA  969
             | ||||||||||||||||||||||| || ||||   ||||||||||||||||||||||||
Sbjct  379   TAGTACAGGCAACCACAACTGTTAACACGACCACCCTGACACAACATCCCTCAGCACCAA  320

Query  970   CAATGCCCTTCACTCCTGATTTCTCCA-A-TGTTGATA-CAT-T-CCACTCAATGGCATA  1024
             ||||||||||||||||||||||||||  | || ||||| ||| | ||| | | ||| | |
Sbjct  319   CAATGCCCTTCACTCCTGATTTCTCCCCAGTGGTGATATCATATGCCATTGAGTGG-A-A  262

Query  1025  TGACATCACCACAGGGGAGAA  1045
             ||  |||| ||  ||||||||
Sbjct  261   TGT-ATCAACATCGGGGAGAA  242


>SRR2298573.524182 524182 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  347  CTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAG  406
            ||||||||||||||||||||||||||| ||||||||||||| ||||||||||||||||||
Sbjct  1    CTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAG  60

Query  407  CGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTT  466
            ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  61   CGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTT  120
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Query  467   TAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAG  526
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  121   TAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAG  180

Query  527   TACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACA  586
             || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   TAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACA  240

Query  587   AGTGACACTA  596
             || |||||||
Sbjct  241   AGCGACACTA  250


 Score = 412 bits (223),  Expect = 7e-111
 Identities = 241/250 (96%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  350   GTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGG  409
             |||||||||||||||||||||||| |||||||| |||| ||||| |||||||||||||||
Sbjct  500   GTGACGTGTGGGAACTTATTGGAAACAACATTTGGCTGTAAAGCTTCCTATTGCCAGCGG  441

Query  410   AACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAG  469
             |||||| ||||||||||||||||||||||||||||||||||||| |||||||||||||||
Sbjct  440   AACAACCCCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAG  381

Query  470   GATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTAC  529
             |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  380   GATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAG  321

Query  530   TGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGT  589
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  320   TGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGC  261

Query  590   GACACTATGG  599
             ||||||||||
Sbjct  260   GACACTATGG  251


>SRR2298573.521950 521950 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  510   ACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAA  569
             |||| |||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  250   ACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAA  309

Query  570   GGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTT  629
             ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  310   GGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTT  369

Query  630   GGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTT  689
             ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  370   GGTGACCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTT  429

Query  690   TATTTTATCAATGCTACAATGGAGACAATTAAAAGTATTGCAGATATGGCGACCGGAGTG  749
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            |||||||||||||| || ||||||||||||||||||||||||||||||||||||||||||
Sbjct  430  TATTTTATCAATGCCACTATGGAGACAATTAAAAGTATTGCAGATATGGCGACCGGAGTG  489

Query  750  GTCAGTTCAG  759
            ||||||||||
Sbjct  490  GTCAGTTCAG  499


 Score = 420 bits (227),  Expect = 4e-113
 Identities = 250/261 (96%), Gaps = 1/261 (0%)
 Strand=Plus/Minus

Query  517  GATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCC  576
            |||| |||||   |||||||  ||||||||||||||||||||||||||||||||||||||
Sbjct  260  GATC-GGTAGGTGTGCAAACCTTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCC  202

Query  577  ATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACC  636
            |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  201  ATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACC  142

Query  637  TGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTTTA  696
            |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  141  TGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTA  82

Query  697  TCAATGCTACAATGGAGACAATTAAAAGTATTGCAGATATGGCGACCGGAGTGGTCAGTT  756
            ||||||| || |||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  81   TCAATGCCACTATGGAGACAATTAAGAGTATTGCAGATATGGCGACCGGAGTGGTCAGTT  22

Query  757  CAGTTGATTCCACTATCAATG  777
            |||||||||||||||||||||
Sbjct  21   CAGTTGATTCCACTATCAATG  1


>SRR2298573.521747 521747 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  451  GGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTA  510
            ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTA  60

Query  511  CCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAG  570
            ||| |||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAG  120

Query  571  GTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTG  630
            |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTG  180

Query  631  GTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTT  690
            |||| ||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTT  240

Query  691  ATTTTATCAA  700
            ||||||||||
Sbjct  241  ATTTTATCAA  250
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 Score = 407 bits (220),  Expect = 3e-109
 Identities = 243/254 (96%), Gaps = 1/254 (0%)
 Strand=Plus/Minus

Query  476  TTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAA  535
            |||||||||||||||||||| |||||| |||||||||| |||||||||||||| ||||||
Sbjct  500  TTCTAAACCTGAGATGTTGTTGAAGATTCTTAGTACCTACCGATCTGGTAGTAGTGCAAA  441

Query  536  CACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACT  595
            ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  440  CACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACT  381

Query  596  ATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGT  655
            ||||||||||||||||||||||||||||||||||||||| ||||||||||| ||||||||
Sbjct  380  ATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGT  321

Query  656  GGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTTTATCAATGCTACAATGGAGAC  715
            |||||||||||||||||||||||||||||||||||||||||||||||| || ||||||||
Sbjct  320  GGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTATCAATGCCACTATGGAGAC  261

Query  716  AATTAAAAGTATTG  729
            |||||| ||| |||
Sbjct  260  AATTAAGAGT-TTG  248


>SRR2298573.521506 521506 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  396  CCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCT  455
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  1    CCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTT  60

Query  456  AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGC  515
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  61   AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTAC  120

Query  516  CGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACC  575
            ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACC  180

Query  576  CATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGAC  635
            ||||||||||||| |||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  181  CATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGGGAT  240

Query  636  CTGGTTAAAA  645
            ||||||||||
Sbjct  241  CTGGTTAAAA  250


 Score = 416 bits (225),  Expect = 6e-112
 Identities = 241/249 (97%), Gaps = 0/249 (0%)
 Strand=Plus/Minus
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Query  417   CCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGT  476
             ||||||||| ||| ||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct  499   CCTGGTAACGGGTTCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGT  440

Query  477   TCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAAC  536
             ||||||||||||||||||||||||||||||||||||| |||||||||||||| |||||||
Sbjct  439   TCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAAC  380

Query  537   ACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTA  596
             |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  379   ACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTA  320

Query  597   TGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTG  656
             |||||||||||||||||||||||||||||||||||||| ||||||||||| |||||||||
Sbjct  319   TGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTG  260

Query  657   GGCCAAACC  665
             |||||||||
Sbjct  259   GGCCAAACC  251


>SRR2298573.502605 502605 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  302   GACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGG  361
             |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  250   GACCTTATGCTCACACCGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGG  191

Query  362   AACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGG  421
             |||||||||||| ||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  190   AACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGG  131

Query  422   TAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAA  481
             |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Sbjct  130   TAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAA  71

Query  482   ACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAG  541
             |||||||||||||||||||||||||||||||| |||||||||||||| ||||||||||||
Sbjct  70    ACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAG  11

Query  542   TTGTAAGGCC  551
             ||||||||||
Sbjct  10    TTGTAAGGCC  1


 Score = 353 bits (191),  Expect = 4e-93
 Identities = 230/249 (92%), Gaps = 1/249 (0%)
 Strand=Plus/Plus

Query  167   GTTGAAGGCAACTTGCAATAAAATGAGTGGGAACAAGACGCTTAAAGCATGGTGTGAACT  226
             |||||||||||||||||||||||||||||| |||||||||||||||||||||||| |  |
Sbjct  252   GTTGAAGGCAACTTGCAATAAAATGAGTGGAAACAAGACGCTTAAAGCATGGTGTAATTT  311

Query  227   AAC-TTTCTAACCCACATTTTGTGTGGGGTGGCAGATGGCGTGCCATAATTCTACTAGTG  285
             | | ||||||||||||||||||||||||||||||||||||||||||||  |||| |||||
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Sbjct  312  AGCTTTTCTAACCCACATTTTGTGTGGGGTGGCAGATGGCGTGCCATAGCTCTATTAGTG  371

Query  286  AGATACCACGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACG  345
            |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  372  AGATACCATGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACG  431

Query  346  TCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCA  405
             |||||||||| |||||||||||||||| ||||||||||| | ||||||||| || ||  
Sbjct  432  GCTGGTGACGTTTGGGAACTTATTGGAAACAACATTTTGCGGTAAAGCATCCAATGGCAC  491

Query  406  GCGGAACAA  414
            |||||||||
Sbjct  492  GCGGAACAA  500


>SRR2298573.502479 502479 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  322  ATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATT  381
            |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  1    ATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATT  60

Query  382  TTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCC  441
            |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCC  120

Query  442  AAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGA  501
            |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGA  180

Query  502  TACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGAT  561
            |||||||||||| |||||||||||||| ||||||||||||| ||||||||||||||||||
Sbjct  181  TACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTGGTAAGGCCCACGAAGGAT  240

Query  562  GCCCAGAAGG  571
            ||||||||||
Sbjct  241  GCCCAGAAGG  250


 Score = 372 bits (201),  Expect = 1e-98
 Identities = 233/249 (94%), Gaps = 0/249 (0%)
 Strand=Plus/Minus

Query  380  TTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGG  439
            ||||| || ||||||||| |||||| ||||||  || ||| | ||| ||| |||||||||
Sbjct  499  TTTTGGTGTAAAGCATCCCATTGCCCGCGGAAACACCCCTTGGAACCGGTTCCTCTGGGG  440

Query  440  CCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAA  499
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  439  CCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAA  380

Query  500  GATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGG  559
            |||||||||||||| |||||||||||||| ||||||||||||||||||||||||||||||
Sbjct  379  GATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGG  320
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Query  560   ATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTA  619
             ||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||||||
Sbjct  319   ATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTAAGGATCTGATCTGGGGCCAGGTA  260

Query  620   CCTCTATCT  628
             |||||||||
Sbjct  259   CCTCTATCT  251


>SRR2298573.499345 499345 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  451   GGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTA  510
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTA  60

Query  511   CCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAG  570
             ||| |||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  61    CCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAG  120

Query  571   GTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTG  630
             |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  121   GTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTG  180

Query  631   GTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTT  690
             |||| ||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   GTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTT  240

Query  691   ATTTTATCAA  700
             ||||||||||
Sbjct  241   ATTTTATCAA  250


 Score = 412 bits (223),  Expect = 7e-111
 Identities = 241/250 (96%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  499   AGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAG  558
             ||||||||||||||| |||||||||||||| ||||||| |||||||||||||||||||||
Sbjct  500   AGATACTTAGTACCTTCCGATCTGGTAGTAGTGCAAACTCTAGTTGTAAGGCCCACGAAG  441

Query  559   GATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGT  618
             |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Sbjct  440   GATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGT  381

Query  619   ACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCC  678
             |||||||||||||||| ||||||||||| |||||||||||||||||||||||||||||||
Sbjct  380   ACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCC  321

Query  679   CGGTTTCCTTTTATTTTATCAATGCTACAATGGAGACAATTAAAAGTATTGCAGATATGG  738
             ||||||||||||||||||||||||| || |||||||||||||| ||||||||||||||||
Sbjct  320   CGGTTTCCTTTTATTTTATCAATGCCACTATGGAGACAATTAAGAGTATTGCAGATATGG  261

Query  739   CGACCGGAGT  748
             ||||||||||
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Sbjct  260  CGACCGGAGT  251


>SRR2298573.484755 484755 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  451  GGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTA  510
            ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTA  60

Query  511  CCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAG  570
            ||| |||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAG  120

Query  571  GTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTG  630
            |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTG  180

Query  631  GTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTT  690
            |||| ||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTT  240

Query  691  ATTTTATCAA  700
            ||||||||||
Sbjct  241  ATTTTATCAA  250


 Score = 381 bits (206),  Expect = 2e-101
 Identities = 236/251 (94%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  475  GTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAA  534
            ||| ||||||||||||||| ||||||||||||||| ||| ||||||| |||||| | |||
Sbjct  500  GTTTTAAACCTGAGATGTTTTGGAAGATACTTAGTCCCTACCGATCTTGTAGTAGTTCAA  441

Query  535  ACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACAC  594
            ||||||||||||||||||| |||||||||||||||||||||||||||||||||| ||| |
Sbjct  440  ACACTAGTTGTAAGGCCCAAGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACTC  381

Query  595  TATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAG  654
            |||||||||||||||||||||||||||||||||||||||| ||||||||||| |||||||
Sbjct  380  TATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAG  321

Query  655  TGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTTTATCAATGCTACAATGGAGA  714
            ||||||||||||||||||||||||||||||||||||||||||||||||| || |||||||
Sbjct  320  TGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTATCAATGCCACTATGGAGA  261

Query  715  CAATTAAAAGT  725
            ||||||| |||
Sbjct  260  CAATTAAGAGT  250


>SRR2298573.477415 477415 length=500
Length=500
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 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  451  GGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTA  510
            ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTA  60

Query  511  CCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAG  570
            ||| |||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAG  120

Query  571  GTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTG  630
            |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTG  180

Query  631  GTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTT  690
            |||| ||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTT  240

Query  691  ATTTTATCAA  700
            ||||||||||
Sbjct  241  ATTTTATCAA  250


 Score = 350 bits (189),  Expect = 6e-92
 Identities = 220/235 (94%), Gaps = 2/235 (1%)
 Strand=Plus/Minus

Query  530  TGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGT  589
            ||||| | || |||||| |||||||||||||||||  ||||||||||||||||||||||
Sbjct  478  TGCAACCCCTTGTTGTATGGCCCACGAAGGATGCCACGAAGGTACCCATAGGTAACAAGC  419

Query  590  GACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCG  649
            ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||| ||
Sbjct  418  GACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACG  359

Query  650  TCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTTTATCAATGCTACAAT  709
            |||||||||||||||||||||||||||||||||||||||||||||||||||||| || ||
Sbjct  358  TCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTATCAATGCCACTAT  299

Query  710  GGAGACAATTAAAAGTATTGCAGATATGGCGACCGGAGTGGTCAGTTCAGTTGAT  764
            |||||||||||| ||||||||||||||||||||||||||||| |||||  |||||
Sbjct  298  GGAGACAATTAAGAGTATTGCAGATATGGCGACCGGAGTGGTAAGTTC--TTGAT  246


>SRR2298573.477266 477266 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  422  TAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAA  481
            |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Sbjct  250  TAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAA  191

Query  482  ACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAG  541
            |||||||||||||||||||||||||||||||| |||||||||||||| ||||||||||||
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Sbjct  190  ACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAG  131

Query  542  TTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGAT  601
            ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  130  TTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGAT  71

Query  602  CTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCA  661
            ||||||||||||||||||||||||||||||||| ||||||||||| ||||||||||||||
Sbjct  70   CTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCA  11

Query  662  AACCCggggg  671
            ||||||||||
Sbjct  10   AACCCGGGGG  1


 Score = 383 bits (207),  Expect = 6e-102
 Identities = 227/237 (96%), Gaps = 0/237 (0%)
 Strand=Plus/Plus

Query  230  TTTCTAACCCACATTTTGTGTGGGGTGGCAGATGGCGTGCCATAATTCTACTAGTGAGAT  289
            ||||||||||||||||||||||||||||||||||||||||||||  |||| |||||||||
Sbjct  264  TTTCTAACCCACATTTTGTGTGGGGTGGCAGATGGCGTGCCATAGCTCTATTAGTGAGAT  323

Query  290  ACCACGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTG  349
            |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  324  ACCATGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTG  383

Query  350  GTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGG  409
            | |||||||||||||||||||||| ||||||||||||| |||||||||||||||||||||
Sbjct  384  GGGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGG  443

Query  410  AACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTT  466
            ||||||||||||||||||| ||| |||||||||||||||||||| ||||||||||||
Sbjct  444  AACAACACCTGGTAACAGGGGCCCCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTT  500


>SRR2298573.474177 474177 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  350  GTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGG  409
            |||||||||||||||||||||||| ||||||||||||| |||||||||||||||||||||
Sbjct  500  GTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGG  441

Query  410  AACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAG  469
            |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Sbjct  440  AACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAG  381

Query  470  GATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTAC  529
            |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  380  GATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAG  321

Query  530  TGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGT  589
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  320  TGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGC  261
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Query  590  GACACTATGG  599
            ||||||||||
Sbjct  260  GACACTATGG  251


 Score = 416 bits (225),  Expect = 6e-112
 Identities = 239/246 (97%), Gaps = 0/246 (0%)
 Strand=Plus/Plus

Query  283  GTGAGATACCACGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAG  342
            ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTGAGATACCATGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAG  60

Query  343  ACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTG  402
            ||||||||||||||||||||||||||||||| ||||||||||||| ||||||||||||||
Sbjct  61   ACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTG  120

Query  403  CCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAAC  462
            ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  121  CCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAAC  180

Query  463  CCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTG  522
            ||||||||||||||||||||||||||||||||||||| |||||||| |||| ||||||||
Sbjct  181  CCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAAATACTTAGAACCTACCGATCTG  240

Query  523  GTAGTA  528
            ||||||
Sbjct  241  GTAGTA  246


>SRR2298573.472684 472684 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  298  TGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTG  357
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTG  60

Query  358  TGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACAC  417
            |||||||||||||||| ||||||||||||| |||||||||||||||||||||||||||||
Sbjct  61   TGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACAC  120

Query  418  CTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTT  477
            |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct  121  CTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTT  180

Query  478  CTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACA  537
            |||||||||||||||||||||||||||||||||||| |||||||||||||| |||||| |
Sbjct  181  CTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAAAA  240

Query  538  CTAGTTGTAA  547
            ||||||||||
Sbjct  241  CTAGTTGTAA  250


 Score = 385 bits (208),  Expect = 2e-102
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 Identities = 236/250 (94%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  465   TTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGT  524
             |||||||||||||| || |||| | ||||||||||||| |||||||||| ||||||||||
Sbjct  500   TTTAGGATTGGTTCAAACCCTGGGGTGTTGTGGAAGATTCTTAGTACCTACCGATCTGGT  441

Query  525   AGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAA  584
             |||| |||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct  440   AGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATACCCAGAAGGTACCCATAGGTAA  381

Query  585   CAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAA  644
             |||| ||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct  380   CAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAA  321

Query  645   AAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTTTATCAATGCT  704
             || ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  320   AAACGTCTAGTGGGCCAAACCCTGGGGGGATCCCCGGTTTCCTTTTATTTTATCAATGCC  261

Query  705   ACAATGGAGA  714
             || |||||||
Sbjct  260   ACTATGGAGA  251


>SRR2298573.471442 471442 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  451   GGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTA  510
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTA  60

Query  511   CCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAG  570
             ||| |||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  61    CCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAG  120

Query  571   GTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTG  630
             |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  121   GTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTG  180

Query  631   GTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTT  690
             |||| ||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   GTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTT  240

Query  691   ATTTTATCAA  700
             ||||||||||
Sbjct  241   ATTTTATCAA  250


 Score = 374 bits (202),  Expect = 3e-99
 Identities = 234/250 (94%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  624   TATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTT  683
             ||||||||||| ||||||||||| ||||||| ||||| ||||||||||||||||||||||
Sbjct  500   TATCTTGGTGATCTGGTTAAAAAACGTCTAGGGGGCCCAACCCGGGGGGGATCCCCGGTT  441
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Query  684  TCCTTTTATTTTATCAATGCTACAATGGAGACAATTAAAAGTATTGCAGATATGGCGACC  743
            ||||||||||||| |||||| || |||||||||||||| |||||||||||||||||||||
Sbjct  440  TCCTTTTATTTTAACAATGCCACTATGGAGACAATTAAGAGTATTGCAGATATGGCGACC  381

Query  744  GGAGTGGTCAGTTCAGTTGATTCCACTATCAATGCAGTTAATGAGAGAGTAGAAAATGTG  803
            |||||||||||||||||||||||||||||||||| ||||||||||||||| ||||||||
Sbjct  380  GGAGTGGTCAGTTCAGTTGATTCCACTATCAATGTAGTTAATGAGAGAGTGGAAAATGTA  321

Query  804  GGCAATGAAATTGGAGGTAACCTATTAACCAAAGTAGCAGATGATGCTTCTAATGTGCTT  863
            || |||||||||||||||||  ||||||||||||| |||||||||||||||||||||||
Sbjct  320  GGTAATGAAATTGGAGGTAATTTATTAACCAAAGTTGCAGATGATGCTTCTAATGTGCTC  261

Query  864  GGACCAAATT  873
            ||||||||||
Sbjct  260  GGACCAAATT  251


>SRR2298573.470122 470122 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  437  GGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTG  496
            ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  250  GGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTG  191

Query  497  GAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGA  556
            ||||||||||||||||| |||||||||||||| |||||||||||||||||||||||||||
Sbjct  190  GAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGA  131

Query  557  AGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAG  616
            |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Sbjct  130  AGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAG  71

Query  617  GTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGCCAAACCCgggggggATC  676
            |||||||||||||||||| ||||||||||| ||||||||||||||||||||||||||||
Sbjct  70   GTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGCCAAACCCGGGGGGGATC  11

Query  677  CCCGGTTTCC  686
            ||||||||||
Sbjct  10   CCCGGTTTCC  1


 Score = 399 bits (216),  Expect = 6e-107
 Identities = 234/243 (96%), Gaps = 0/243 (0%)
 Strand=Plus/Plus

Query  389  AAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCC  448
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  253  AAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCC  312

Query  449  AAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAG  508
            ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  313  AAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAG  372

Query  509  TACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGA  568
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                ||||| |||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct  373  TACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGA  432

Query  569  AGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCT  628
            ||||||||| ||| |||||| ||||||||||| | |||||||||||||||||||||| ||
Sbjct  433  AGGTACCCAAAGGAAACAAGCGACACTATGGACCGGATCTGGGGCCAGGTACCTCTACCT  492

Query  629  TGG  631
            |||
Sbjct  493  TGG  495


>SRR2298573.466202 466202 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  443  AAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGAT  502
            ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  250  AAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGAT  191

Query  503  ACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATG  562
            ||||||||||| |||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  190  ACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATG  131

Query  563  CCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCT  622
            |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  130  CCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCT  71

Query  623  CTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGT  682
            |||||||||||| ||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  70   CTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGT  11

Query  683  TTCCTTTTAT  692
            ||||||||||
Sbjct  10   TTCCTTTTAT  1


 Score = 429 bits (232),  Expect = 7e-116
 Identities = 242/247 (98%), Gaps = 0/247 (0%)
 Strand=Plus/Plus

Query  375  CAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTC  434
            ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  251  CAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTC  310

Query  435  TGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTG  494
            ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  311  TGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTG  370

Query  495  TGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCAC  554
            ||||||||||||||||||| |||||||||||||| |||||||||||||||||||||||||
Sbjct  371  TGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCAC  430

Query  555  GAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCC  614
            |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  431  GAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCC  490
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Query  615  AGGTACC  621
            |||||||
Sbjct  491  AGGTACC  497


>SRR2298573.464947 464947 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 242/247 (98%), Gaps = 0/247 (0%)
 Strand=Plus/Plus

Query  319  GCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAAC  378
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  1    GCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAAC  60

Query  379  ATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGG  438
            ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGG  120

Query  439  GCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGA  498
            ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGA  180

Query  499  AGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAG  558
            ||||||||||||||| |||||||||||||| |||||||||||||||||||||||||||||
Sbjct  181  AGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAG  240

Query  559  GATGCCC  565
            |||||||
Sbjct  241  GATGCCC  247


 Score = 368 bits (199),  Expect = 2e-97
 Identities = 229/244 (94%), Gaps = 0/244 (0%)
 Strand=Plus/Minus

Query  352  GACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAA  411
            |||||| ||||| ||||||||| ||||||||||||| ||||| |||||| ||||||||||
Sbjct  493  GACGTGGGGGAATTTATTGGAAACAACATTTTGCTGTAAAGCTTCCTATGGCCAGCGGAA  434

Query  412  CAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGA  471
            |||||||||| |||||||||||||||||||||||||||| || |||||| ||||||||||
Sbjct  433  CAACACCTGGGAACAGGTGCCTCTGGGGCCAAAAGCCAATGTTTAACAAGCCCTTTAGGA  374

Query  472  TTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTG  531
            ||||||||||||||||||||||||||||||| |||||||||| |||||||||||||| ||
Sbjct  373  TTGGTTCTAAACCTGAGATGTTGTGGAAGATCCTTAGTACCTACCGATCTGGTAGTAGTG  314

Query  532  CAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGA  591
            |||||||||||||||||||||||||||||||||| |||||||||||||||||||||| ||
Sbjct  313  CAAACACTAGTTGTAAGGCCCACGAAGGATGCCCTGAAGGTACCCATAGGTAACAAGCGA  254

Query  592  CACT  595
            ||||
Sbjct  253  CACT  250
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>SRR2298573.460111 460111 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  444  AAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATA  503
            |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  250  AAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATA  191

Query  504  CTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGC  563
            |||||||||| |||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  190  CTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGC  131

Query  564  CCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTC  623
            ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  130  CCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTC  71

Query  624  TATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTT  683
            ||||||||||| ||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  70   TATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTT  11

Query  684  TCCTTTTATT  693
            ||||||||||
Sbjct  10   TCCTTTTATT  1


 Score = 396 bits (214),  Expect = 7e-106
 Identities = 238/250 (95%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  372  AAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGC  431
            || ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  251  AAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGC  310

Query  432  CTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATG  491
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  311  CTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATG  370

Query  492  TTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCC  551
            |||||||||||||||||||||| |||||||||||||| ||||||||||||||||||||||
Sbjct  371  TTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCC  430

Query  552  CACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGG  611
            |||||||||||||||||||| ||||||||| |||||| | ||| ||||| |||| |||||
Sbjct  431  CACGAAGGATGCCCAGAAGGAACCCATAGGAAACAAGCGCCACCATGGACCTGACCTGGG  490

Query  612  GCCAGGTACC  621
            ||||||||||
Sbjct  491  GCCAGGTACC  500


>SRR2298573.445246 445246 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus
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Query  445  AGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATAC  504
            ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    AGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATAC  60

Query  505  TTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCC  564
            ||||||||| |||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  61   TTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCC  120

Query  565  CAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCT  624
            |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  121  CAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCT  180

Query  625  ATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTT  684
            |||||||||| ||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  181  ATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTT  240

Query  685  CCTTTTATTT  694
            ||||||||||
Sbjct  241  CCTTTTATTT  250


 Score = 407 bits (220),  Expect = 3e-109
 Identities = 240/250 (96%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  540  AGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGG  599
            |||||||||||||| | |||||||||||||||||||||||||||||||| ||| ||||||
Sbjct  499  AGTTGTAAGGCCCAAGGAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACCCTATGG  440

Query  600  ATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGC  659
            ||||||||||||||||||||||||||||||||||| ||||||||||| ||||||||||||
Sbjct  439  ATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGC  380

Query  660  CAAACCCgggggggATCCCCGGTTTCCTTTTATTTTATCAATGCTACAATGGAGACAATT  719
            |||||||||||||||||||||||||||||||||||||||||||| || ||||||||||||
Sbjct  379  CAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTATCAATGCCACTATGGAGACAATT  320

Query  720  AAAAGTATTGCAGATATGGCGACCGGAGTGGTCAGTTCAGTTGATTCCACTATCAATGCA  779
            || ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  319  AAGAGTATTGCAGATATGGCGACCGGAGTGGTCAGTTCAGTTGATTCCACTATCAATGTA  260

Query  780  GTTAATGAGA  789
            ||||||||||
Sbjct  259  GTTAATGAGA  250


>SRR2298573.439597 439597 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  369  TGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGG  428
            ||||| ||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  250  TGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGG  191

Query  429  TGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAG  488
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            ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  190  TGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAG  131

Query  489  ATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAG  548
            ||||||||||||||||||||||||| |||||||||||||| |||||||||||||||||||
Sbjct  130  ATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAG  71

Query  549  GCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCT  608
            |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  70   GCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCT  11

Query  609  GGGGCCAGGT  618
            ||||||||||
Sbjct  10   GGGGCCAGGT  1


 Score = 427 bits (231),  Expect = 3e-115
 Identities = 243/249 (98%), Gaps = 0/249 (0%)
 Strand=Plus/Plus

Query  333  AGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAG  392
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||||| ||||
Sbjct  250  AGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAG  309

Query  393  CATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGG  452
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  310  CATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGG  369

Query  453  TCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACC  512
            | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  370  TTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACC  429

Query  513  TGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGT  572
            | |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  430  TACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGA  489

Query  573  ACCCATAGG  581
            |||||||||
Sbjct  490  ACCCATAGG  498


>SRR2298573.434018 434018 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  313  CACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGA  372
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGA  60

Query  373  AGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCC  432
            | ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCC  120

Query  433  TCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGT  492
            ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  121  TCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGT  180
```

```
Query  493  TGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCC  552
            ||||||||||||||||||||| |||||||||||||| ||||||||| |||||||||||||
Sbjct  181  TGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACAAGTTGTAAGGCCC  240

Query  553  ACGAAGGATG  562
            ||||||||||
Sbjct  241  ACGAAGGATG  250


 Score = 407 bits (220),  Expect = 3e-109
 Identities = 240/250 (96%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  337  TGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATC  396
            |||| | ||| |||||||||| ||||||||||||||| ||||||||||||| ||||||||
Sbjct  500  TGTGGGGCGTTTGGTGACGTGGGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATC  441

Query  397  CTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTA  456
            ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||| ||
Sbjct  440  CTATTGCCAGCGGAACAACCCCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTA  381

Query  457  ACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCC  516
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  380  ACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACC  321

Query  517  GATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCC  576
            |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  320  GATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCC  261

Query  577  ATAGGTAACA  586
            ||||||||||
Sbjct  260  ATAGGTAACA  251


>SRR2298573.432649 432649 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  377  ACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTG  436
            ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    ACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTG  60

Query  437  GGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTG  496
            ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTG  120

Query  497  GAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGA  556
            ||||||||||||||||| |||||||||||||| |||||||||||||||||||||||||||
Sbjct  121  GAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGA  180

Query  557  AGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAG  616
            |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Sbjct  181  AGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAG  240

Query  617  GTACCTCTAT  626
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            | ||||||||
Sbjct  241  GAACCTCTAT  250


 Score = 407 bits (220),  Expect = 3e-109
 Identities = 241/251 (96%), Gaps = 1/251 (0%)
 Strand=Plus/Minus

Query  444  AAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATA  503
            |||| ||||| ||||||||||||||||||||||||||| |||||||| ||||||||||||
Sbjct  500  AAGCAAAGGTTTAACAAACCCTTTAGGATTGGTTCTAACCCTGAGATTTTGTGGAAGATA  441

Query  504  CTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGC  563
            |||||||||| |||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  440  CTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGC  381

Query  564  CCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTC  623
            ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  380  CCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTC  321

Query  624  TATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTT  683
            ||||||||||| ||||||||||| ||||||||||||||||||||||||| ||||||||||
Sbjct  320  TATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGG-ATCCCCGGTT  262

Query  684  TCCTTTTATTT  694
            |||||||||||
Sbjct  261  TCCTTTTATTT  251


>SRR2298573.428971 428971 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  407  CGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTT  466
            ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  250  CGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTT  191

Query  467  TAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAG  526
            ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  190  TAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAG  131

Query  527  TACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACA  586
            || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  130  TAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACA  71

Query  587  AGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAA  646
            || ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  70   AGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAA  11

Query  647  GCGTCTAGTG  656
             |||||||||
Sbjct  10   ACGTCTAGTG  1


 Score = 394 bits (213),  Expect = 3e-105
 Identities = 237/249 (95%), Gaps = 0/249 (0%)
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 Strand=Plus/Plus

Query  377  ACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTG  436
            |||||| |||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  251  ACATTTAGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTG  310

Query  437  GGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTG  496
            ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  311  GGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTG  370

Query  497  GAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGA  556
            ||||||||||||||||| |||||||||||||| |||||||||||||||||||||||||||
Sbjct  371  GAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGA  430

Query  557  AGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAG  616
            ||||||||||||||||||||| |||||||||| ||| | ||||| |||||||||||||||
Sbjct  431  AGGATGCCCAGAAGGTACCCAAAGGTAACAAGCGACCCCATGGAACTGATCTGGGGCCAG  490

Query  617  GTACCTCTA  625
            | ||| |||
Sbjct  491  GGACCCCTA  499


>SRR2298573.400359 400359 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  445  AGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATAC  504
            ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  500  AGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATAC  441

Query  505  TTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCC  564
            ||||||||| |||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  440  TTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCC  381

Query  565  CAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCT  624
            |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  380  CAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCT  321

Query  625  ATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTT  684
            |||||||||| ||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  320  ATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTT  261

Query  685  CCTTTTATTT  694
            ||||||||||
Sbjct  260  CCTTTTATTT  251


 Score = 416 bits (225),  Expect = 6e-112
 Identities = 241/249 (97%), Gaps = 0/249 (0%)
 Strand=Plus/Plus

Query  417  CCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGT  476
            ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct  1    CCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGT  60
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Query  477  TCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAAC  536
            ||||||||||||||||||||||||||||||||||||| |||||||||||||| |||||||
Sbjct  61   TCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAAC  120

Query  537  ACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTA  596
            |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  121  ACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTA  180

Query  597  TGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTG  656
            ||||||||||||||||||||||||||||||||||| || ||||||||||| ||||||| |
Sbjct  181  TGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGGGATCTGGTTAAAAAACGTCTAGGG  240

Query  657  GGCCAAACC  665
            |||||||||
Sbjct  241  GGCCAAACC  249


>SRR2298573.372955 372955 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  420  GGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCT  479
            |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  1    GGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCT  60

Query  480  AAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACT  539
            |||||||||||||||||||||||||||||||||| |||||||||||||| ||||||||||
Sbjct  61   AAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACT  120

Query  540  AGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGG  599
            ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  121  AGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGG  180

Query  600  ATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGC  659
            ||||||||||||||||||||||||||||||||||| ||||||||||| ||||||||||||
Sbjct  181  ATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGC  240

Query  660  CAAACCCggg  669
            ||||||||||
Sbjct  241  CAAACCCGGG  250


 Score = 355 bits (192),  Expect = 1e-93
 Identities = 231/250 (92%), Gaps = 1/250 (0%)
 Strand=Plus/Minus

Query  483  CCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGT  542
            |||| ||| ||||||||| ||||| || ||| ||| |  ||||||| ||||||| |||||
Sbjct  499  CCTGGGATTTTGTGGAAGTTACTTTGTTCCTTCCGTTTGGGTAGTAGTGCAAACCCTAGT  440

Query  543  TGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATC  602
            |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Sbjct  439  TGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATC  380

Query  603  TGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAA  662
            |||||||||||||||||||||||||||||||| ||||||||||| |||||||||||||||
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```
Sbjct  379  TGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAA  320

Query  663  ACCCgggggggATCCCCGGTTTCCTTTTATTTTATCAATGCTACAATGGAGACAATTAAA  722
            |||||||||| ||| |||||||||||||||||||||||||| || |||||||||||||| 
Sbjct  319  ACCCGGGGGG-ATCACCGGTTTCCTTTTATTTTATCAATGCCACTATGGAGACAATTAAG  261

Query  723  AGTATTGCAG  732
            ||||||||||
Sbjct  260  AGTATTGCAG  251


>SRR2298573.356978 356978 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  430  GCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGA  489
            |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  250  GCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGA  191

Query  490  TGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGG  549
            |||||||||||||||||||||||| |||||||||||||| ||||||||||||||||||||
Sbjct  190  TGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGG  131

Query  550  CCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTG  609
            ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  130  CCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTG  71

Query  610  GGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCggg  669
            ||||||||||||||||||||||||| ||||||||||| ||||||||||||||||||||||
Sbjct  70   GGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGG  11

Query  670  ggggATCCCC  679
            ||||||||||
Sbjct  10   GGGGATCCCC  1


 Score = 363 bits (196),  Expect = 7e-96
 Identities = 235/254 (93%), Gaps = 2/254 (1%)
 Strand=Plus/Plus

Query  340  GAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTA  399
            ||| |||||||||||||||||||||||||||||| ||||||||||||| |||||||||||
Sbjct  246  GAGGCGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTA  305

Query  400  TTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACA  459
            |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  306  TTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACA  365

Query  460  AACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGAT  519
            |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  366  AACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGAT  425

Query  520  CTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACC-CAT  578
            |||| ||||  |||||||||| ||| ||||||| ||||||| ||||| |||| ||| || 
Sbjct  426  CTGGAAGTATGGCAAACACTAATTGAAAGGCCCCCGAAGGAGGCCCAAAAGGGACCGCAG  485
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Query  579  AGGTAACAAGTGAC  592
             || |||||| |||
Sbjct  486  -GGAAACAAGGGAC  498


>SRR2298573.318184 318184 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  396  CCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCT  455
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  1    CCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTT  60

Query  456  AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGC  515
            ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||| |
Sbjct  61   AACAAACCCTTTAGGATTGGTCCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTAC  120

Query  516  CGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACC  575
            ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACC  180

Query  576  CATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGAC  635
            ||||||||||||| |||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  181  CATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGGGAC  240

Query  636  CTGGTTAAAA  645
            ||||||||||
Sbjct  241  CTGGTTAAAA  250


 Score = 394 bits (213),  Expect = 3e-105
 Identities = 237/249 (95%), Gaps = 0/249 (0%)
 Strand=Plus/Minus

Query  458  CAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCG  517
            ||||||||||||||||||| ||||||||| | |||||||||| || |||||||||| |||
Sbjct  499  CAAACCCTTTAGGATTGGTCCTAAACCTGGGTTGTTGTGGAATATTCTTAGTACCTACCG  440

Query  518  ATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCA  577
            ||||||||||| ||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  439  ATCTGGTAGTAGTGCAAACCCTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCA  380

Query  578  TAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCT  637
            ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  379  TAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCT  320

Query  638  GGTTAAAAAGCGTCTAGTGGGCCAAACCCggggggATCCCCGGTTTCCTTTTATTTTAT  697
            ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  319  GGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTAT  260

Query  698  CAATGCTAC  706
            |||||| ||
Sbjct  259  CAATGCCAC  251


>SRR2298573.314513 314513 length=500
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Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  378  CATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGG  437
            |||||||||| ||||||||||||||||||||||||||| |||||||||||||||||||||
Sbjct  250  CATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACCCCTGGTAACAGGTGCCTCTGG  191

Query  438  GGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGG  497
            |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  190  GGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGG  131

Query  498  AAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAA  557
            |||||||||||||||| |||||||||||||| ||||||||||||||||||||||||||||
Sbjct  130  AAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAA  71

Query  558  GGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGG  617
            ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  70   GGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGG  11

Query  618  TACCTCTATC  627
            ||||||||||
Sbjct  10   TACCTCTATC  1


 Score = 425 bits (230),  Expect = 9e-115
 Identities = 242/248 (98%), Gaps = 0/248 (0%)
 Strand=Plus/Plus

Query  324  CCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTT  383
            |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct  251  CCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTT  310

Query  384  GCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAA  443
            |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  311  GCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAA  370

Query  444  AAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATA  503
            |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  371  AAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATA  430

Query  504  CTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGC  563
            |||||||||| |||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  431  CTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGC  490

Query  564  CCAGAAGG  571
            || |||||
Sbjct  491  CCGGAAGG  498


>SRR2298573.309719 309719 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus
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Query  396   CCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCT  455
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  1     CCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTT  60

Query  456   AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGC  515
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  61    AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTAC  120

Query  516   CGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACC  575
             ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   CGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACC  180

Query  576   CATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGAC  635
             ||||||||||||| |||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  181   CATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGGGAT  240

Query  636   CTGGTTAAAA  645
             ||||||||||
Sbjct  241   CTGGTTAAAA  250


 Score = 381 bits (206),  Expect = 2e-101
 Identities = 238/254 (94%), Gaps = 0/254 (0%)
 Strand=Plus/Minus

Query  475   GTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAA  534
             ||| ||||||||||||||| ||||| || |||||| ||| ||||| |||||||| |||||
Sbjct  500   GTTTTAAACCTGAGATGTTTTGGAAAATCCTTAGTTCCTACCGATTTGGTAGTAGTGCAA  441

Query  535   ACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACAC  594
             || ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  440   ACCCTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACAC  381

Query  595   TATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAG  654
             |||||||||||||||||||||||||||||||||||||||| ||||||||||| |||||||
Sbjct  380   TATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAG  321

Query  655   TGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTTTATCAATGCTACAATGGAGA  714
             ||||||||||||||||||||||||||||||||||||||||||||||||| || |||||||
Sbjct  320   TGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTATCAATGCCACTATGGAGA  261

Query  715   CAATTAAAAGTATT  728
             ||||||| ||| ||
Sbjct  260   CAATTAAGAGTTTT  247


>SRR2298573.304269 304269 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 249/257 (97%), Gaps = 2/257 (1%)
 Strand=Plus/Minus

Query  372   AAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGC  431
             |||| || |||||||| |||||| ||||||||||||||||||||||||||||||||||||
Sbjct  255   AAGC-AC-TTTTGCTGTAAAGCAACCTATTGCCAGCGGAACAACACCTGGTAACAGGTGC  198

Query  432   CTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATG  491
             |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
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Sbjct  197  CTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATG  138

Query  492  TTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCC  551
            |||||||||||||||||||||| |||||||||||||| ||||||||||||||||||||||
Sbjct  137  TTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCC  78

Query  552  CACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGG  611
            ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct  77   CACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGG  18

Query  612  GCCAGGTACCTCTATCT  628
            |||||||||||||||||
Sbjct  17   GCCAGGTACCTCTATCT  1


 Score = 366 bits (198),  Expect = 6e-97
 Identities = 222/234 (95%), Gaps = 0/234 (0%)
 Strand=Plus/Plus

Query  295  GCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGAC  354
            ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  252  GCTTGTGGACCTTATGCTCACACAGCCATCCTCCAGTAAGTTTGTGAGACGTCTGGTGAC  311

Query  355  GTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAA  414
            | ||||||||||||||||| ||||||||||||| ||||||||||||||||||||||||||
Sbjct  312  GCGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAA  371

Query  415  CACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTG  474
            ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  372  CACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTG  431

Query  475  GTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTA  528
            ||||||||||||||| ||  |||||  |||||||||||| ||||| ||||||||
Sbjct  432  GTTCTAAACCTGAGAGGTGTTGGAAATTACTTAGTACCTACCGATTTGGTAGTA  485


>SRR2298573.271506 271506 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  420  GGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCT  479
            |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  1    GGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCT  60

Query  480  AAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACT  539
            |||||||||||||||||||||||||||||||||| |||||||||||||| ||||||||||
Sbjct  61   AAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACT  120

Query  540  AGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGG  599
            ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  121  AGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGG  180

Query  600  ATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGC  659
            ||||||||||||||||||||||||||||||||||| ||||||||||| ||||||||||||
Sbjct  181  ATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGC  240
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```
Query  660  CAAACCCggg  669
            ||||||||||
Sbjct  241  CAAACCCGGG  250


 Score = 396 bits (214),  Expect = 7e-106
 Identities = 239/251 (95%), Gaps = 1/251 (0%)
 Strand=Plus/Minus

Query  475  GTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAA  534
            ||| |||||||||||||||||||||| | ||| |||||| |||||||||||||| |||||
Sbjct  500  GTT-TAAACCTGAGATGTTGTGGAAGTTTCTTGGTACCTACCGATCTGGTAGTAGTGCAA  442

Query  535  ACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACAC  594
            |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  441  ACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACAC  382

Query  595  TATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAG  654
            |||||||||||||||||||||||||||||||||||||||| ||||||||||| |||||||
Sbjct  381  TATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAG  322

Query  655  TGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTTTATCAATGCTACAATGGAGA  714
            ||||||||||||||||||||||||||||||||||||||||||||||||| || |||||||
Sbjct  321  TGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTATCAATGCCACTATGGAGA  262

Query  715  CAATTAAAAGT  725
            ||||||| |||
Sbjct  261  CAATTAAGAGT  251


>SRR2298573.248619 248619 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  409  GAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTA  468
            ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  1    GAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTA  60

Query  469  GGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTA  528
            ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  61   GGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTA  120

Query  529  CTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAG  588
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAG  180

Query  589  TGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGC  648
             ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||| |
Sbjct  181  CGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAAC  240

Query  649  GTCTAGTGGG  658
            ||||||||||
Sbjct  241  GTCTAGTGGG  250


 Score = 368 bits (199),  Expect = 2e-97
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 Identities = 233/250 (93%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  640  TTAAAAAGCGTCTAGTGGGCCAAACCCggggggGATCCCCGGTTTCCTTTTATTTTATCA  699
            ||||||| || |||| ||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  500  TTAAAAAACGGCTAGGGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTAGCA  441

Query  700  ATGCTACAATGGAGACAATTAAAAGTATTGCAGATATGGCGACCGGAGTGGTCAGTTCAG  759
            |||| || |||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  440  ATGCCACTATGGAGACAATTAAGAGTATTGCAGATATGGCGACCGGAGTGGTCAGTTCAG  381

Query  760  TTGATTCCACTATCAATGCAGTTAATGAGAGAGTAGAAAATGTGGGCAATGAAATTGGAG  819
            |||||||||||||||||| ||||||||||||||| |||||||| || |||||||||||||
Sbjct  380  TTGATTCCACTATCAATGTAGTTAATGAGAGAGTGGAAAATGTAGGTAATGAAATTGGAG  321

Query  820  GTAACCTATTAACCAAAGTAGCAGATGATGCTTCTAATGTGCTTGGACCAAATTGTTATG  879
            ||||  ||||||||||||| ||||||||||||||||||||||| ||||||||| | ||||
Sbjct  320  GTAATTTATTAACCAAAGTTGCAGATGATGCTTCTAATGTGCTCGGACCAAATCGCTATG  261

Query  880  CTACAACAGC  889
            ||||||||||
Sbjct  260  CTACAACAGC  251


>SRR2298573.246804 246804 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 249/257 (97%), Gaps = 1/257 (0%)
 Strand=Plus/Plus

Query  319  GCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAAC  378
            |||||||||||||||||||| ||||||||||||||||||||||||||||||||||| ||||
Sbjct  1    GCCATCCTCTAGTAAGTTTGCGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAAC  60

Query  379  ATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGG  438
            ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGG  120

Query  439  GCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGA  498
            ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGA  180

Query  499  AGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAG  558
            ||||||||||||||| |||||||||||||| |||||||||||||||||||||||||||||
Sbjct  181  AGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAG  240

Query  559  GATGCCCAGAAGGTACC  575
            |||||||||  ||||||
Sbjct  241  GATGCCCAGG-GGTACC  256


 Score = 405 bits (219),  Expect = 1e-108
 Identities = 239/249 (96%), Gaps = 0/249 (0%)
 Strand=Plus/Minus

Query  328  TAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTG  387
            ||||||||| | |||||| |||||||||| |||||||||||||||| |||||||||||||
Sbjct  498  TAGTAAGTTGGGGAGACGGCTGGTGACGTTTGGGAACTTATTGGAAACAACATTTTGCTG  439
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Query  388   CAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGC  447
              ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Sbjct  438   TAAAGCATCCTATTGCCAGCGGAACAACCCCTGGTAACAGGTGCCTCTGGGGCCAAAAGC  379

Query  448   CAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTA  507
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  378   CAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTA  319

Query  508   GTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAG  567
             |||||| |||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  318   GTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAG  259

Query  568   AAGGTACCC  576
             |||||||||
Sbjct  258   AAGGTACCC  250


>SRR2298573.246257 246257 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  409   GAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTA  468
             ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  1     GAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTA  60

Query  469   GGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTA  528
             ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  61    GGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTA  120

Query  529   CTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAG  588
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   GTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAG  180

Query  589   TGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGC  648
              ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||| |
Sbjct  181   CGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGAACTGGTTAAAAAAC  240

Query  649   GTCTAGTGGG  658
             ||||||||||
Sbjct  241   GTCTAGTGGG  250


 Score = 424 bits (229),  Expect = 3e-114
 Identities = 243/250 (97%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  417   CCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGT  476
             ||||||||| ||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct  500   CCTGGTAACCGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGT  441

Query  477   TCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAAC  536
             ||||||||||||||||||||||||||||||||||||| |||||||||||||| |||||||
Sbjct  440   TCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAAC  381

Query  537   ACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTA  596
```

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          |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  380  ACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTA  321

Query  597  TGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTG  656
            |||||||||||||||||||||||||||||||||||||| ||||||||||| |||||||||
Sbjct  320  TGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTG  261

Query  657  GGCCAAACCC  666
            ||||||||||
Sbjct  260  GGCCAAACCC  251


>SRR2298573.240979 240979 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  300  TGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTG  359
            ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  250  TGGCCCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTG  191

Query  360  GGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCT  419
            |||||||||||||| ||||||||||||| |||||||||||||||||||||||||||||||
Sbjct  190  GGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCT  131

Query  420  GGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCT  479
            |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  130  GGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCT  71

Query  480  AAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACT  539
            |||||||||||||||||||||||||||||||||| |||||||||||||| ||||||||||
Sbjct  70   AAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACT  11

Query  540  AGTTGTAAGG  549
            ||||||||||
Sbjct  10   AGTTGTAAGG  1


 Score = 379 bits (205),  Expect = 7e-101
 Identities = 235/250 (94%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  286  AGATACCACGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACG  345
            |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  250  AGATACCATGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACG  309

Query  346  TCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCA  405
            |||||||||||||||||||||||||||| ||||||||||||| |||||||||||||||||
Sbjct  310  TCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCA  369

Query  406  GCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCT  465
            |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  370  GCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCT  429

Query  466  TTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTA  525
            ||||||||||||||||||||  |||||||||||||| ||| || |||  |||  |||| |
Sbjct  430  TTAGGATTGGTTCTAAACCTAGGATGTTGTGGAAGAAACTAAGAACCAACCGTCCTGGGA  489
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Query  526  GTACTGCAAA  535
            ||| ||||||
Sbjct  490  GTAGTGCAAA  499


>SRR2298573.223650 223650 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  345  GTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCC  404
            ||||||||||||||||||||||||||||| ||||||||||||| ||||||||||||||||
Sbjct  250  GTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCC  191

Query  405  AGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCC  464
            ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  190  AGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCC  131

Query  465  TTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGT  524
            ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  130  TTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGT  71

Query  525  AGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAA  584
            |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  70   AGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAA  11

Query  585  CAAGTGACAC  594
            |||| |||||
Sbjct  10   CAAGCGACAC  1


 Score = 377 bits (204),  Expect = 3e-100
 Identities = 230/243 (95%), Gaps = 0/243 (0%)
 Strand=Plus/Plus

Query  333  AGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAG  392
            |||||| |||||||||||||||||||||||||||||||||| ||||||||||||| ||||
Sbjct  258  AGTTTGCGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAG  317

Query  393  CATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGG  452
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  318  CATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGG  377

Query  453  TCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACC  512
            | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  378  TTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACC  437

Query  513  TGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGT  572
            | ||||||||||||||  |||||  | ||||  |||||||||||||||||||||||||| 
Sbjct  438  TACCGATCTGGTAGTAGGGCAAAACCCAGTTTAAAGGCCCACGAAGGATGCCCAGAAGGG  497

Query  573  ACC  575
            |||
Sbjct  498  ACC  500
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>SRR2298573.223439 223439 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  327  CTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCT  386
            |||||||||||||| |||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  500  CTAGTAAGTTTGTGGGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCT  441

Query  387  GCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAG  446
            | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  440  GTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAG  381

Query  447  CCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTT  506
            ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  380  CCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTT  321

Query  507  AGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCA  566
            ||||||| |||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  320  AGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCA  261

Query  567  GAAGGTACCC  576
            ||||||||||
Sbjct  260  GAAGGTACCC  251


 Score = 414 bits (224),  Expect = 2e-111
 Identities = 240/248 (97%), Gaps = 0/248 (0%)
 Strand=Plus/Plus

Query  312  TCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGG  371
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGG  60

Query  372  AAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGC  431
            || ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGC  120

Query  432  CTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATG  491
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  121  CTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATG  180

Query  492  TTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCC  551
            |||||||||||||||||||||| |||||||||||  | |||||| |||||||||||||||
Sbjct  181  TTGTGGAAGATACTTAGTACCTACCGATCTGGTATAAGTGCAAAAACTAGTTGTAAGGCC  240

Query  552  CACGAAGG  559
            ||||||||
Sbjct  241  CACGAAGG  248


>SRR2298573.223034 223034 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus
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Query  330  GTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCA  389
            |||||||| ||||||||||||||||||||||||||||||||||| ||||||||||||| |
Sbjct  500  GTAAGTTTTTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTA  441

Query  390  AAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCA  449
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  440  AAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCA  381

Query  450  AGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGT  509
            |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  380  AGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGT  321

Query  510  ACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAA  569
            |||| |||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  320  ACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAA  261

Query  570  GGTACCCATA  579
            ||||||||||
Sbjct  260  GGTACCCATA  251


 Score = 405 bits (219),  Expect = 1e-108
 Identities = 235/243 (97%), Gaps = 0/243 (0%)
 Strand=Plus/Plus

Query  281  TAGTGAGATACCACGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTG  340
            ||||||||||||| ||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  7    TAGTGAGATACCATGCTTGTGTACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTG  66

Query  341  AGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTAT  400
            ||||||||||||||||||||||||||||||||| ||||||||||||| ||||||||||||
Sbjct  67   AGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTAT  126

Query  401  TGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAA  460
            ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  127  TGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAA  186

Query  461  ACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATC  520
            ||||||||||||||||||||||||||||| ||||||||||| ||||||||||| ||||||
Sbjct  187  ACCCTTTAGGATTGGTTCTAAACCTGAGAGGTTGTGGAAGAAACTTAGTACCTACCGATC  246

Query  521  TGG  523
            |||
Sbjct  247  TGG  249


>SRR2298573.207601 207601 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  415  CACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTG  474
            ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  500  CACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTG  441

Query  475  GTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAA  534
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            ||||||||||||||||||||||||||||||||||||||| |||||||||||||| |||||
Sbjct  440  GTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAA  381

Query  535  ACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACAC  594
            |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  380  ACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACAC  321

Query  595  TATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAG  654
            |||||||||||||||||||||||||||||||||||||||| ||||||||||| |||||||
Sbjct  320  TATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAG  261

Query  655  TGGGCCAAAC  664
            ||||||||||
Sbjct  260  TGGGCCAAAC  251


 Score = 407 bits (220),  Expect = 3e-109
 Identities = 243/254 (96%), Gaps = 2/254 (1%)
 Strand=Plus/Plus

Query  336  TTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCAT  395
            |||| ||||||||||||||||||||||||||||||||| ||||||||||||| |||||||
Sbjct  1    TTGTCAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCAT  60

Query  396  CCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCT  455
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  61   CCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTT  120

Query  456  AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGC  515
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  121  AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTAC  180

Query  516  CGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACC  575
            ||||||||||||| ||||||||||||||||||||||| |||||||||||||||||| |||
Sbjct  181  CGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCCCGAAGGATGCCCAGAAGGGACC  240

Query  576  CATAGGTAACAAGT  589
            ||| || || ||||
Sbjct  241  CATGGG-AA-AAGT  252


>SRR2298573.204285 204285 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  424  ACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAAC  483
            |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Sbjct  250  ACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAAC  191

Query  484  CTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTT  543
            |||||||||||||||||||||||||||||| |||||||||||||| ||||||||||||||
Sbjct  190  CTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTT  131

Query  544  GTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCT  603
            ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  130  GTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCT  71
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Query  604  GATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAA  663
            ||||||||||||||||||||||||||||||| ||||||||||| ||||||||||||||||
Sbjct  70   GATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAA  11

Query  664  CCCggggggg  673
            ||||||||||
Sbjct  10   CCCGGGGGGG  1


 Score = 412 bits (223),  Expect = 7e-111
 Identities = 237/244 (97%), Gaps = 0/244 (0%)
 Strand=Plus/Plus

Query  344  CGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGC  403
            |||||||||||||||||||||||||||||| ||||||||||||| |||||||||||||||
Sbjct  251  CGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGC  310

Query  404  CAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACC  463
            |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct  311  CAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACC  370

Query  464  CTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGG  523
            |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct  371  CTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGG  430

Query  524  TAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTA  583
            ||||| |||||||||||||||||||||||||||||||||||||||||| ||||||||| |
Sbjct  431  TAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGGACCCATAGGGA  490

Query  584  ACAA  587
            ||||
Sbjct  491  ACAA  494


>SRR2298573.190220 190220 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  446  GCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACT  505
            |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACT  60

Query  506  TAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCC  565
            |||||||| |||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  61   TAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCC  120

Query  566  AGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTA  625
            ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  121  AGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTA  180

Query  626  TCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTC  685
            ||||||||| ||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  181  TCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTC  240

Query  686  CTTTTATTTT  695
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           ||||||||||
Sbjct  241  CTTTTATTTT  250


 Score = 414 bits (224),  Expect = 2e-111
 Identities = 240/248 (97%), Gaps = 0/248 (0%)
 Strand=Plus/Minus

Query  503  ACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATG  562
            ||||||||||| |||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  498  ACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATG  439

Query  563  CCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCT  622
            |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  438  CCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCT  379

Query  623  CTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGT  682
            |||||||||||| ||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  378  CTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGT  319

Query  683  TTCCTTTTATTTTATCAATGCTACAATGGAGACAATTAAAAGTATTGCAGATATGGCGAC  742
            ||||||||||||||||||||| || |||||||||||||| ||||||||||||||||||||
Sbjct  318  TTCCTTTTATTTTATCAATGCCACTATGGAGACAATTAAGAGTATTGCAGATATGGCGAC  259

Query  743  CGGAGTGG  750
            ||||||||
Sbjct  258  CGGAGTGG  251


>SRR2298573.178633 178633 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  427  GGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTG  486
            ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  250  GGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTG  191

Query  487  AGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTA  546
            ||||||||||||||||||||||||||| |||||||||||||| |||||||||||||||||
Sbjct  190  AGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTA  131

Query  547  AGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGAT  606
            |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Sbjct  130  AGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGAT  71

Query  607  CTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCC  666
            |||||||||||||||||||||||||||| ||||||||||| |||||||||||||||||||
Sbjct  70   CTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCC  11

Query  667  gggggggATC  676
            ||||||||||
Sbjct  10   GGGGGGGATC  1


 Score = 427 bits (231),  Expect = 3e-115
 Identities = 243/249 (98%), Gaps = 0/249 (0%)
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 Strand=Plus/Plus

Query  324  CCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTT  383
            |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct  251  CCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTT  310

Query  384  GCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAA  443
            |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  311  GCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAA  370

Query  444  AAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATA  503
            |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  371  AAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATA  430

Query  504  CTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGC  563
            |||||||||| |||||||||||||| ||||||||||||||||||||||| ||||||||||
Sbjct  431  CTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCCCGAAGGATGC  490

Query  564  CCAGAAGGT  572
            |||||||||
Sbjct  491  CCAGAAGGT  499


>SRR2298573.167573 167573 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  436  GGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGT  495
            |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  250  GGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGT  191

Query  496  GGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACG  555
            |||||||||||||||||| |||||||||||||| ||||||||||||||||||||||||||
Sbjct  190  GGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACG  131

Query  556  AAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCA  615
            ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  130  AAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCA  71

Query  616  GGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggAT  675
            ||||||||||||||||||| ||||||||||| ||||||||||||||||||||||||||||
Sbjct  70   GGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGAT  11

Query  676  CCCCGGTTTC  685
            ||||||||||
Sbjct  10   CCCCGGTTTC  1


 Score = 392 bits (212),  Expect = 9e-105
 Identities = 236/248 (95%), Gaps = 0/248 (0%)
 Strand=Plus/Plus

Query  431  CCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGAT  490
            ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  251  CCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGAT  310
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Query  491   GTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGC  550
             ||||||||||||||||||||||| |||||||||||||| |||||||||||||||||||||
Sbjct  311   GTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGC  370

Query  551   CCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGG  610
             |||||||||||||||||||||||||||||||||||||| |||||||||||||||| ||||
Sbjct  371   CCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGACCTGG  430

Query  611   GGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggg  670
             ||||||| |||||||||| || |||||||||||||| || | || |||||||||||||||
Sbjct  431   GGCCAGGAACCTCTATCTGGGGGACCTGGTTAAAAAACGCCCAGGGGGCCAAACCCGGGG  490

Query  671   gggATCCC  678
             ||||||||
Sbjct  491   GGGATCCC  498


>SRR2298573.129131 129131 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  394   ATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGT  453
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     ATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGT  60

Query  454   CTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCT  513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    TTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCT  120

Query  514   GCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTA  573
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   ACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTA  180

Query  574   CCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTG  633
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  181   CCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGGG  240

Query  634   ACCTGGTTAA  643
             | ||||||||
Sbjct  241   ATCTGGTTAA  250


 Score = 372 bits (201),  Expect = 1e-98
 Identities = 233/249 (94%), Gaps = 0/249 (0%)
 Strand=Plus/Minus

Query  629   TGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTT  688
             |||||| ||||||||||| ||||||||||||||||||||||| |||||||||||||||||
Sbjct  496   TGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGAGGGGATCCCCGGTTTCCTT  437

Query  689   TTATTTTATCAATGCTACAATGGAGACAATTAAAAGTATTGCAGATATGGCGACCGGAGT  748
             |||||||| |||||| || |||||||||||||| ||||||||||||||||||||||||||
Sbjct  436   TTATTTTAGCAATGCCACTATGGAGACAATTAAGAGTATTGCAGATATGGCGACCGGAGT  377

Query  749   GGTCAGTTCAGTTGATTCCACTATCAATGCAGTTAATGAGAGAGTAGAAAATGTGGGCAA  808
             |||||||||||||||||||||||| |||| ||||||||||||||| |||||||| || ||
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Sbjct  376  GGTCAGTTCAGTTGATTCCACTATGAATGTAGTTAATGAGAGAGTGGAAAATGTAGGTAA  317

Query  809  TGAAATTGGAGGTAACCTATTAACCAAAGTAGCAGATGATGCTTCTAATGTGCTTGGACC  868
            |||||||||||||||  ||||||||||||| ||||||||||||||||||||||| |||||
Sbjct  316  TGAAATTGGAGGTAATTTATTAACCAAAGTTGCAGATGATGCTTCTAATGTGCTCGGACC  257

Query  869  AAATTGTTA  877
            |||||||||
Sbjct  256  AAATTGTTA  248


>SRR2298573.122310 122310 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  451  GGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTA  510
            ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTA  60

Query  511  CCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAG  570
            ||| |||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAG  120

Query  571  GTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTG  630
            |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTG  180

Query  631  GTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTT  690
            |||| ||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTT  240

Query  691  ATTTTATCAA  700
            ||||||||||
Sbjct  241  ATTTTATCAA  250


 Score = 379 bits (205),  Expect = 7e-101
 Identities = 236/251 (94%), Gaps = 2/251 (1%)
 Strand=Plus/Minus

Query  499  AGATAC-TTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAA  557
            |||||| ||||  |||  |||| |||||||  |||||||||| |||||||||||||||||
Sbjct  499  AGATACTTTAG-CCCTTGCGATTTGGTAGTTGTGCAAACACTTGTTGTAAGGCCCACGAA  441

Query  558  GGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGG  617
            ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  440  GGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGG  381

Query  618  TACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCC  677
            ||||||||||||||||| ||||||||||| ||||||||||||||||||||||||||||||
Sbjct  380  TACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCC  321

Query  678  CCGGTTTCCTTTTATTTTATCAATGCTACAATGGAGACAATTAAAAGTATTGCAGATATG  737
            |||||||||||||||||||||||||| || |||||||||||||| |||||||||||||||
Sbjct  320  CCGGTTTCCTTTTATTTTATCAATGCCACTATGGAGACAATTAAGAGTATTGCAGATATG  261
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Query  738  GCGACCGGAGT  748
            |||||||||||
Sbjct  260  GCGACCGGAGT  250


>SRR2298573.121752 121752 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  313  CACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGA  372
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGA  60

Query  373  AGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCC  432
            | ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCC  120

Query  433  TCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGT  492
            ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  121  TCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGT  180

Query  493  TGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCC  552
            ||||||||||||||||||||| |||||||||||||| |||||||||||||||||||||||
Sbjct  181  TGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCC  240

Query  553  ACGAAGGATG  562
             |||||||||
Sbjct  241  CCGAAGGATG  250


 Score = 412 bits (223),  Expect = 7e-111
 Identities = 241/250 (96%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  334  GTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGC  393
            ||||||||  |||||||||||||| ||||||||||||||| |||| |||||||| |||||
Sbjct  500  GTTTGTGAAGCGTCTGGTGACGTGGGGGAACTTATTGGAAACAACTTTTTGCTGTAAAGC  441

Query  394  ATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGT  453
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  440  ATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGT  381

Query  454  CTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCT  513
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  380  TTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCT  321

Query  514  GCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTA  573
             |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  320  ACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTA  261

Query  574  CCCATAGGTA  583
            ||||||||||
Sbjct  260  CCCATAGGTA  251


>SRR2298573.106244 106244 length=500
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Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  321  CATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACAT  380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  500  CATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACAT  441

Query  381  TTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGC  440
            ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  440  TTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGC  381

Query  441  CAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAG  500
            ||| ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  380  CAAGAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAG  321

Query  501  ATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGA  560
            ||||||||||||| |||||||||||||| |||||||||||||||||||||||||||||||
Sbjct  320  ATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGA  261

Query  561  TGCCCAGAAG  570
            ||||||||||
Sbjct  260  TGCCCAGAAG  251


 Score = 412 bits (223),  Expect = 7e-111
 Identities = 239/247 (97%), Gaps = 0/247 (0%)
 Strand=Plus/Plus

Query  276  TCTACTAGTGAGATACCACGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGT  335
            |||| ||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  4    TCTATTAGTGAGATACCATGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGT  63

Query  336  TTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCAT  395
            |||||||||||||||||||||||||||||||||||||| ||||||||||||| |||||||
Sbjct  64   TTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCAT  123

Query  396  CCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCT  455
            |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||| |
Sbjct  124  CCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAGAGCCAAGGTTT  183

Query  456  AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGC  515
            |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||| |
Sbjct  184  AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAAATACTTAGTACCTAC  243

Query  516  CGATCTG  522
            |||||||
Sbjct  244  CGATCTG  250


>SRR2298573.96228 96228 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus
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Query  407  CGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTT  466
            ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  250  CGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTT  191

Query  467  TAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAG  526
            ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  190  TAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAG  131

Query  527  TACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACA  586
            || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  130  TAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACA  71

Query  587  AGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAA  646
            || ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  70   AGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAA  11

Query  647  GCGTCTAGTG  656
             |||||||||
Sbjct  10   ACGTCTAGTG  1


 Score = 401 bits (217),  Expect = 2e-107
 Identities = 239/250 (96%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  289  TACCACGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCT  348
            ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  251  TACCATGCTTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCT  310

Query  349  GGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCG  408
            ||||||||||||||||||||||||| ||||||||||||| ||||||||||||||||||||
Sbjct  311  GGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCG  370

Query  409  GAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTA  468
            ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  371  GAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTA  430

Query  469  GGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTA  528
            ||||||||||||||||||||||||||||||| ||||||||||||| |||| ||||  |||
Sbjct  431  GGATTGGTTCTAAACCTGAGATGTTGTGGAACATACTTAGTACCTCCCGAGCTGGAGGTA  490

Query  529  CTGCAAACAC  538
              ||||||||
Sbjct  491  GGGCAAACAC  500


>SRR2298573.90787 90787 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  421  GTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTA  480
            ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  500  GTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTA  441

Query  481  AACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTA  540
            ||||||||||||||||||||||||||||||||| |||||||||||||| |||||||||||
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Sbjct  440   AACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTA  381

Query  541   GTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGA  600
             |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  380   GTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGA  321

Query  601   TCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCC  660
             |||||||||||||||||||||||||||||||||| ||||||||||| |||||||||||||
Sbjct  320   TCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCC  261

Query  661   AAACCCgggg  670
             ||||||||||
Sbjct  260   AAACCCGGGG  251


 Score = 424 bits (229),  Expect = 3e-114
 Identities = 243/250 (97%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  396   CCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCT  455
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  1     CCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTT  60

Query  456   AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGC  515
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  61    AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTAC  120

Query  516   CGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACC  575
             ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   CGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACC  180

Query  576   CATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGAC  635
             ||||||||||||| |||||||||||||||||||||||||||| ||||| ||||||||||
Sbjct  181   CATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGAACCTCAATCTTGGTGAT  240

Query  636   CTGGTTAAAA  645
             ||||||||||
Sbjct  241   CTGGTTAAAA  250


>SRR2298573.71711 71711 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 242/247 (98%), Gaps = 0/247 (0%)
 Strand=Plus/Plus

Query  335   TTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCA  394
             ||||||||||||||||||||||||||||||||||||||| ||||||||||||| ||||||
Sbjct  5     TTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCA  64

Query  395   TCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTC  454
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  65    TCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTT  124

Query  455   TAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTG  514
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  125   TAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTA  184
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Query  515   CCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTAC  574
             |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  185   CCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTAC  244

Query  575   CCATAGG  581
             |||||||
Sbjct  245   CCATAGG  251


 Score = 390 bits (211),  Expect = 3e-104
 Identities = 237/250 (95%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  481   AACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTA  540
             |||||||||||||  ||||||| |||||||||| |||||||||||||| |||||||||||
Sbjct  500   AACCTGAGATGTTTGGGAAGATTCTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTA  441

Query  541   GTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGA  600
             |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  440   GTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGA  381

Query  601   TCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCC  660
             |||||||||||||||||||||||||||||||||| ||||||||||| |||||||||||||
Sbjct  380   TCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCC  321

Query  661   AAACCCgggggggATCCCCGGTTTCCTTTTATTTTATCAATGCTACAATGGAGACAATTA  720
             || |||||||||||||||||||||||||||||| ||||||||| || |||||||||||||
Sbjct  320   AACCCCGGGGGGGATCCCCGGTTTCCTTTTATTGTATCAATGCCACTATGGAGACAATTA  261

Query  721   AAAGTATTGC  730
             | ||||||||
Sbjct  260   AGAGTATTGC  251


>SRR2298573.49960 49960 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  445   AGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATAC  504
             ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     AGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATAC  60

Query  505   TTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCC  564
             ||||||||| |||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  61    TTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCC  120

Query  565   CAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCT  624
             |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  121   CAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCT  180

Query  625   ATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTT  684
             |||||||||| ||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  181   ATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTT  240

Query  685   CCTTTTATTT  694
             ||||||||||
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Sbjct  241  CCTTTTATTT  250


 Score = 405 bits (219),  Expect = 1e-108
 Identities = 239/249 (96%), Gaps = 0/249 (0%)
 Strand=Plus/Minus

Query  490  TGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGG  549
            ||||| ||||||| |||||||||| |||||||||||||| ||||||||||||||||||||
Sbjct  499  TGTTGGGGAAGATTCTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGG  440

Query  550  CCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTG  609
            ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  439  CCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTG  380

Query  610  GGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCggg  669
            ||||||||||||||||||||||||| ||||||||||| ||||||||||||||||||||||
Sbjct  379  GGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGG  320

Query  670  ggggATCCCCGGTTTCCTTTTATTTTATCAATGCTACAATGGAGACAATTAAAAGTATTG  729
            |||||||||||||||||||||||||||||||||| || |||||||||||||| |||||||
Sbjct  319  GGGGATCCCCGGTTTCCTTTTATTTTATCAATGCCACTATGGAGACAATTAAGAGTATTG  260

Query  730  CAGATATGG  738
            |||||||||
Sbjct  259  CAGATATGG  251


>SRR2298573.48192 48192 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  436  GGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGT  495
            |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  250  GGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGT  191

Query  496  GGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACG  555
            |||||||||||||||||| |||||||||||||| ||||||||||||||||||||||||||
Sbjct  190  GGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACG  131

Query  556  AAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCA  615
            ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  130  AAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCA  71

Query  616  GGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCggggggAT  675
            ||||||||||||||||||| ||||||||||| ||||||||||||||||||||||||||||
Sbjct  70   GGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGAT  11

Query  676  CCCCGGTTTC  685
            ||||||||||
Sbjct  10   CCCCGGTTTC  1


 Score = 412 bits (223),  Expect = 7e-111
 Identities = 241/250 (96%), Gaps = 0/250 (0%)
 Strand=Plus/Plus
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Query  396  CCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCT  455
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  251  CCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTT  310

Query  456  AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGC  515
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  311  AACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTAC  370

Query  516  CGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACC  575
            |||||||||||||  |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  371  CGATCTGGTAGTAGGGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACC  430

Query  576  CATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGAC  635
            ||||||||||||| ||||||||||| |||||||||||||||||||||||||||||| |
Sbjct  431  CATAGGTAACAAGCGACACTATGGAACTGATCTGGGGCCAGGTACCTCTATCTTGGGGCT  490

Query  636  CTGGTTAAAA  645
            ||||||||||
Sbjct  491  CTGGTTAAAA  500


>SRR2298573.42949 42949 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 259/272 (95%), Gaps = 1/272 (0%)
 Strand=Plus/Minus

Query  415  CACCTGGTAACAGGTGCCTCT-GGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATT  473
            |||||| || ||||||    | |||||||||||||||||| |||||||||||||||||||
Sbjct  272  CACCTGTTACCAGGTGTTGTTCGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATT  213

Query  474  GGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCA  533
            |||||||||||||||||||||||||||||||||||||||| |||||||||||||| ||||
Sbjct  212  GGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCA  153

Query  534  AACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACA  593
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  152  AACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACA  93

Query  594  CTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTA  653
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||| ||||||
Sbjct  92   CTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTA  33

Query  654  GTGGGCCAAACCCgggggggATCCCCGGTTTC  685
            ||||||||||||||||||||||||||||||||
Sbjct  32   GTGGGCCAAACCCGGGGGGGATCCCCGGTTTC  1


 Score = 401 bits (217),  Expect = 2e-107
 Identities = 239/250 (96%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  409  GAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTA  468
            ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  251  GAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTA  310

Query  469  GGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTA  528
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            ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  311  GGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTA  370

Query  529  CTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAG  588
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  371  GTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAG  430

Query  589  TGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGC  648
             ||||| |||||||||||||||||||||| ||||||| ||||| || ||||||||||| |
Sbjct  431  CGACACCATGGATCTGATCTGGGGCCAGGAACCTCTAACTTGGGGATCTGGTTAAAAAAC  490

Query  649  GTCTAGTGGG  658
            | ||||||||
Sbjct  491  GGCTAGTGGG  500


>SRR2298573.25832 25832 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  464  CTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGG  523
            |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct  1    CTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGG  60

Query  524  TAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTA  583
            ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTA  120

Query  584  ACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAA  643
            ||||| ||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  121  ACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAA  180

Query  644  AAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTTTATCAATGC  703
            ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTATCAATGC  240

Query  704  TACAATGGAG  713
             |||||||||
Sbjct  241  CACAATGGAG  250


 Score = 374 bits (202),  Expect = 3e-99
 Identities = 234/250 (94%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  475  GTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAA  534
            |||| ||||||||||| ||| ||||| ||||||||||||||| || |||| ||| |||||
Sbjct  500  GTTCAAAACCTGAGATTTTGGGGAAGGTACTTAGTACCTGCCTATTTGGTTGTAGTGCAA  441

Query  535  ACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACAC  594
            || |||||||||||||||| |||||||||||||||||||||||||||||||||| |||||
Sbjct  440  ACCCTAGTTGTAAGGCCCAAGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACAC  381

Query  595  TATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAG  654
            |||||||||||||||||||||||||||||||||||||||| ||||||||||| |||||||
Sbjct  380  TATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAG  321
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Query  655  TGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTTTATCAATGCTACAATGGAGA  714
            ||||||||||||||||||||||||||||||||||||||||||||||||| || |||||||
Sbjct  320  TGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTATCAATGCCACTATGGAGA  261

Query  715  CAATTAAAAG  724
            ||||||| ||
Sbjct  260  CAATTAAGAG  251


>SRR2298573.22802 22802 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 248/256 (97%), Gaps = 0/256 (0%)
 Strand=Plus/Plus

Query  313  CACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGA  372
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGA  60

Query  373  AGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCC  432
            | ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCC  120

Query  433  TCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGT  492
            ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  121  TCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGT  180

Query  493  TGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCC  552
            ||||||||||||||||||||| |||||||||||||| ||||||||| ||||| |||||||
Sbjct  181  TGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACAAGTTGAAAGGCCC  240

Query  553  ACGAAGGATGCCCAGA  568
            |||||||||||| |||
Sbjct  241  ACGAAGGATGCCAAGA  256


 Score = 418 bits (226),  Expect = 2e-112
 Identities = 242/250 (97%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  382  TTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCC  441
            |||||| ||||| |||||||||||||||| |||| |||||||||||||||||||||||||
Sbjct  500  TTGCTGTAAAGCCTCCTATTGCCAGCGGACCAACCCCTGGTAACAGGTGCCTCTGGGGCC  441

Query  442  AAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGA  501
            |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  440  AAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGA  381

Query  502  TACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGAT  561
            |||||||||||| |||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  380  TACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGAT  321

Query  562  GCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACC  621
            ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  320  GCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACC  261

Query  622  TCTATCTTGG  631
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            ||||||||||
Sbjct  260  TCTATCTTGG  251


>SRR2298573.22004 22004 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  394  ATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGT  453
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    ATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGT  60

Query  454  CTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCT  513
             |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  61   TTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGGTACTTAGTACCT  120

Query  514  GCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTA  573
             |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTA  180

Query  574  CCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTG  633
            ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTG  240

Query  634  ACCTGGTTAA  643
            | ||||||||
Sbjct  241  ATCTGGTTAA  250


 Score = 388 bits (210),  Expect = 1e-103
 Identities = 236/249 (95%), Gaps = 0/249 (0%)
 Strand=Plus/Minus

Query  455  TAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTG  514
            |||||| ||||||||||||||||||||||||| ||| ||||||||| | |||||| ||| 
Sbjct  500  TAACAACCCCTTTAGGATTGGTTCTAAACCTGGGATTTTGTGGAAGGTTCTTAGTTCCTA  441

Query  515  CCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTAC  574
            |||||||||||||| ||||||||||||||| ||||||||||||||||||||||||||||||
Sbjct  440  CCGATCTGGTAGTAGTGCAAACACTAGTTTTAAGGCCCACGAAGGATGCCCAGAAGGTAC  381

Query  575  CCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGA  634
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  380  CCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGA  321

Query  635  CCTGGTTAAAAAGCGTCTAGTGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTT  694
             ||||||||||| ||||||||||||||||||||||||| |||||||||||||||||||||
Sbjct  320  TCTGGTTAAAAAACGTCTAGTGGCCAAACCCGGGGGGGGTCCCCGGTTTCCTTTTATTT  261

Query  695  TATCAATGC  703
            |||||||||
Sbjct  260  TATCAATGC  252


>SRR2298573.21098 21098 length=500
Length=500
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```
 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  309  TGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTAT  368
            |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Sbjct  250  TGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTTTGGTGACGTGTGGGAACTTAT  191

Query  369  TGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGG  428
            ||||| ||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  190  TGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGG  131

Query  429  TGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAG  488
            ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  130  TGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAG  71

Query  489  ATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAG  548
            ||||||||||||||||||||||||| |||||||||||||| |||||||||||||||||||
Sbjct  70   ATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAG  11

Query  549  GCCCACGAAG  558
            ||||||||||
Sbjct  10   GCCCACGAAG  1


 Score = 407 bits (220),  Expect = 3e-109
 Identities = 240/250 (96%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  258  CAGATGGCGTGCCATAATTCTACTAGTGAGATACCACGCTTGTGGACCTTATGCTCACAC  317
            || |||||||||||||  ||||| |||||||||||| |||||||||||||||||||||||
Sbjct  251  CAAATGGCGTGCCATAGCTCTATTAGTGAGATACCATGCTTGTGGACCTTATGCTCACAC  310

Query  318  AGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAA  377
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  311  AGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAA  370

Query  378  CATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGG  437
            |||||||||| |||||||||||||||||||||||||||||||||||||||  ||||||||
Sbjct  371  CATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGTGGCCTCTGG  430

Query  438  GGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGG  497
            |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  431  GGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGG  490

Query  498  AAGATACTTA  507
            ||||||||||
Sbjct  491  AAGATACTTA  500


>SRR2298573.20649 20649 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  451  GGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTA  510
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            ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTA  60

Query  511  CCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAG  570
            ||| |||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAG  120

Query  571  GTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTG  630
            |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GTACCCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTG  180

Query  631  GTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTT  690
            |||| ||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTT  240

Query  691  ATTTTATCAA  700
            ||||||||||
Sbjct  241  ATTTTATCAA  250


 Score = 387 bits (209),  Expect = 4e-103
 Identities = 237/251 (94%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  475  GTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAA  534
            |||||||||||| ||||||||||||| | ||| || ||| ||||||| |||||| |||||
Sbjct  500  GTTCTAAACCTGGGATGTTGTGGAAGTTTCTTTGTTCCTACCGATCTTGTAGTAGTGCAA  441

Query  535  ACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACAC  594
            |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  440  ACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACAC  381

Query  595  TATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAG  654
            |||||||||||||||||||||||||||||||||||||||| ||||||||||| |||||||
Sbjct  380  TATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAG  321

Query  655  TGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTTTATCAATGCTACAATGGAGA  714
            ||||||||||||||||||||||||||||||||||||||||||||||||| || |||||||
Sbjct  320  TGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTATCAATGCCACTATGGAGA  261

Query  715  CAATTAAAAGT  725
            ||||||| |||
Sbjct  260  CAATTAAGAGT  250


>SRR2298573.19115 19115 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  352  GACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAA  411
            |||||||||||||||||||||| ||||||||||||| |||||||||||||||||||||||
Sbjct  250  GACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAA  191

Query  412  CAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGA  471
            |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Sbjct  190  CAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGA  131
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Query  472  TTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTG  531
            |||||||||||||||||||||||||||||||||||||||||| |||||||||||||| ||
Sbjct  130  TTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTG  71

Query  532  CAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGA  591
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  70   CAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGA  11

Query  592  CACTATGGAT  601
            ||||||||||
Sbjct  10   CACTATGGAT  1


 Score = 420 bits (227),  Expect = 4e-113
 Identities = 241/248 (97%), Gaps = 0/248 (0%)
 Strand=Plus/Plus

Query  330  GTAAGTTTGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCA  389
            ||||||  |||||||||||||||||||||||||||||||||||| ||||||||||||| |
Sbjct  252  GTAAGTCGGTGAGACGTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTA  311

Query  390  AAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCA  449
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  312  AAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCA  371

Query  450  AGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGT  509
            |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  372  AGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGT  431

Query  510  ACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAA  569
            |||| |||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  432  ACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAA  491

Query  570  GGTACCCA  577
            ||||||||
Sbjct  492  GGTACCCA  499


>SRR2298573.12663 12663 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  409  GAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTA  468
            ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  1    GAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTA  60

Query  469  GGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTA  528
            ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  61   GGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTA  120

Query  529  CTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAG  588
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAG  180

Query  589  TGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGC  648
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             ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||| |
Sbjct  181  CGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAAC  240

Query  649  GTCTAGTGGG  658
            ||||||||||
Sbjct  241  GTCTAGTGGG  250


 Score = 355 bits (192),  Expect = 1e-93
 Identities = 230/249 (92%), Gaps = 0/249 (0%)
 Strand=Plus/Minus

Query  455  TAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTG  514
            |||||| |||||||||||||||||||| |||| |||||||||||| || |||||| |||
Sbjct  500  TAACAACCCCTTTAGGATTGGTTCTAACCCTGTGATGTTGTGGAAAATCCTTAGTCCCTA  441

Query  515  CCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTAC  574
            |||||||||||||| ||||||||||   ||||||||| |||||||||||||||||||| |
Sbjct  440  CCGATCTGGTAGTAGTGCAAACACTGCGTGTAAGGCCGACGAAGGATGCCCAGAAGGTGC  381

Query  575  CCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGA  634
            ||||||||||| || ||||| |||||||||||||||||||||||||||||| ||||||||
Sbjct  380  CCATAGGTAACTAGCGACACGATGGATCTGATCTGGGGCCAGGTACCTCTAGCTTGGTGA  321

Query  635  CCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTT  694
             ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  320  TCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTT  261

Query  695  TATCAATGC  703
            |||||||||
Sbjct  260  TATCAATGC  252


>SRR2298573.7958 7958 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  297  TTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGT  356
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  251  TTGTGGACCTTATGCTCACACAGCCATCCTCTAGTAAGTTTGTGAGACGTCTGGTGACGT  310

Query  357  GTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACA  416
            ||||||||||||||||| ||||||||||||| ||||||||||||||||||||||||||||
Sbjct  311  GTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACA  370

Query  417  CCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGT  476
            ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct  371  CCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGT  430

Query  477  TCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAAC  536
            ||||||||||||||||||||||||||||||||| |||| ||||||||||||| |||||||
Sbjct  431  TCTAAACCTGAGATGTTGTGGAAGATACTTAGAACCTACCGATCTGGTAGTAGTGCAAAC  490

Query  537  ACTAGTTGTA  546
            ||||||||||
Sbjct  491  ACTAGTTGTA  500
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 Score = 411 bits (222),  Expect = 3e-110
 Identities = 240/249 (96%), Gaps = 0/249 (0%)
 Strand=Plus/Minus

Query  455  TAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTG  514
            ||||||||||||||||||||||| |||||||||||||||| ||||||| |||||||||| 
Sbjct  250  TAACAAACCCTTTAGGATTGGTTTTAAACCTGAGATGTTGGGGAAGATTCTTAGTACCTA  191

Query  515  CCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTAC  574
            |||||||||||||| |||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  190  CCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCGGAAGGTAC  131

Query  575  CCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGA  634
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  130  CCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGA  71

Query  635  CCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTT  694
             ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  70   TCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTT  11

Query  695  TATCAATGC  703
            |||||||||
Sbjct  10   TATCAATGC  2


>SRR2298566.575132 575132 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  1281  GTTGTGACATATGACTCAAAGTTAGAATTTGGAGCATTTACCAATTTACCACATGTATTG  1340
             ||||||||||||||||||||||||||||||||||||||||||||| |||||||||| |||
Sbjct  251   GTTGTGACATATGACTCAAAGTTAGAATTTGGAGCATTTACCAATCTACCACATGTGTTG  310

Query  1341  ATGAATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAAC  1400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  311   ATGAATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAAC  370

Query  1401  TATGTTAAAACGGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTA  1460
             ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  371   TATGTTAAAACAGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTA  430

Query  1461  TCTATACCTTCAGGTTCTGCGACACAAGTTGATGTAACCATATTGGGTAGTTTATTGCAA  1520
             || ||||||||||||||||| ||||||||||||||||||||||||||||| |||||||||
Sbjct  431   TCCATACCTTCAGGTTCTGCTACACAAGTTGATGTAACCATATTGGGTAGCTTATTGCAA  490

Query  1521  TTGGACTTCC  1530
             ||||||||||
Sbjct  491   TTGGACTTCC  500


 Score = 346 bits (187),  Expect = 7e-91
 Identities = 228/248 (92%), Gaps = 1/248 (0%)
 Strand=Plus/Minus
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Query  1328  ACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGT  1387
             ||| ||||  ||||||||||||||||| |||||  ||||||||||||||||||| |||||
Sbjct  252   ACC-CATGGGTTGATGAATTTGGCTGATACCACTTAGGCTGATTTATGTATCCCTTATGT  194

Query  1388  TGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGT  1447
             |||||||||||||||| |||||||  ||||||||| ||||||||||||||||||||||||
Sbjct  193   TGCTGACACAAACTATTTTAAAACATATTCGTCAGTCTTAGGGCAACTAAAAGTCTATGT  134

Query  1448  TTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGATGTAACCATATTGGG  1507
             ||||||||||||||| || |||||||||||||| ||||||||||||||||||||||||||
Sbjct  133   TTGGACACCTTTATCCATTCCTTCAGGTTCTGCTACACAAGTTGATGTAACCATATTGGG  74

Query  1508  TAGTTTATTGCAATTGGACTTCCAAAATCCTAGGGTGTTTGGCCAAGACGTTGGTATCTA  1567
             ||| |||||||||||||||||||||||||||||||| || || |||||||||||||| ||
Sbjct  73    TAGCTTATTGCAATTGGACTTCCAAAATCCTAGGGTATTCGGTCAAGACGTTGGTATTTA  14

Query  1568  TGATAATG  1575
             ||| ||||
Sbjct  13    TGACAATG  6


>SRR2298566.451439 451439 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  1239  GGAACAGCTGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCA  1298
             ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  250   GGAACAGCTGGTAGTGCATTGGTTGTGTATGAACCCAAACCTGTTGTGACATATGACTCA  191

Query  1299  AAGTTAGAATTTGGAGCATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACC  1358
             ||||||||||||||||||||||||||| |||||||||| |||||||||||||||||||||
Sbjct  190   AAGTTAGAATTTGGAGCATTTACCAATCTACCACATGTGTTGATGAATTTGGCTGAGACC  131

Query  1359  ACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCG  1418
             ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  130   ACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCG  71

Query  1419  TCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCT  1478
             |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Sbjct  70    TCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCT  11

Query  1479  GCGACACAAG  1488
             || |||||||
Sbjct  10    GCTACACAAG  1


 Score = 424 bits (229),  Expect = 3e-114
 Identities = 243/250 (97%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  1218  GTGCAAGTGAATGTTAACCAAGGAACAGCTGGTAGTGCATTGGTGGTGTATGAACCCAAA  1277
             || |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  251   GTACAAGTGAATGTTAATCAAGGAACAGCTGGTAGTGCATTGGTGGTGTATGAACCCAAA  310

Query  1278  CCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCATTTACCAATTTACCACATGTA  1337
             |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
```

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Sbjct  311   CCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCATTTACCAATCTACCACATGTG  370

Query  1338  TTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACA  1397
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  371   TTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACA  430

Query  1398  AACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCT  1457
             |||||||||||||| ||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct  431   AACTATGTTAAAACAGATTCGTCAGACTTAGGGCAACTAAAAGCCTATGTTTGGACACCT  490

Query  1458  TTATCTATAC  1467
             ||||| ||||
Sbjct  491   TTATCCATAC  500


>SRR2298566.378213 378213 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  1271  ACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCATTTACCAATTTACC  1330
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  1     ACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCATTTACCAATCTACC  60

Query  1331  ACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGC  1390
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    ACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGC  120

Query  1391  TGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTG  1450
             ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  121   TGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTG  180

Query  1451  GACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGATGTAACCATATTGGGTAG  1510
             |||||||||||| ||||||||||||||||| |||||||||||||||||||||||||||||
Sbjct  181   GACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGATGTAACCATATTGGGTAG  240

Query  1511  TTTATTGCAA  1520
              |||||||||
Sbjct  241   CTTATTGCAA  250


 Score = 357 bits (193),  Expect = 3e-94
 Identities = 233/253 (92%), Gaps = 0/253 (0%)
 Strand=Plus/Minus

Query  1430  GCAACTAAAAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGT  1489
             ||||||||| || |  ||| |||| |||||||| |||||||||| |||||| ||||||||
Sbjct  500   GCAACTAAATGTTTTGGTTGGGACCCCTTTATCCATACCTTCAGTTTCTGCTACACAAGT  441

Query  1490  TGATGTAACCATATTGGGTAGTTTATTGCAATTGGACTTCCAAAATCCTAGGGTGTTTGG  1549
             ||||||||||||||||||||| |||||||||||||||||||||||||||||||| || ||
Sbjct  440   TGATGTAACCATATTGGGTAGCTTATTGCAATTGGACTTCCAAAATCCTAGGGTATTCGG  381

Query  1550  CCAAGACGTTGGTATCTATGATAATGCACCAACGCGGAAACAAAATCTTAAAAAGATTCT  1609
              |||||||||||||| ||||| ||||||||||||||||||||||| || ||||||| |||
Sbjct  380   TCAAGACGTTGGTATTTATGACAATGCACCAACGCGGAAACAAAACCTAAAAAAGACTCT  321
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Query  1610  TACAATGAGCACTAAATACAAGTGGACTAGGGGAAAAATTGACATTGCAGAAGGGCCAGG  1669
             ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  320   TACAATGAGCACTAAATACAATTGGACTAGGGGAAAAATTGACATTGCAGAAGGGCCAGG  261

Query  1670  TTCTATGAACATG  1682
             |||||||||| ||
Sbjct  260   TTCTATGAACTTG  248


>SRR2298546.989298 989298 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 250/259 (97%), Gaps = 0/259 (0%)
 Strand=Plus/Plus

Query  1285  TGACATATGACTCAAAGTTAGAATTTGGAGCATTTACCAATTTACCACATGTATTGATGA  1344
             ||||  ||||||||||||||||||||||||| |||||||||||||||||||| |||||||
Sbjct  242   TGACGAATGACTCAAAGTTAGAATTTGGAGCGTTTACCAATTTACCACATGTGTTGATGA  301

Query  1345  ATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATG  1404
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  302   ATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATG  361

Query  1405  TTAAAACGGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCTA  1464
             ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  362   TTAAAACAGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCCA  421

Query  1465  TACCTTCAGGTTCTGCGACACAAGTTGATGTAACCATATTGGGTAGTTTATTGCAATTGG  1524
             |||||||||||||||| |||||||||||||| |||||||||||||| |||||||||||||
Sbjct  422   TACCTTCAGGTTCTGCTACACAAGTTGATGTTACCATATTGGGTAGCTTATTGCAATTGG  481

Query  1525  ACTTCCAAAATCCTAGGGT  1543
             |||||||||||||||||||
Sbjct  482   ACTTCCAAAATCCTAGGGT  500


 Score = 394 bits (213),  Expect = 3e-105
 Identities = 237/249 (95%), Gaps = 0/249 (0%)
 Strand=Plus/Minus

Query  1414  ATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCTATACCTTCAG  1473
             ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  249   ATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCCATACCTTCAG  190

Query  1474  GTTCTGCGACACAAGTTGATGTAACCATATTGGGTAGTTTATTGCAATTGGACTTCCAAA  1533
             ||||||| |||||||||||||| |||||||||||||||| ||||||||||||||||||||||
Sbjct  189   GTTCTGCTACACAAGTTGATGTTACCATATTGGGTAGCTTATTGCAATTGGACTTCCAAA  130

Query  1534  ATCCTAGGGTGTTTGGCCAAGACGTTGGTATCTATGATAATGCACCAACGCGGAAACAAA  1593
             |||||||||| || || |||||||||||||| ||||| ||||||||||||||||| ||||
Sbjct  129   ATCCTAGGGTATTCGGTCAAGACGTTGGTATTTATGACAATGCACCAACGCGGAAGCAAA  70

Query  1594  ATCTTAAAAAGATTCTTACAATGAGCACTAAATACAAGTGGACTAGGGGAAAAATTGACA  1653
             ||||||| || |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  69    ATCTTAAGAAAATTCTTACAATGAGCACTAAATACAAGTGGACTAGGGGAAAAATTGACA  10

Query  1654  TTGCAGAAG  1662
             |||||||||
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Sbjct  9     TTGCAGAAG  1


>SRR2298546.892755 892755 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  1228  ATGTTAACCAAGGAACAGCTGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGA  1287
              ||||||| ||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  1     ATGTTAATCAAGGAACAGCCGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGA  60

Query  1288  CATATGACTCAAAGTTAGAATTTGGAGCATTTACCAATTTACCACATGTATTGATGAATT  1347
              |||||||||||||||||||||||||||| |||||||||||||||||||| ||||||||||
Sbjct  61    CATATGACTCAAAGTTAGAATTTGGAGCGTTTACCAATTTACCACATGTGTTGATGAATT  120

Query  1348  TGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTA  1407
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   TGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTA  180

Query  1408  AAACGGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCTATAC  1467
              |||| |||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  181   AAACAGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCCATAC  240

Query  1468  CTTCAGGTTC  1477
              ||||||||||
Sbjct  241   CTTCAGGTTC  250


 Score = 425 bits (230),  Expect = 9e-115
 Identities = 244/251 (97%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  1292  TGACTCAAAGTTAGAATTTGGAGCATTTACCAATTTACCACATGTATTGATGAATTTGGC  1351
              |||||||||||||||||||||||| |||||||||||||||||||| ||||||||||||||
Sbjct  500   TGACTCAAAGTTAGAATTTGGAGCGTTTACCAATTTACCACATGTGTTGATGAATTTGGC  441

Query  1352  TGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAAC  1411
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  440   TGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAAC  381

Query  1412  GGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCTATACCTTC  1471
               |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  380   AGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCCATACCTTC  321

Query  1472  AGGTTCTGCGACACAAGTTGATGTAACCATATTGGGTAGTTTATTGCAATTGGACTTCCA  1531
              ||||||||| |||||||||||||| |||||||||||||| ||||||||||||||||||||
Sbjct  320   AGGTTCTGCTACACAAGTTGATGTTACCATATTGGGTAGCTTATTGCAATTGGACTTCCA  261

Query  1532  AAATCCTAGGG  1542
              |||||||||||
Sbjct  260   AAATCCTAGGG  250


>SRR2298546.846783 846783 length=501
Length=501
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 Score = 429 bits (232),  Expect = 7e-116
 Identities = 242/247 (98%), Gaps = 0/247 (0%)
 Strand=Plus/Plus

Query  1249  GTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAAT  1308
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAAT  60

Query  1309  TTGGAGCATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTG  1368
             ||||||| |||||||||||||||||||| |||||||||||||||||||||||||||||||
Sbjct  61    TTGGAGCGTTTACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTG  120

Query  1369  ATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAG  1428
             ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct  121   ATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAG  180

Query  1429  GGCAACTAAAAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAG  1488
             |||||||||||||||||||||||||||||||||| ||||||||||||||||| |||||||
Sbjct  181   GGCAACTAAAAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAG  240

Query  1489  TTGATGT  1495
             |||||||
Sbjct  241   TTGATGT  247


 Score = 392 bits (212),  Expect = 9e-105
 Identities = 238/251 (95%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  1379  CCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACTAAA  1438
             ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  501   CCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAACTAAA  442

Query  1439  AGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGATGTAAC  1498
             |||||||||||||||||||||||| ||||||||||||||||| |||||||||||||| ||
Sbjct  441   AGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGATGTTAC  382

Query  1499  CATATTGGGTAGTTTATTGCAATTGGACTTCCAAAATCCTAGGGTGTTTGGCCAAGACGT  1558
             |||||||||||| |||||||||||||||||||||||||||||||| || || ||||||||
Sbjct  381   CATATTGGGTAGCTTATTGCAATTGGACTTCCAAAATCCTAGGGTATTCGGTCAAGACGT  322

Query  1559  TGGTATCTATGATAATGCACCAACGCGGAAACAAAATCTTAAAAAGATTCTTACAATGAG  1618
             |||||| ||||| ||||||||||||||||| ||||||||||| || ||||||||||||||
Sbjct  321   TGGTATTTATGACAATGCACCAACGCGGAAGCAAAATCTTAAGAAAATTCTTACAATGAG  262

Query  1619  CACTAAATACA  1629
             |||||||||||
Sbjct  261   CACTAAATACA  251


>SRR2298546.823945 823945 length=502
Length=502

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  1236  CAAGGAACAGCTGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGAC  1295
             |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  250   CAAGGAACAGCCGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGAC  191

Query  1296  TCAAAGTTAGAATTTGGAGCATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAG  1355
              |||||||||||||||||||| |||||||||||||||||||| ||||||||||||||||||
Sbjct  190   TCAAAGTTAGAATTTGGAGCGTTTACCAATTTACCACATGTGTTGATGAATTTGGCTGAG  131

Query  1356  ACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGAT  1415
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  130   ACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGAT  71

Query  1416  TCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGT  1475
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  70    TCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGT  11

Query  1476  TCTGCGACAC  1485
              ||||| ||||
Sbjct  10    TCTGCTACAC  1


 Score = 398 bits (215),  Expect = 2e-106
 Identities = 239/251 (95%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  1041  GAGAAGAATCCTAGCAAATTAGTTAGATTAGAGACACATGAGTGGACACCAACATGGGCT  1100
              ||||| |||||||||||||| |||||||| ||||||||||||||||||||||| ||||||
Sbjct  252   GAGAAAAATCCTAGCAAATTGGTTAGATTGGAGACACATGAGTGGACACCAACCTGGGCT  311

Query  1101  AGAGGACATCAGATAACCCATGTGGAATTGCCAAAAGTCTTTTGGGACAAAAACAGTAAG  1160
              ||||||||||||||||||||||||||| | |||||||||||||||||||||||||| |||
Sbjct  312   AGAGGACATCAGATAACCCATGTGGAACTACCAAAAGTCTTTTGGGACAAAAACAGCAAG  371

Query  1161  CCAGCCTATGGCCAATCAAGATACTTTGCAGCAGTACGGTGTGGCTTTCATTTTCAGGTG  1220
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||| ||
Sbjct  372   CCAGCCTATGGCCAATCAAGATACTTTGCAGCAGTACGGTGTGGTTTTCATTTTCAAGTA  431

Query  1221  CAAGTGAATGTTAACCAAGGAACAGCTGGTAGTGCATTGGTGGTGTATGAACCCAAACCT  1280
              |||||||||||||| ||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  432   CAAGTGAATGTTAATCAAGGAACAGCCGGTAGTGCATTGGTGGTGTATGAACCCAAACCT  491

Query  1281  GTTGTGACATA  1291
              |||||||||||
Sbjct  492   GTTGTGACATA  502


>SRR2298546.818952 818952 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 250/259 (97%), Gaps = 0/259 (0%)
 Strand=Plus/Minus

Query  381  TTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGC  440
            ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  500  TTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGC  441

Query  441  CAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAG  500
            ||||||||||||| ||||||||||||||||||||||| |||||||||| |||||||||||
Sbjct  440  CAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTATAAACCTGAGGTGTTGTGGAAG  381
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Query  501  ATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGA  560
            ||||||||||||| |||||||||||||| |||||||||||||||||||||||||||||||
Sbjct  380  ATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGA  321

Query  561  TGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTAC  620
            |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Sbjct  320  TGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATTTGGGGCCAGGTAC  261

Query  621  CTCTATCTTGGTGACCTGG  639
            |||||||||||  ||||||
Sbjct  260  CTCTATCTTGGGTACCTGG  242


 Score = 407 bits (220),  Expect = 3e-109
 Identities = 240/250 (96%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  372  AAGCAACATTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGC  431
            || ||| | ||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    AAACAATACTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGC  60

Query  432  CTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATG  491
            |||||||||||||||||||||| ||||||||||||||||||||||| |||||||||| ||
Sbjct  61   CTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTATAAACCTGAGGTG  120

Query  492  TTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCC  551
            |||||||||||||||||||||| |||||||||||||| ||||||||||||||||||||||
Sbjct  121  TTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCC  180

Query  552  CACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGG  611
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  181  CACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATTTGGG  240

Query  612  GCCAGGTACC  621
            ||||||||||
Sbjct  241  GCCAGGTACC  250


>SRR2298546.568253 568253 length=501
Length=501

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  1221  CAAGTGAATGTTAACCAAGGAACAGCTGGTAGTGCATTGGTGGTGTATGAACCCAAACCT  1280
             |||||||||||||| ||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  252   CAAGTGAATGTTAATCAAGGAACAGCCGGTAGTGCATTGGTGGTGTATGAACCCAAACCT  311

Query  1281  GTTGTGACATATGACTCAAAGTTAGAATTTGGAGCATTTACCAATTTACCACATGTATTG  1340
             ||||||||||||||||||||||||||||||||||| |||||||||||||||||||| |||
Sbjct  312   GTTGTGACATATGACTCAAAGTTAGAATTTGGAGCGTTTACCAATTTACCACATGTGTTG  371

Query  1341  ATGAATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAAC  1400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  372   ATGAATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAAC  431

Query  1401  TATGTTAAAACGGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTA  1460
             ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  432   TATGTTAAAACAGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTA  491

Query  1461  TCTATACCTT  1470
             || |||||||
Sbjct  492   TCCATACCTT  501


 Score = 403 bits (218),  Expect = 4e-108
 Identities = 240/251 (96%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  1470  TCAGGTTCTGCGACACAAGTTGATGTAACCATATTGGGTAGTTTATTGCAATTGGACTTC  1529
             ||||||||||| |||||||||||||| |||||||||||||| ||||||||||||||||||
Sbjct  251   TCAGGTTCTGCTACACAAGTTGATGTTACCATATTGGGTAGCTTATTGCAATTGGACTTC  192

Query  1530  CAAAATCCTAGGGTGTTTGGCCAAGACGTTGGTATCTATGATAATGCACCAACGCGGAAA  1589
             |||||||||||||| || || |||||||||||||| ||||| ||||||||||||||||| 
Sbjct  191   CAAAATCCTAGGGTATTCGGTCAAGACGTTGGTATTTATGACAATGCACCAACGCGGAAG  132

Query  1590  CAAAATCTTAAAAAGATTCTTACAATGAGCACTAAATACAAGTGGACTAGGGGAAAAATT  1649
             ||||||||||| || |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  131   CAAAATCTTAAGAAAATTCTTACAATGAGCACTAAATACAAGTGGACTAGGGGAAAAATT  72

Query  1650  GACATTGCAGAAGGGCCAGGTTCTATGAACATGGCGAACGTATTGAGTACCACTGCAGCG  1709
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  71    GACATTGCAGAAGGGCCAGGTTCTATGAACATGGCGAACGTATTGAGTACCACTGCAGCG  12

Query  1710  CAATCAATTGC  1720
             |||||||||||
Sbjct  11    CAATCAATTGC  1


>SRR2298546.429759 429759 length=502
Length=502

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 246/253 (97%), Gaps = 0/253 (0%)
 Strand=Plus/Plus

Query  1221  CAAGTGAATGTTAACCAAGGAACAGCTGGTAGTGCATTGGTGGTGTATGAACCCAAACCT  1280
             |||||||||||||| ||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  250   CAAGTGAATGTTAATCAAGGAACAGCCGGTAGTGCATTGGTGGTGTATGAACCCAAACCT  309

Query  1281  GTTGTGACATATGACTCAAAGTTAGAATTTGGAGCATTTACCAATTTACCACATGTATTG  1340
             ||||||||||||||||||||||||||||||||||| ||||||||||| |||||||| |||
Sbjct  310   GTTGTGACATATGACTCAAAGTTAGAATTTGGAGCGTTTACCAATTTGCCACATGTGTTG  369

Query  1341  ATGAATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAAC  1400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  370   ATGAATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAAC  429

Query  1401  TATGTTAAAACGGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTA  1460
             ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  430   TATGTTAAAACAGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTA  489

Query  1461  TCTATACCTTCAG  1473
             || ||||||||||
Sbjct  490   TCCATACCTTCAG  502
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 Score = 420 bits (227),  Expect = 4e-113
 Identities = 243/251 (97%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  1292  TGACTCAAAGTTAGAATTTGGAGCATTTACCAATTTACCACATGTATTGATGAATTTGGC  1351
             |||||||||||||||||||||||| ||||||||||| |||||||| ||||||||||||||
Sbjct  251   TGACTCAAAGTTAGAATTTGGAGCGTTTACCAATTTGCCACATGTGTTGATGAATTTGGC  192

Query  1352  TGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAAC  1411
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  191   TGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAAC  132

Query  1412  GGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCTATACCTTC  1471
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  131   AGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCCATACCTTC  72

Query  1472  AGGTTCTGCGACACAAGTTGATGTAACCATATTGGGTAGTTTATTGCAATTGGACTTCCA  1531
             ||||||||| |||||||||||||| |||||||||||||| ||||||||||||||||||||
Sbjct  71    AGGTTCTGCTACACAAGTTGATGTTACCATATTGGGTAGCTTATTGCAATTGGACTTCCA  12

Query  1532  AAATCCTAGGG  1542
             |||||||||||
Sbjct  11    AAATCCTAGGG  1


>SRR2298546.424373 424373 length=501
Length=501

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 246/253 (97%), Gaps = 0/253 (0%)
 Strand=Plus/Plus

Query  380  TTTTGCTGCAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGG  439
            |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  249  TTTTGCTGTAAAGCATCCTATTGCCAGCGGAACAACACCTGGTAACAGGTGCCTCTGGGG  308

Query  440  CCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAA  499
            |||||||||||||| ||||||||||||||||||||||| |||||||||| ||||||||||
Sbjct  309  CCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTATAAACCTGAGGTGTTGTGGAA  368

Query  500  GATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGG  559
            |||||||||||||| |||||||||||||| ||||||||||||||||||||||||||||||
Sbjct  369  GATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGG  428

Query  560  ATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTA  619
            ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  429  ATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATTTGGGGCCAGGTA  488

Query  620  CCTCTATCTTGGT  632
            |||||||||||||
Sbjct  489  CCTCTATCTTGGT  501


 Score = 407 bits (220),  Expect = 3e-109
 Identities = 240/250 (96%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  498  AAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAA  557
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                ||||||||||||||||| ||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  250  AAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAA  191

Query  558  GGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGG  617
            ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  190  GGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATTTGGGGCCAGG  131

Query  618  TACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCC  677
            ||||||||||||||||| ||||||||||| ||||||||||||||||||||||||||||||
Sbjct  130  TACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCC  71

Query  678  CCGGTTTCCTTTTATTTTATCAATGCTACAATGGAGACAATTAAAAGTATTGCAGATATG  737
            |||||||||||||||||||||||||| |  |||||||||||||| |||||||||||||||
Sbjct  70   CCGGTTTCCTTTTATTTTATCAATGCCATTATGGAGACAATTAAGAGTATTGCAGATATG  11

Query  738  GCGACCGGAG  747
            || |||||||
Sbjct  10   GCAACCGGAG  1


>SRR2298546.317425 317425 length=500
Length=500

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  1231  TTAACCAAGGAACAGCTGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACAT  1290
             |||| ||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  250   TTAATCAAGGAACAGCCGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACAT  191

Query  1291  ATGACTCAAAGTTAGAATTTGGAGCATTTACCAATTTACCACATGTATTGATGAATTTGG  1350
             ||||||||||||||||||||||||| |||||||||||||||||||| |||||||||||||
Sbjct  190   ATGACTCAAAGTTAGAATTTGGAGCGTTTACCAATTTACCACATGTGTTGATGAATTTGG  131

Query  1351  CTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAA  1410
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  130   CTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAA  71

Query  1411  CGGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCTATACCTT  1470
             | |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  70    CAGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCCATACCTT  11

Query  1471  CAGGTTCTGC  1480
             ||||||||||
Sbjct  10    CAGGTTCTGC  1


 Score = 418 bits (226),  Expect = 2e-112
 Identities = 242/250 (97%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  1146  GACAAAAACAGTAAGCCAGCCTATGGCCAATCAAGATACTTTGCAGCAGTACGGTGTGGC  1205
             ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  251   GACAAAAACAGCAAGCCAGCCTATGGCCAATCAAGATACTTTGCAGCAGTACGGTGTGGT  310

Query  1206  TTTCATTTTCAGGTGCAAGTGAATGTTAACCAAGGAACAGCTGGTAGTGCATTGGTGGTG  1265
             ||||||||||| || |||||||||||||| ||||||||||| ||||||||||||||||||
Sbjct  311   TTTCATTTTCAAGTACAAGTGAATGTTAATCAAGGAACAGCCGGTAGTGCATTGGTGGTG  370
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Query  1266  TATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCATTTACCAAT  1325
             |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct  371   TATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCGTTTACCAAT  430

Query  1326  TTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTAT  1385
             ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  431   TTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTAT  490

Query  1386  GTTGCTGACA  1395
             ||||||||||
Sbjct  491   GTTGCTGACA  500


>SRR2298546.264343 264343 length=501
Length=501

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 242/247 (98%), Gaps = 0/247 (0%)
 Strand=Plus/Plus

Query  1249  GTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAAT  1308
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  252   GTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAAT  311

Query  1309  TTGGAGCATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTG  1368
             ||||||| |||||||||||||||||||| |||||||||||||||||||||||||||||||
Sbjct  312   TTGGAGCGTTTACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTG  371

Query  1369  ATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAG  1428
             ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct  372   ATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAG  431

Query  1429  GGCAACTAAAAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAG  1488
             |||||||||||||||||||||||||||||||||| ||||||||||||||||| |||||||
Sbjct  432   GGCAACTAAAAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAG  491

Query  1489  TTGATGT  1495
             |||||||
Sbjct  492   TTGATGT  498


 Score = 409 bits (221),  Expect = 9e-110
 Identities = 241/251 (96%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  1307  ATTTGGAGCATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGC  1366
             ||||||||| |||||||||||||||||||| |||||||||||||||||||||||||||||
Sbjct  251   ATTTGGAGCGTTTACCAATTTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGC  192

Query  1367  TGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTT  1426
             ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  191   TGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTT  132

Query  1427  AGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACA  1486
             |||||||||||||||||||||||||||||||||||| ||||||||||||||||| |||||
Sbjct  131   AGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACA  72

Query  1487  AGTTGATGTAACCATATTGGGTAGTTTATTGCAATTGGACTTCCAAAATCCTAGGGTGTT  1546
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             ||||||||| |||||||||||||| |||||||||||||||||||||||||||||||| ||
Sbjct  71    AGTTGATGTTACCATATTGGGTAGCTTATTGCAATTGGACTTCCAAAATCCTAGGGTATT  12

Query  1547  TGGCCAAGACG  1557
              || |||||||
Sbjct  11    CGGTCAAGACG  1


>SRR2298382.75729 75729 length=501
Length=501

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  428  GTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATTGGTTCTAAACCTGA  487
            |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  1    GTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATTGGTTCTAAACCTGA  60

Query  488  GATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTTGTAA  547
            |||||||||||||||||||||||||| |||||||||||||| ||||||||||||||||||
Sbjct  61   GATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTTGTAA  120

Query  548  GGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCTGATC  607
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  121  GGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCTGATC  180

Query  608  TGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCg  667
            ||||||||||||||||||||||||||| ||||||||||| ||||||||||||||||||||
Sbjct  181  TGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAACCCG  240

Query  668  ggggggATCC  677
            ||||||||||
Sbjct  241  GGGGGGATCC  250


 Score = 414 bits (224),  Expect = 2e-111
 Identities = 242/251 (96%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  484  CTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTAGTT  543
            ||||||||||||||||||| |||||||||| |||||||||||||| ||||||||||||||
Sbjct  501  CTGAGATGTTGTGGAAGATTCTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTAGTT  442

Query  544  GTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGATCT  603
            ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  441  GTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGATCT  382

Query  604  GATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCCAAA  663
            ||||||||||||||||||||||||||||||| ||||||||||| ||||||||||||||||
Sbjct  381  GATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCCAAA  322

Query  664  CCCgggggggATCCCCGGTTTCCTTTTATTTTATCAATGCTACAATGGAGACAATTAAAA  723
            |||||||||||||||||||||||||||||||||||||||| || |||||||||||||| |
Sbjct  321  CCCGGGGGGGATCCCCGGTTTCCTTTTATTTTATCAATGCCACTATGGAGACAATTAAGA  262

Query  724  GTATTGCAGAT  734
            |||||||||||
Sbjct  261  GTATTGCAGAT  251
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>SRR2298382.11686 11686 length=501
Length=501

 Score = 429 bits (232),  Expect = 7e-116
 Identities = 244/250 (98%), Gaps = 0/250 (0%)
 Strand=Plus/Plus

Query  414  ACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCCTTTAGGATT  473
            |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  1    ACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCCTTTAGGATT  60

Query  474  GGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCA  533
            |||||||||||||||||||||||||||||||||||||||| |||||||||||||| ||||
Sbjct  61   GGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCA  120

Query  534  AACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACA  593
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  121  AACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACA  180

Query  594  CTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTA  653
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||| ||||||
Sbjct  181  CTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTA  240

Query  654  GTGGGCCAAA  663
            ||||||||||
Sbjct  241  GTGGGCCAAA  250


 Score = 418 bits (226),  Expect = 2e-112
 Identities = 242/250 (97%), Gaps = 0/250 (0%)
 Strand=Plus/Minus

Query  481  AACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGTAGTACTGCAAACACTA  540
            ||||||||||||||||||||||||||||||||| |||||||||||||| |||||||||||
Sbjct  500  AACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGTAGTAGTGCAAACACTA  441

Query  541  GTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGGA  600
            |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  440  GTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGCGACACTATGGA  381

Query  601  TCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGCC  660
            |||||||||||||||||||||||||||||||||| ||||||||||| |||||||||||||
Sbjct  380  TCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGCC  321

Query  661  AAACCCgggggggATCCCCGGTTTCCTTTTATTTTATCAATGCTACAATGGAGACAATTA  720
            ||||||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Sbjct  320  AAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTATCAATGCCACTATGGAGACAATTA  261

Query  721  AAAGTATTGC  730
            | ||||||||
Sbjct  260  AGAGTATTGC  251


>SRR2298578.1031647 1031647 length=500
Length=500

 Score = 427 bits (231),  Expect = 3e-115
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 Identities = 243/249 (98%), Gaps = 0/249 (0%)
 Strand=Plus/Minus

Query  1227  AATGTTAACCAAGGAACAGCTGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTG  1286
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  249   AATGTTAATCAAGGAACAGCTGGTAGTGCATTGGTGGTGTATGAACCCAAACCCGTTGTG  190

Query  1287  ACATATGACTCAAAGTTAGAATTTGGAGCATTTACCAATTTACCACATGTATTGATGAAT  1346
             ||||||||||||||||||||||||||||||||||||||| |||||||||| |||||||||
Sbjct  189   ACATATGACTCAAAGTTAGAATTTGGAGCATTTACCAATCTACCACATGTGTTGATGAAT  130

Query  1347  TTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTT  1406
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  129   TTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTT  70

Query  1407  AAAACGGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCTATA  1466
             ||||| |||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  69    AAAACAGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCCATA  10

Query  1467  CCTTCAGGT  1475
             |||||||||
Sbjct  9     CCTTCAGGT  1


 Score = 137 bits (74),  Expect = 5e-28
 Identities = 88/95 (93%), Gaps = 0/95 (0%)
 Strand=Plus/Plus

Query  1190  AGCAGTACGGTGTGGCTTTCATTTTCAGGTGCAAGTGAATGTTAACCAAGGAACAGCTGG  1249
             ||||||||||||||| ||||| ||||| ||||||| ||||||||| ||||||||||||||
Sbjct  394   AGCAGTACGGTGTGGTTTTCACTTTCAAGTGCAAGGGAATGTTAATCAAGGAACAGCTGG  453

Query  1250  TAGTGCATTGGTGGTGTATGAACCCAAACCTGTTG  1284
             ||||||||||||||||||||||| |||||| ||||
Sbjct  454   TAGTGCATTGGTGGTGTATGAACCAAAACCCGTTG  488


>SRR2298578.969663 969663 length=500
Length=500

 Score = 427 bits (231),  Expect = 3e-115
 Identities = 243/249 (98%), Gaps = 0/249 (0%)
 Strand=Plus/Plus

Query  1252  GTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTG  1311
             |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Sbjct  1     GTGCATTGGTGGTGTATGAACCCAAACCCGTTGTGACATATGACTCAAAGTTAGAATTTG  60

Query  1312  GAGCATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATT  1371
             |||||||||||||| |||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  61    GAGCATTTACCAATCTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATT  120

Query  1372  TATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGC  1431
             |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  121   TATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGC  180

Query  1432  AACTAAAAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTG  1491
             ||||||||||||||||||||||||||||||| ||||||||||||||||| ||||||||||
Sbjct  181   AACTAAAAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTG  240
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Query  1492  ATGTAACCA  1500
             |||||||||
Sbjct  241   ATGTAACCA  249


 Score = 375 bits (203),  Expect = 9e-100
 Identities = 235/251 (94%), Gaps = 0/251 (0%)
 Strand=Plus/Minus

Query  1312  GAGCATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATT  1371
             |||| ||| ||||| | || ||||| |||||||||||||||||||||| |||||||||||
Sbjct  500   GAGCCTTTTCCAATCTTCCCCATGTGTTGATGAATTTGGCTGAGACCAAACAGGCTGATT  441

Query  1372  TATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGC  1431
             |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  440   TATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGC  381

Query  1432  AACTAAAAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTG  1491
             ||||||||||||||||||||||||||||||| ||||||||||||||||| ||||||||||
Sbjct  380   AACTAAAAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTG  321

Query  1492  ATGTAACCATATTGGGTAGTTTATTGCAATTGGACTTCCAAAATCCTAGGGTGTTTGGCC  1551
             |||||||||||||||||||  |||||||||||||||||||||| |||||||| || ||||
Sbjct  320   ATGTAACCATATTGGGTAGCCTATTGCAATTGGACTTCCAAAACCCTAGGGTATTCGGCC  261

Query  1552  AAGACGTTGGT  1562
             | |||||||||
Sbjct  260   AGGACGTTGGT  250


>SRR2298578.960513 960513 length=500
Length=500

 Score = 427 bits (231),  Expect = 3e-115
 Identities = 246/253 (97%), Gaps = 1/253 (0%)
 Strand=Plus/Minus

Query  1211  TTT-TCAGGTGCAAGTGAATGTTAACCAAGGAACAGCTGGTAGTGCATTGGTGGTGTATG  1269
             ||| ||| ||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  254   TTTGTCAAGTGCAAGTGAATGTTAATCAAGGAACAGCTGGTAGTGCATTGGTGGTGTATG  195

Query  1270  AACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCATTTACCAATTTAC  1329
             |||||||||| ||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  194   AACCCAAACCCGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCATTTACCAATCTAC  135

Query  1330  CACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTG  1389
             ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  134   CACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTG  75

Query  1390  CTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTT  1449
             |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  74    CTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTT  15

Query  1450  GGACACCTTTATC  1462
             |||||||||||||
Sbjct  14    GGACACCTTTATC  2
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 Score = 353 bits (191),  Expect = 4e-93
 Identities = 229/248 (92%), Gaps = 0/248 (0%)
 Strand=Plus/Plus

Query  1128  TTGCCAAAAGTCTTTTGGGACAAAAACAGTAAGCCAGCCTATGGCCAATCAAGATACTTT  1187
             ||| ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Sbjct  247   TTGACAAAAGTCTTTTGGGACAAAAACAGCAAGCCAGCCTATGGCCAATCAAGATACTTT  306

Query  1188  GCAGCAGTACGGTGTGGCTTTCATTTTCAGGTGCAAGTGAATGTTAACCAAGGAACAGCT  1247
             ||||||||||||||||| ||||| ||||| ||||||||||||||||| ||||||||||||
Sbjct  307   GCAGCAGTACGGTGTGGTTTTCACTTTCAAGTGCAAGTGAATGTTAATCAAGGAACAGCT  366

Query  1248  GGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAA  1307
             |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Sbjct  367   GGTAGTGCATTGGTGGTGTATGAACCCAAACCAGTTGTGACATATGACTCAAAGTTAGAA  426

Query  1308  TTTGGAGCATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCT  1367
             ||||||||| |||||||  ||||| |||  |||||||| ||||||||||||| ||  | |
Sbjct  427   TTTGGAGCAATTACCAAACTACCAAATGGGTTGATGAAATTGGCTGAGACCAAACCAGAT  486

Query  1368  GATTTATG  1375
             | ||||||
Sbjct  487   GGTTTATG  494


>SRR2298578.398520 398520 length=500
Length=500

 Score = 427 bits (231),  Expect = 3e-115
 Identities = 247/255 (97%), Gaps = 0/255 (0%)
 Strand=Plus/Minus

Query  1272  CCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCATTTACCAATTTACCA  1331
             |||| ||| ||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  255   CCCAGACCCGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCATTTACCAATCTACCA  196

Query  1332  CATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCT  1391
             ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  195   CATGTTTTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTGCT  136

Query  1392  GACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGG  1451
             |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct  135   GACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTTGG  76

Query  1452  ACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGATGTAACCATATTGGGTAGT  1511
             ||||||||||| ||||||||||||||||| |||||||||||||||||||||||||||||
Sbjct  75    ACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGATGTAACCATATTGGGTAGC  16

Query  1512  TTATTGCAATTGGAC  1526
             |||||||||||||||
Sbjct  15    TTATTGCAATTGGAC  1


 Score = 392 bits (212),  Expect = 9e-105
 Identities = 234/245 (96%), Gaps = 0/245 (0%)
 Strand=Plus/Plus

Query  1194  GTACGGTGTGGCTTTCATTTTCAGGTGCAAGTGAATGTTAACCAAGGAACAGCTGGTAGT  1253
             ||||||||||| ||||| ||||| ||||||||||||||||| ||||||||||||||||||
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Sbjct  256   GTACGGTGTGGTTTTCACTTTCAAGTGCAAGTGAATGTTAATCAAGGAACAGCTGGTAGT  315

Query  1254  GCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGA  1313
             |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  316   GCATTGGTGGTGTATGAACCCAAACCCGTTGTGACATATGACTCAAAGTTAGAATTTGGA  375

Query  1314  GCATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTTA  1373
             |||||||||||| |||||||||| |||||||||||||||||||| |||||||||||||||
Sbjct  376   GCATTTACCAATCTACCACATGTGTTGATGAATTTGGCTGAGACAACACAGGCTGATTTA  435

Query  1374  TGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAA  1433
             ||||||||||||||||||||||||||| || ||||||| |||||||||||||||||||||
Sbjct  436   TGTATCCCCTATGTTGCTGACACAAACCATCTTAAAACAGATTCGTCAGACTTAGGGCAA  495

Query  1434  CTAAA  1438
             |||||
Sbjct  496   CTAAA  500


>SRR2298578.380777 380777 length=500
Length=500

 Score = 427 bits (231),  Expect = 3e-115
 Identities = 243/249 (98%), Gaps = 0/249 (0%)
 Strand=Plus/Plus

Query  1252  GTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTG  1311
             |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Sbjct  1     GTGCATTGGTGGTGTATGAACCCAAACCCGTTGTGACATATGACTCAAAGTTAGAATTTG  60

Query  1312  GAGCATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATT  1371
             |||||||||||||| |||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  61    GAGCATTTACCAATCTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATT  120

Query  1372  TATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGC  1431
             |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  121   TATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGC  180

Query  1432  AACTAAAAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTG  1491
             ||||||||||||||||||||||||||||||| ||||||||||||||||| ||||||||||
Sbjct  181   AACTAAAAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTG  240

Query  1492  ATGTAACCA  1500
             |||||||||
Sbjct  241   ATGTAACCA  249


 Score = 388 bits (210),  Expect = 1e-103
 Identities = 236/249 (95%), Gaps = 0/249 (0%)
 Strand=Plus/Minus

Query  1270  AACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCATTTACCAATTTAC  1329
             |||||||||| ||||| |||| || || |||||||||||||||||||||||||||| | |
Sbjct  499   AACCCAAACCCGTTGTTACATTTGCCTTAAAGTTAGAATTTGGAGCATTTACCAATCTTC  440

Query  1330  CACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTG  1389
             ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  439   CACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGTATCCCCTATGTTG  380
```

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Query  1390   CTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTT  1449
              ||||||||| |||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  379    CTGACACAAGCTATGTTAAAACAGATTCGTCAGACTTAGGGCAACTAAAAGTCTATGTTT  320

Query  1450   GGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGATGTAACCATATTGGGTA  1509
              ||||||||||||| ||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  319    GGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGATGTAACCATATTGGGTA  260

Query  1510   GTTTATTGC  1518
              | |||||||
Sbjct  259    GCTTATTGC  251


>SRR2298578.377864 377864 length=500
Length=500

 Score = 427 bits (231),  Expect = 3e-115
 Identities = 280/304 (92%), Gaps = 1/304 (0%)
 Strand=Plus/Plus

Query  1716   ATTGCTTTGGTTGGAGAAAGAGCATTCTATGATCCAAGAACAGCAGGAAGCAAGAGTAGG  1775
              ||||| |||||||||||||| ||||||||||| |||||||||||||||||||||||||||
Sbjct  3      ATTGCCTTGGTTGGAGAAAGGGCATTCTATGACCCAAGAACAGCAGGAAGCAAGAGTAGG  62

Query  1776   TTTGATGATTTAGTGAAAATATCCCAACTTTTTTCTGTGATGAGTGACTCCACAACTCCC  1835
              |||||||||||||| |||||||| |||||||||||||||||||||||||| ||||| ||
Sbjct  63     TTTGATGATTTAGTAAAAATATCTCAACTTTTTTCTGTGATGAGTGACTCAACAACCCCT  122

Query  1836   TCAGCCAACCATGGTATAGATGCAAAAGGTTATTTCACATGGTCATCCACAACTGCACCA  1895
              ||||||||||||||||||||||||||||| ||||| |  |||||||||||||| |||||
Sbjct  123    TCAGCCAACCATGGTATAGATGCAAAAGGCTATTTTAAGTGGTCATCCACAACAGCACCC  182

Query  1896   CAATCTGTAGTACATAGGAATATTGTTTACTTAAAATTATTTCCCAACTTGAATGTTTTT  1955
              || |||||||| |||||||| ||||||||  ||||||| |||||||||||||||||||||
Sbjct  183    CAGTCTGTAGTGCATAGGAAAATTGTTTATCTAAAATTGTTTCCCAACTTGAATGTTTTT  242

Query  1956   GTCAATA-GCTACTCATATTTTAGAGGCTCAATAGTGCTGAGGTTGAGTGTATATGCCAG  2014
              ||||| | ||||||||||||||||||| |||||||||||||||||||| |||||||||||
Sbjct  243    GTCAACAGGCTACTCATATTTTAGAGGATCAATAGTGCTGAGGTTGAGCGTATATGCCAG  302

Query  2015   CACT  2018
              ||||
Sbjct  303    CACT  306


 Score = 267 bits (144),  Expect = 6e-67
 Identities = 178/195 (91%), Gaps = 0/195 (0%)
 Strand=Plus/Minus

Query  1800   CAACTTTTTTCTGTGATGAGTGACTCCACAACTCCCTCAGCCAACCATGGTATAGATGCA  1859
              |||||||||||||||||||||||||| ||| | || ||||||||||||||||||||||||
Sbjct  494    CAACTTTTTTCTGTGATGAGTGACTCAACACCCCCTTCAGCCAACCATGGTATAGATGCA  435

Query  1860   AAAGGTTATTTCACATGGTCATCCACAACTGCACCACAATCTGTAGTACATAGGAATATT  1919
              ||||| ||||| |  |||||||||||||| || ||||| |||||||| ||||||||||||
Sbjct  434    AAAGGCTATTTTAAGTGGTCATCCACAACAGCCCCACAGTCTGTAGTGCATAGGAATATT  375

Query  1920   GTTTACTTAAAATTATTTCCCAACTTGAATGTTTTTGTCAATAGCTACTCATATTTTAGA  1979
              |||||  ||||||| |||||||||||||||||||||||||| ||||||||||||||||||
```

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Sbjct  374   GTTTATCTAAAATTGTTTCCCAACTTGAATGTTTTTGTCAACAGCTACTCATATTTTAGA  315

Query  1980  GGCTCAATAGTGCTG  1994
             || ||||||||||||
Sbjct  314   GGATCAATAGTGCTG  300


>SRR2298578.142685 142685 length=500
Length=500

 Score = 427 bits (231),  Expect = 3e-115
 Identities = 246/253 (97%), Gaps = 1/253 (0%)
 Strand=Plus/Minus

Query  1256  ATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGC  1315
             ||||||||| |||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  252   ATTGGTGGT-TATGAACCCAAACCCGTTGTGACATATGACTCAAAGTTAGAATTTGGAGC  194

Query  1316  ATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTTATG  1375
             |||||||||| |||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  193   ATTTACCAATCTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATTTATG  134

Query  1376  TATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACT  1435
             |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct  133   TATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAACT  74

Query  1436  AAAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGATGT  1495
             |||||||||||||||||||||||||| ||||||||||||||||| |||||||||||||||
Sbjct  73    AAAAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGATGT  14

Query  1496  AACCATATTGGGT  1508
             |||||||||||||
Sbjct  13    AACCATATTGGGT  1


 Score = 392 bits (212),  Expect = 9e-105
 Identities = 238/251 (95%), Gaps = 0/251 (0%)
 Strand=Plus/Plus

Query  1047  AATCCTAGCAAATTAGTTAGATTAGAGACACATGAGTGGACACCAACATGGGCTAGAGGA  1106
             |||||||||||||| |||||||| ||||||||||||||||||||||| ||||||||||||
Sbjct  250   AATCCTAGCAAATTGGTTAGATTGGAGACACATGAGTGGACACCAACCTGGGCTAGAGGA  309

Query  1107  CATCAGATAACCCATGTGGAATTGCCAAAAGTCTTTTGGGACAAAAACAGTAAGCCAGCC  1166
             ||||||||||| ||||||||||| |||||||||||||||||||||||||| |||||||||
Sbjct  310   CATCAGATAACTCATGTGGAATTACCAAAAGTCTTTTGGGACAAAAACAGCAAGCCAGCC  369

Query  1167  TATGGCCAATCAAGATACTTTGCAGCAGTACGGTGTGGCTTTCATTTTCAGGTGCAAGTG  1226
             |||||||||||||||||||||||||||||||||||||| ||||| ||||| |||||||||
Sbjct  370   TATGGCCAATCAAGATACTTTGCAGCAGTACGGTGTGGTTTTCACTTTCAAGTGCAAGTG  429

Query  1227  AATGTTAACCAAGGAACAGCTGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTG  1286
             |||||||| |||||||||||||| ||||||||||||||||||||||||||||| ||||||
Sbjct  430   AATGTTAATCAAGGAACAGCTGGAAGTGCATTGGTGGTGTATGAACCCAAACCCGTTGTG  489

Query  1287  ACATATGACTC  1297
             ||| |||||||
Sbjct  490   ACAAATGACTC  500
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>SRR2298578.41611 41611 length=500
Length=500

 Score = 427 bits (231),  Expect = 3e-115
 Identities = 245/252 (97%), Gaps = 0/252 (0%)
 Strand=Plus/Minus

Query  1257  TTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTTAGAATTTGGAGCA  1316
             ||||||||||||||||||||||| ||||||||||||| ||||||||||||||||||||||
Sbjct  252   TTGGTGGTGTATGAACCCAAACCCGTTGTGACATATGGCTCAAAGTTAGAATTTGGAGCA  193

Query  1317  TTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGT  1376
             ||||||||| |||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct  192   TTTACCAATCTACCACATGTGTTGATGAATTTGGCTGAGACCACACAGGCTGATTTATGT  133

Query  1377  ATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGACTTAGGGCAACTA  1436
             ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  132   ATCCCCTATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGACTTAGGGCAACTA  73

Query  1437  AAAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGACACAAGTTGATGTA  1496
             |||||||||||||||||||||||||| ||||||||||||||||| |||||||||||||||
Sbjct  72    AAAGTCTATGTTTGGACACCTTTATCCATACCTTCAGGTTCTGCTACACAAGTTGATGTA  13

Query  1497  ACCATATTGGGT  1508
             ||||||||||||
Sbjct  12    ACCATATTGGGT  1


 Score = 344 bits (186),  Expect = 3e-90
 Identities = 228/249 (92%), Gaps = 0/249 (0%)
 Strand=Plus/Plus

Query  1244  AGCTGGTAGTGCATTGGTGGTGTATGAACCCAAACCTGTTGTGACATATGACTCAAAGTT  1303
             ||||| ||| |||||||||||| ||||||||||||| |||||||||||||||||||||||
Sbjct  252   AGCTGATAGGGCATTGGTGGTGCATGAACCCAAACCCGTTGTGACATATGACTCAAAGTT  311

Query  1304  AGAATTTGGAGCATTTACCAATTTACCACATGTATTGATGAATTTGGCTGAGACCACACA  1363
             |||||||||||||| ||||||| || || |||  ||||||||||||||||||||||||||
Sbjct  312   AGAATTTGGAGCATATACCAATCTATCAAATGCGTTGATGAATTTGGCTGAGACCACACA  371

Query  1364  GGCTGATTTATGTATCCCCTATGTTGCTGACACAAACTATGTTAAAACGGATTCGTCAGA  1423
             |||||||||||||||||| ||||||||||||||||||||||||||||| |||||||||||
Sbjct  372   GGCTGATTTATGTATCCCATATGTTGCTGACACAAACTATGTTAAAACAGATTCGTCAGA  431

Query  1424  CTTAGGGCAACTAAAAGTCTATGTTTGGACACCTTTATCTATACCTTCAGGTTCTGCGAC  1483
             ||||||||||||||||||||||||| | ||| ||||||| ||||| | |||||||||
Sbjct  432   CTTAGGGCAACTAAAAGTCTATGTTCGAACAACTTTATCCATACCATAAGGTTCTGCTCA  491

Query  1484  ACAAGTTGA  1492
             |||||||||
Sbjct  492   ACAAGTTGA  500


>SRR2298573.879666 879666 length=500
Length=500

 Score = 427 bits (231),  Expect = 3e-115
 Identities = 243/249 (98%), Gaps = 0/249 (0%)
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 Strand=Plus/Plus

Query  345  GTCTGGTGACGTGTGGGAACTTATTGGAAGCAACATTTTGCTGCAAAGCATCCTATTGCC  404
            ||||||||||||||||||||||||||||| ||||||||||||| ||||||||||||||||
Sbjct  1    GTCTGGTGACGTGTGGGAACTTATTGGAAACAACATTTTGCTGTAAAGCATCCTATTGCC  60

Query  405  AGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTCTAACAAACCC  464
            ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  61   AGCGGAACAACACCTGGTAACAGGTGCCTCTGGGGCCAAAAGCCAAGGTTTAACAAACCC  120

Query  465  TTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTGCCGATCTGGT  524
            ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  121  TTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTACCGATCTGGT  180

Query  525  AGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAA  584
            |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAA  240

Query  585  CAAGTGACA  593
            |||| ||||
Sbjct  241  CAAGCGACA  249


 Score = 368 bits (199),  Expect = 2e-97
 Identities = 231/247 (94%), Gaps = 0/247 (0%)
 Strand=Plus/Minus

Query  530  TGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGT  589
            |||||||||| ||| |||||||| || ||| | |||||||||||||||  |||||| || 
Sbjct  497  TGCAAACACTTGTTTTAAGGCCCCCGGAGGTTTCCCAGAAGGTACCCAATGGTAACCAGC  438

Query  590  GACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCG  649
            |||||||||||||||||||||||||||||||||||| |||||||| ||||||||||| ||
Sbjct  437  GACACTATGGATCTGATCTGGGGCCAGGTACCTCTAGCTTGGTGATCTGGTTAAAAAACG  378

Query  650  TCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTTTATCAATGCTACAAT  709
            |||||||||||||||||||||||||||||||||||||||||||||||||||||| || ||
Sbjct  377  TCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTATCAATGCCACTAT  318

Query  710  GGAGACAATTAAAAGTATTGCAGATATGGCGACCGGAGTGGTCAGTTCAGTTGATTCCAC  769
            |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  317  GGAGACAATTAAGAGTATTGCAGATATGGCGACCGGAGTGGTCAGTTCAGTTGATTCCAC  258

Query  770  TATCAAT  776
            |||||||
Sbjct  257  TATCAAT  251


>SRR2298573.865740 865740 length=500
Length=500

 Score = 427 bits (231),  Expect = 3e-115
 Identities = 243/249 (98%), Gaps = 0/249 (0%)
 Strand=Plus/Plus

Query  455  TAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTG  514
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  251  TAACAAACCCTTTAGGATTGGTTCTAAACCTGAGATGTTGTGGAAGATACTTAGTACCTA  310
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Query  515  CCGATCTGGTAGTACTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTAC  574
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  311  CCGATCTGGTAGTAGTGCAAACACTAGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTAC  370

Query  575  CCATAGGTAACAAGTGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGA  634
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  371  CCATAGGTAACAAGCGACACTATGGATCTGATCTGGGGCCAGGTACCTCTATCTTGGGGA  430

Query  635  CCTGGTTAAAAAGCGTCTAGTGGGCCAAACCCgggggggATCCCCGGTTTCCTTTTATTT  694
             ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  431  TCTGGTTAAAAAACGTCTAGTGGGCCAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTT  490

Query  695  TATCAATGC  703
            |||||||||
Sbjct  491  TATCAATGC  499


 Score = 405 bits (219),  Expect = 1e-108
 Identities = 239/249 (96%), Gaps = 0/249 (0%)
 Strand=Plus/Minus

Query  540  AGTTGTAAGGCCCACGAAGGATGCCCAGAAGGTACCCATAGGTAACAAGTGACACTATGG  599
            |||||||||||||||||||||| |||||||||| ||||||||||||||| ||||||||||
Sbjct  249  AGTTGTAAGGCCCACGAAGGATTCCCAGAAGGTTCCCATAGGTAACAAGCGACACTATGG  190

Query  600  ATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGACCTGGTTAAAAAGCGTCTAGTGGGC  659
            ||||||||||||||||||||||||||||||||||| ||||||||||| ||||||||||||
Sbjct  189  ATCTGATCTGGGGCCAGGTACCTCTATCTTGGTGATCTGGTTAAAAAACGTCTAGTGGGC  130

Query  660  CAAACCCgggggggATCCCCGGTTTCCTTTTATTTTATCAATGCTACAATGGAGACAATT  719
            |||||||||||||||||||||||||||||||||||||||||||| || ||||||||||||
Sbjct  129  CAAACCCGGGGGGGATCCCCGGTTTCCTTTTATTTTATCAATGCCACTATGGAGACAATT  70

Query  720  AAAAGTATTGCAGATATGGCGACCGGAGTGGTCAGTTCAGTTGATTCCACTATCAATGCA  779
            || ||||||||||||| ||||||||||||||||||||||||||||||||||||||||| |
Sbjct  69   AAGAGTATTGCAGATACGGCGACCGGAGTGGTCAGTTCAGTTGATTCCACTATCAATGTA  10

Query  780  GTTAATGAG  788
            |||||||||
Sbjct  9    GTTAATGAG  1




Lambda      K        H
    1.33    0.621     1.12

Gapped
Lambda      K        H
    1.28    0.460    0.850

Effective search space used: 143028841133916


  Database: virome_reads.fasta
    Posted date:  Aug 31, 2017  9:43 AM
  Number of letters in database: 21,830,462,082
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  Number of sequences in database:  64,922,850



Matrix: blastn matrix 1 -2
Gap Penalties: Existence: 0, Extension: 2.5

BLASTN 2.6.0+


Reference: Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb
Miller (2000), "A greedy algorithm for aligning DNA sequences", J
Comput Biol 2000; 7(1-2):203-14.



Database: virome_reads.fasta
           64,922,850 sequences; 21,830,462,082 total letters
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The full length reads that gave significant hits for LCDV-Sa.

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>SRR2298382.126301 126301 length=502
GATAGGCCCACAAGGCCCTCAAGGCTTGACTGGCCCACAAGGGCAACGTGGGGAAACTGGTCAACAAGGTTTGCAAGGAC
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TTGCAAGGCGAGCAAGGCCGTGACGGCGTAGGAATCCCGCAAAAGCTGACCTTATCAGGAAACACACTCACGCTGTCAGA
CGGTGGGGGAAACTTGGTAGCGTTACACTTCCCCCACCGTCTGACAGCGTGAGTGTGTTTCCTGATAAGGTCAGCTTTTG
CGGGATTCCTACGCCGTCACGGCCTTGCTCGCCTTGCAAACCTTGAGGGCCAATAGGGCCTTGTAGTCCGTCCGCTCCTT
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>SRR2298382.124650 124650 length=156
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>SRR2298382.122212 122212 length=190
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>SRR2298382.118813 118813 length=192
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>SRR2298382.112002 112002 length=344
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>SRR2298382.111826 111826 length=502
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>SRR2298382.108909 108909 length=194
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>SRR2298382.106152 106152 length=342
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>SRR2298382.104887 104887 length=164
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