Blast Result Interpretation with Multiple HSPs

Result 1 (has 1 Hit):
      Hit accession: parC0.000 (Hit has 2 Hsps)
          Hsp identity: 100
          Hsp identity: 100

Result 2 (has 1 Hit):
      Hit accession: penA0.000
          Hsp identity: 100

Result 3 (has 1 Hit):
      Hit accession: mtrR0.000
          Hsp identity: 100

We got 2 Hsps for parC because we have a sequence stored in the database that looks like this:

GTTTCAGACGGCCAAAAGCCCGTGCAGCGGCGCATTTTGTTTGCCATGCGCGATATGGGTTTGACGGCGGGGGCG
AAGCCGGTGAAATCGGCGCGCGTGGTCGGCGAGATTTTGGGTAAATACCATCCGCACGGCGACAGTTCCGCCTAT
GAGGCGATGGTGCGCATGGTTTCAGACGGCCAAAAGCCCGTGCAGCGGCGCATTTTGTTTGCCATGCGCGATATG
GGTTTGACGGCGGGGGCGAAGCCGGTGAAATCGGCGCGCGTGGTCGGCGAGATTTTGGGTAAATACCATCCGCAC
GGCGACAGTTCCGCCTATGAGGCGATGGTGCGCATG

The first half and the last half of the sequence are identitcal.

We made a query using this sequence for parC:

GTTTCAGACGGCCAAAAGCCCGTGCAGCGGCGCATTTTGTTTGCCATGCGCGATATGGGTTTGACGGCGGGGGCG
AAGCCGGTGAAATCGGCGCGCGTGGTCGGCGAGATTTTGGGTAAATACCATCCGCACGGCGACAGTTCCGCCTAT
GAGGCGATGGTGCGCATG

This sequence will hit in 2 places in the parC sequence stored in the database. In the first half, and the last half. This results in 2 Hsps for parC. We get multiple Hsps if there is more than one hit in a particular sequence in the database.

Allele Query Results

mtrR	0	Full	703 / 703 (100.00%)	703 / 703 (100.00%)
parC	0	Partial	168 / 168 (100.00%)	168 / 336 (50.00%)
parC	0	Partial	168 / 168 (100.00%)	168 / 336 (50.00%)
penA	0.000	Full	1746 / 1746 (100.00%)	1746 / 1746 (100.00%)

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BLASTN 2.2.28+


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: /home/irish_m/ng-star-test-2/ng-
star/BusinessLogic/data/allele_db_UAR3efEh.fasta
           3 sequences; 2,785 total letters



Query=
Length=168
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                                                               Score      E
Sequences producing significant alignments:                   (Bits)   Value

  parC0.000                                                     311     8e-89


> parC0.000
Length=336

 Score =  311 bits (168),  Expect = 8e-89
 Identities = 168/168 (100%), Gaps = 0/168 (0%)
 Strand=Plus/Plus

Query  1    GTTTCAGACGGCCAAAAGCCCGTGCAGCGGCGCATTTTGTTTGCCATGCGCGATATGGGT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTTTCAGACGGCCAAAAGCCCGTGCAGCGGCGCATTTTGTTTGCCATGCGCGATATGGGT  60

Query  61   TTGACGGCGGGGGCGAAGCCGGTGAAATCGGCGCGCGTGGTCGGCGAGATTTTGGGTAAA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TTGACGGCGGGGGCGAAGCCGGTGAAATCGGCGCGCGTGGTCGGCGAGATTTTGGGTAAA  120

Query  121  TACCATCCGCACGGCGACAGTTCCGCCTATGAGGCGATGGTGCGCATG  168
            ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TACCATCCGCACGGCGACAGTTCCGCCTATGAGGCGATGGTGCGCATG  168


 Score =  311 bits (168),  Expect = 8e-89
 Identities = 168/168 (100%), Gaps = 0/168 (0%)
 Strand=Plus/Plus

Query  1    GTTTCAGACGGCCAAAAGCCCGTGCAGCGGCGCATTTTGTTTGCCATGCGCGATATGGGT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  169  GTTTCAGACGGCCAAAAGCCCGTGCAGCGGCGCATTTTGTTTGCCATGCGCGATATGGGT  228

Query  61   TTGACGGCGGGGGCGAAGCCGGTGAAATCGGCGCGCGTGGTCGGCGAGATTTTGGGTAAA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  229  TTGACGGCGGGGGCGAAGCCGGTGAAATCGGCGCGCGTGGTCGGCGAGATTTTGGGTAAA  288

Query  121  TACCATCCGCACGGCGACAGTTCCGCCTATGAGGCGATGGTGCGCATG  168
            ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  289  TACCATCCGCACGGCGACAGTTCCGCCTATGAGGCGATGGTGCGCATG  336



Lambda      K        H
    1.33    0.621     1.12

Gapped
Lambda      K        H
    1.28    0.460     0.850

Effective search space used: 428844


Query=
Length=1752
                                                               Score      E
Sequences producing significant alignments:                   (Bits)   Value

  penA0.000                                                     3225     0.0


> penA0.000
Length=1746

 Score = 3225 bits (1746),  Expect = 0.0
 Identities = 1746/1746 (100%), Gaps = 0/1746 (0%)
 Strand=Plus/Plus

Query  7     ATGTTGATTAAAAGCGAATATAAGCCCCGGATGCTGCCCAAAGAAGAGCAGGTCAAAAAG  66
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1      ATGTTGATTAAAAGCGAATATAAGCCCCGGATGCTGCCCAAAGAAGAGCAGGTCAAAAAG  60

Query  67     CCGATGACCAGTAACGGACGGATTAGCTTCGTCCTGATGGCAATGGCGGTCTTGTTTGCC  126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61     CCGATGACCAGTAACGGACGGATTAGCTTCGTCCTGATGGCAATGGCGGTCTTGTTTGCC  120

Query  127    TGTCTGATTGCCCGCGGGCTGTATCTGCAGACGGTAACGTATAACTTTTTGAAAGAACAG  186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121    TGTCTGATTGCCCGCGGGCTGTATCTGCAGACGGTAACGTATAACTTTTTGAAAGAACAG  180

Query  187    GGCGACAACCGGATTGTGCGGACTCAAGCATTGCCGGCTACACGCGGTACGGTTTCGGAC  246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181    GGCGACAACCGGATTGTGCGGACTCAAGCATTGCCGGCTACACGCGGTACGGTTTCGGAC  240

Query  247    CGGAACGGTGCGGTTTTGGCGTTGAGCGCGCCGACGGAGTCCCTGTTTGCCGTGCCTAAA  306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241    CGGAACGGTGCGGTTTTGGCGTTGAGCGCGCCGACGGAGTCCCTGTTTGCCGTGCCTAAA  300

Query  307    GATATGAAGGAAATGCCGTCTGCCGCCCAATTGGAACGCCTGTCCGAGCTTGTCGATGTG  366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301    GATATGAAGGAAATGCCGTCTGCCGCCCAATTGGAACGCCTGTCCGAGCTTGTCGATGTG  360

Query  367    CCGGTCGATGTTTTGAGGAACAAACTCGAACAGAAAGGCAAGTCGTTTATTTGGATCAAG  426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361    CCGGTCGATGTTTTGAGGAACAAACTCGAACAGAAAGGCAAGTCGTTTATTTGGATCAAG  420

Query  427    CGGCAGCTCGATCCCAAGGTTGCCGAAGAGGTCAAAGCCTTGGGTTTGGAAAACTTTGTA  486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421    CGGCAGCTCGATCCCAAGGTTGCCGAAGAGGTCAAAGCCTTGGGTTTGGAAAACTTTGTA  480

Query  487    TTTGAAAAAGAATTAAAACGCCATTACCCGATGGGCAACCTGTTTGCACACGTCATCGGA  546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481    TTTGAAAAAGAATTAAAACGCCATTACCCGATGGGCAACCTGTTTGCACACGTCATCGGA  540

Query  547    TTTACCGATATTGACGGCAAAGGTCAGGAAGGTTTGGAACTTTCGCTTGAAGACAGCCTG  606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541    TTTACCGATATTGACGGCAAAGGTCAGGAAGGTTTGGAACTTTCGCTTGAAGACAGCCTG  600

Query  607    TATGGCGAAGACGGCGCGGAAGTTGTTTTGCGGGACCGGCAGGGCAATATTGTGGACAGC  666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601    TATGGCGAAGACGGCGCGGAAGTTGTTTTGCGGGACCGGCAGGGCAATATTGTGGACAGC  660

Query  667    TTGGACTCCCCGCGCAATAAAGCACCGCAAAACGGCAAAGACATCATCCTTTCCCTCGAT  726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661    TTGGACTCCCCGCGCAATAAAGCACCGCAAAACGGCAAAGACATCATCCTTTCCCTCGAT  720

Query  727    CAGAGGATTCAGACCTTGGCCTATGAAGAGTTGAACAAGGCGGTCGAATACCATCAGGCA  786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721    CAGAGGATTCAGACCTTGGCCTATGAAGAGTTGAACAAGGCGGTCGAATACCATCAGGCA  780

Query  787    AAAGCCGGAACGGTGGTGGTTTTGGATGCCCGCACGGGGGAAATCCTCGCCTTGGCCAAT  846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  781    AAAGCCGGAACGGTGGTGGTTTTGGATGCCCGCACGGGGGAAATCCTCGCCTTGGCCAAT  840

Query  847    ACGCCCGCCTACGATCCCAACAGACCCGGCCGGGCAGACAGCGAACAGCGGCGCAACCGT  906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  841    ACGCCCGCCTACGATCCCAACAGACCCGGCCGGGCAGACAGCGAACAGCGGCGCAACCGT  900

Query  907    GCCGTAACCGATATGATCGAACCTGGTTCGGCAATCAAACCGTTCGTGATTGCGAAGGCA  966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  901    GCCGTAACCGATATGATCGAACCTGGTTCGGCAATCAAACCGTTCGTGATTGCGAAGGCA  960

Query  967    TTGGATGCGGGCAAAACCGATTTGAACGAACGGCTGAATACGCAGCCTTATAAAATCGGA  1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  961    TTGGATGCGGGCAAAACCGATTTGAACGAACGGCTGAATACGCAGCCTTATAAAATCGGA  1020

Query  1027   CCGTCTCCCGTGCGCGATACCCATGTTTACCCCTCTTTGGATGTGCGCGGCATTATGCAG  1086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1021   CCGTCTCCCGTGCGCGATACCCATGTTTACCCCTCTTTGGATGTGCGCGGCATTATGCAG  1080
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Query  1087   AAATCGTCCAACGTCGGCACAAGCAAACTGTCTGCGCGTTTCGGCGCCGAAGAAATGTAT   1146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1081   AAATCGTCCAACGTCGGCACAAGCAAACTGTCTGCGCGTTTCGGCGCCGAAGAAATGTAT   1140

Query  1147   GACTTCTATCATGAATTGGGCATCGGTGTGCGTATGCACTCGGGCTTTCCGGGGGAAACT   1206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1141   GACTTCTATCATGAATTGGGCATCGGTGTGCGTATGCACTCGGGCTTTCCGGGGGAAACT   1200

Query  1207   GCAGGTTTGTTGAGAAATTGGCGCAGGTGGCGGCCCATCGAACAGGCGACGATGTCTTTC   1266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1201   GCAGGTTTGTTGAGAAATTGGCGCAGGTGGCGGCCCATCGAACAGGCGACGATGTCTTTC   1260

Query  1267   GGTTACGGTCTGCAATTGAGCCTGCTGCAATTGGCGCGCGCCTATACCGCACTGACGCAC   1326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1261   GGTTACGGTCTGCAATTGAGCCTGCTGCAATTGGCGCGCGCCTATACCGCACTGACGCAC   1320

Query  1327   GACGGCGTTTTGCTGCCGCTCAGCTTTGAGAAGCAGGCGGTTGCGCCGCAAGGCAAACGC   1386
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1321   GACGGCGTTTTGCTGCCGCTCAGCTTTGAGAAGCAGGCGGTTGCGCCGCAAGGCAAACGC   1380

Query  1387   ATATTCAAAGAATCGACCGCGCGCGAGGTACGCAATCTGATGGTTTCCGTAACCGAGCCG   1446
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1381   ATATTCAAAGAATCGACCGCGCGCGAGGTACGCAATCTGATGGTTTCCGTAACCGAGCCG   1440

Query  1447   GGCGGCACCGGTACGGCGGGTGCGGTGGACGGTTTCGATGTCGGCGCTAAAACCGGCACG   1506
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1441   GGCGGCACCGGTACGGCGGGTGCGGTGGACGGTTTCGATGTCGGCGCTAAAACCGGCACG   1500

Query  1507   GCGCGCAAGTTCGTCAACGGGCGTTATGCCGACAACAAACACGTCGCTACCTTTATCGGT   1566
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1501   GCGCGCAAGTTCGTCAACGGGCGTTATGCCGACAACAAACACGTCGCTACCTTTATCGGT   1560

Query  1567   TTTGCCCCCGCCAAAAACCCCCGTGTGATTGTGGCGGTAACCATCGACGAACCGACTGCC   1626
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1561   TTTGCCCCCGCCAAAAACCCCCGTGTGATTGTGGCGGTAACCATCGACGAACCGACTGCC   1620

Query  1627   CACGGCTATTACGGCGGCGTAGTGGCAGGGCCGCCCTTCaaaaaaaTTATGGGCGGCAGC   1686
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1621   CACGGCTATTACGGCGGCGTAGTGGCAGGGCCGCCCTTCAAAAAAATTATGGGCGGCAGC   1680

Query  1687   CTGAACATCTTGGGCATTTCCCCGACCAAGCCACTGACCGCCGCAGCCGTCAAAACACCG   1746
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1681   CTGAACATCTTGGGCATTTCCCCGACCAAGCCACTGACCGCCGCAGCCGTCAAAACACCG   1740

Query  1747   TCTTAA  1752
              ||||||
Sbjct  1741   TCTTAA  1746




Lambda      K        H
    1.33    0.621     1.12

Gapped
Lambda      K        H
    1.28    0.460    0.850

Effective search space used: 4759380


Query=
Length=715
                                                              Score     E
Sequences producing significant alignments:                  (Bits)  Value

  mtrR0.000                                                   1299    0.0


> mtrR0.000
```

```
Length=703

 Score = 1299 bits (703),  Expect = 0.0
 Identities = 703/703 (100%), Gaps = 0/703 (0%)
 Strand=Plus/Plus

Query  7     TTGCACGGATAAAAAGTCttttttttATAATCCGCCCTCGTCAAACCGACCCGAAACGAAA  66
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     TTGCACGGATAAAAAGTCTTTTTTTATAATCCGCCCTCGTCAAACCGACCCGAAACGAAA  60

Query  67    ACGCCATTATGAGAAAAACCAAAACCGAAGCCTTGAAAACCAAAGAACACCTGATGCTTG  126
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    ACGCCATTATGAGAAAAACCAAAACCGAAGCCTTGAAAACCAAAGAACACCTGATGCTTG  120

Query  127   CCGCCTTGGAAACCTTTTACCGCAAAGGGATTGCCCGCACCTCGCTCAACGAAATCGCCC  186
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   CCGCCTTGGAAACCTTTTACCGCAAAGGGATTGCCCGCACCTCGCTCAACGAAATCGCCC  180

Query  187   AAGCCGCCGGCGTAACGCGCGGCGCGCTTTATTGGCATTTCAAAAATAAGGAAGACTTGT  246
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   AAGCCGCCGGCGTAACGCGCGGCGCGCTTTATTGGCATTTCAAAAATAAGGAAGACTTGT  240

Query  247   TCGACGCGCTGTTCCAACGTATCTGCGACGACATCGAAAACTGCATCGCGCAAGATGCCG  306
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   TCGACGCGCTGTTCCAACGTATCTGCGACGACATCGAAAACTGCATCGCGCAAGATGCCG  300

Query  307   CAGATGCCGAAGGAGGGTCTTGGGCGGTATTCCGCCACACGCTGCTGCACTTTTTCGAGC  366
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   CAGATGCCGAAGGAGGGTCTTGGGCGGTATTCCGCCACACGCTGCTGCACTTTTTCGAGC  360

Query  367   GGCTGCAAAGCAACGACATCTACTACAAATTCCACAACATCCTGTTTTTAAAATGCGAAC  426
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   GGCTGCAAAGCAACGACATCTACTACAAATTCCACAACATCCTGTTTTTAAAATGCGAAC  420

Query  427   ACACGGAGCAAAACGCCGCCGTTATCGCCATTGCCCGCAAGCATCAGGCAATCTGGCGCG  486
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   ACACGGAGCAAAACGCCGCCGTTATCGCCATTGCCCGCAAGCATCAGGCAATCTGGCGCG  480

Query  487   AGAAAATTACCGCCGTTTTGACCGAAGCGGTGGAAAATCAGGATTTGGCTGACGATTTGG  546
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   AGAAAATTACCGCCGTTTTGACCGAAGCGGTGGAAAATCAGGATTTGGCTGACGATTTGG  540

Query  547   ACAAGGAAACGGCGGTCATCTTCATCAAATCGACGTTGGACGGGCTGATTTGGCGTTGGT  606
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   ACAAGGAAACGGCGGTCATCTTCATCAAATCGACGTTGGACGGGCTGATTTGGCGTTGGT  600

Query  607   TCTCTTCCGGCGAAAGTTTCGATTTGGGCAAAACCGCCCCCCGCGCATCATCGGGATAAT  666
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601   TCTCTTCCGGCGAAAGTTTCGATTTGGGCAAAACCGCCCCCCGCGCATCATCGGGATAAT  660

Query  667   GATGGACAACTTGGAAAACCATCCCTGCCTGCGCCGGAAATAA  709
             |||||||||||||||||||||||||||||||||||||||||||
Sbjct  661   GATGGACAACTTGGAAAACCATCCCTGCCTGCGCCGGAAATAA  703


Lambda      K         H
    1.33    0.621     1.12

Gapped
Lambda      K         H
    1.28    0.460     0.850

Effective search space used: 1922843


  Database: /home/irish_m/ng-star-test-2/ng-
star/BusinessLogic/data/allele_db_UAR3efEh.fasta
    Posted date:  May 29, 2015  10:59 AM
  Number of letters in database: 2,785
```

Number of sequences in database: 3

Matrix: blastn matrix 1 -2
Gap Penalties: Existence: 0, Extension: 2.5