```
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|50512980|gb|AY644953.1| Andropadus virens clone AviAAGG18
microsatellite sequence
         (816 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr2                                                                  264   2e-068

>chr2
          Length = 147590765

 Score =  264 bits (166), Expect = 2e-068
 Identities = 332/474 (70%), Gaps = 44/474 (9%)
 Strand = Plus / Plus


Query: 315      tgtttcccttgttttgaaacaattccagattatctctttatctatctccatgca--caca 372
                |||||| |||| ||||||| ||||||| | ||||| ||||||||||| ||||||  ||||
Sbjct: 59721817 tgtttcacttgctttgaaataattccaaaatatctgtttatctatctgcatgcatacaca 59721876


Query: 373      cactcaaggatgca----------cacacgaagcgtgtacaga-aataacttgagg---- 417
                |||||| ||||  |          |||| ||||  |   |  | |||||   ||||
Sbjct: 59721877 cactcatggatctaggcctatgtgcacatgaagtattcccgcagaataatgcgaggcaca 59721936


Query: 418      ----------taaacacgttcaaacccatcttgtgtcttaaggtgaaagcaggccgagcc 467
                          || | | |  |||||| ||||||||| | |||||||  |||  | |||
Sbjct: 59721937 tgtccctacatacagaagcacaaaccaatcttgtgtttcaaggtgatggcaaacagaggg 59721996


Query: 468      cttgtggaattagatgaggacaatcctttga-----gtaaactctcctcacaggtggtcc 522
                 ||||| |  ||||||||||||||||||||      ||||||||||   |||||||| ||
Sbjct: 59721997 -ttgtgaaggtagatgaggacaatcctttgcttagtgtaaactctc---acaggtggccc 59722052


Query: 523      tggatggagcagctgtggtgtaggttgagtgctcagcaccttgtatctacactgggtcag 582
                  || ||||  ||||||| | | ||| | |||| | |    ||||| ||   | |||||
Sbjct: 59722053 cagaaggagtggctgtggaggaagtttactgctgacc----tgtatttatgttaggtcat 59722108


Query: 583      ggttatatggaaggcgttgtcttccagagagcaacaaac-agattccctactttgac-ca 640
                | |||| |||||||| |||||||| | |||||| ||| | | ||||   | |||||  ||
Sbjct: 59722109 gattatgtggaaggcattgtcttctacagagcagcaagccatattcttga-tttgaggca 59722167


Query: 641      agtgcttgaattcaagagcagaaaggtgggtgtgaagaagtgccaaacctgcctttggaa 700
                ||||||  ||| |||| |||   |  ||||||| ||||||||| |||  || || |||||
Sbjct: 59722168 agtgctcaaatccaagtgcaatcaaatgggtgtaaagaagtgctaaaaatgtctgtggaa 59722227


Query: 701      gtcagagccaaaagatatttccttgaccctctactcagtatctgtgacatggca 754
                |  ||||    |||| |||||||||| ||||| ||||||| |||||| |  |||
Sbjct: 59722228 gggagagttggaagacatttccttga-cctctgctcagtagctgtgaaacagca 59722280


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
```

```
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 432,067
Number of Sequences: 54
Number of extensions: 432067
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 816
length of database: 1,133,629,576
effective HSP length: 48
effective length of query: 768
effective length of database: 1,133,626,984
effective search space: 870625523712
effective search space used: 870625523712
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|50512989|gb|AY644962.1| Andropadus virens clone AviAAGG28m
microsatellite sequence
         (366 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr15                                                                 247   1e-063
chrUn                                                                  76   5e-012

>chr15
          Length = 12438626

 Score =  247 bits (155), Expect = 1e-063
 Identities = 241/348 (69%), Gaps = 22/348 (6%)
 Strand = Plus / Plus


Query: 22      cttaccaggatggccacgaagctgatgaggaaggaggtgaggaagacgccgatgccgtag 81
               |||||||| ||||| | ||||||||| || |||||    |||||||| || ||||| |||
Sbjct: 6195626 cttaccagaatggctatgaagctgatcagaaaggaaacaaggaagaccccaatgccatag 6195685


Query: 82      aaatgcatcgcgctggcaaacggagccgctcagctctggg-gctcgctgg-gggctcngn 139
               |||||||| ||  |||||||| ||||| ||||||  | |  ||||| ||| |||||| |
Sbjct: 6195686 aaatgcattgct-tggcaaacagagccactcagcgttagcagctcgttggtgggctcagc 6195744


Query: 140     cacctccgtgtgcatcaggagacacctgtggg-acacagggaagagcctgagctcctgcc 198
               ||  || |||||||||| |||||| ||| ||| | | |||||  ||||||||||| ||||
Sbjct: 6195745 catttctgtgtgcatcaagagacatctgcggggagaaagggagcagcctgagctcttgcc 6195804
```

```
Query: 199     cacccccagcagccctnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnng 258
                   | ||| ||                                               |
Sbjct: 6195805 atgactcagaag-----------------tggtgaggctgtttcagagagaatcatgagg 6195847


Query: 259     ctcacccgtgcttctggctgaagttctggnagcaattactgctgttgtccaggcaaaaca 318
               || |||| ||||| || |||||||||||| |||| |||||||||||| ||||||||||||
Sbjct: 6195848 cttacccatgcttttgactgaagttctggtagcagttactgctgttgcccaggcaaaaca 6195907


Query: 319     ccggcaccatgaggaggaaagggatcaaggctgagaggagagaggaca 366
               | |||||||| |  || ||||||||| |||||  ||| ||||||||||
Sbjct: 6195908 caggcaccattaaaagaaaagggatc-aggctaggagaagagaggaca 6195954


>chrUn
          Length = 165033910

 Score = 76.1 bits (47), Expect = 5e-012
 Identities = 78/100 (78%), Gaps = 6/100 (6%)
 Strand = Plus / Minus


Query: 267      tgcttctggctgaagttctggnag-caattactgctgttgtccaggc-aaaacaccggca 324
                ||||| || |||||||||||| || |||||| |||| ||  |||||| |||||||||||
Sbjct: 48796624 tgcttttgactgaagttctggtagccaattattgct-tttcccaggcaaaaacaccggcc 48796566


Query: 325      ccatgaggaggaaagggatcaaggctgagaggagagagga 364
                |||| |  | | ||||||||  || |  | | ||||||||
Sbjct: 48796565 ccataa--aagcaagggatc-cggtttggggaagagagga 48796529


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 214,795
Number of Sequences: 54
Number of extensions: 214795
Number of successful extensions: 8
Number of sequences better than 1.0e-005: 2
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 1
Number of HSP's that attempted gapping in prelim test: 6
Number of HSP's gapped (non-prelim): 2
length of query: 366
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 320
effective length of database: 1,133,627,092
effective search space: 362760669440
effective search space used: 362760669440
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
```

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"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|50512982|gb|AY644955.1| Andropadus virens clone AviAAGG30
microsatellite sequence
         (218 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr24                                                                 106   2e-021

>chr24
          Length = 5910111

 Score =  106 bits (66), Expect = 2e-021
 Identities = 70/75 (93%)
 Strand = Plus / Plus


Query: 1       gatcttgctggggttggcaaactcgtactnggagctcatggggtaggcgtggggcacggt 60
               |||||||||||||||||||||||||||||  |||||||||||||||||||||||||| ||
Sbjct: 5876700 gatcttgctggggttggcaaactcgtactctgagctcatggggtaggcgtggggcaccgt 5876759


Query: 61      gcgggcagccatggc 75
                ||||| ||||||||
Sbjct: 5876760 ccgggcggccatggc 5876774


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 62,889
Number of Sequences: 54
Number of extensions: 62889
Number of successful extensions: 2
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 1
Number of HSP's gapped (non-prelim): 1
length of query: 218
length of database: 1,133,629,576
effective HSP length: 45
effective length of query: 173
effective length of database: 1,133,627,146
effective search space: 196117496258
effective search space used: 196117496258
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
```

```
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|50512983|gb|AY644956.1| Andropadus virens clone AviAAGG41
microsatellite sequence
         (590 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr5                                                                   86   1e-014

>chr5
          Length = 56310377

 Score = 85.6 bits (53), Expect = 1e-014
 Identities = 136/203 (66%), Gaps = 13/203 (6%)
 Strand = Plus / Minus


Query: 130      gcagcagaagtaaatggtacctac-acagttggcattttaaatgttaaagagctccc-ct 187
                |||| ||| |||| ||| |||||| | | |||| |||| |||||||     |||  | ||
Sbjct: 31210490 gcagtagaggtaa-tggcacctactaaaattggtattt-aaatgttct---gctggctct 31210436


Query: 188      tcttaaagacattaatggtactta---aagacattaatggtacttcctactatccca--g 242
                |  |||   ||  |   || ||||   |||||  |||  ||||||  || | || |   |
Sbjct: 31210435 tggtaactccaagagctgtccttacgaaagacgctaacagtactttttagtctcactagg 31210376


Query: 243      agtttttatggcaaaggcatactaagaggaggtacatgtgacacaagtattgtgtctcct 302
                ||||||||||    |   ||||||| |||||||| ||||||||  | |   |||| ||||
Sbjct: 31210375 agtttttatgtggcacatatactaaaaggaggtaaatgtgacatga-tcccgtgtttcct 31210317


Query: 303      ttcccaaaacattatatagacag 325
                | ||  |||||   || || |||
Sbjct: 31210316 tccctgaaacaacttagaggcag 31210294


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 332,754
Number of Sequences: 54
Number of extensions: 332754
Number of successful extensions: 2
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 0
Number of HSP's successfully gapped in prelim test: 1
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 1
length of query: 590
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 543
effective length of database: 1,133,627,038
effective search space: 615559481634
```

```
effective search space used: 615559481634
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|50512985|gb|AY644958.1| Andropadus virens clone AviAAGG117
microsatellite sequence
         (373 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr28                                                                 103   4e-020

>chr28
          Length = 4731479

 Score =  103 bits (64), Expect = 4e-020
 Identities = 94/118 (79%), Gaps = 5/118 (4%)
 Strand = Plus / Minus


Query: 260     gtaccttggtcagcgaagacacggacgatgttcccggggacattcagctcctccacccta 319
               ||||||||||||||||||||||||| ||||||||| |||||||| | |||||||||||||
Sbjct: 3110254 gtaccttggtcagcgaagacacggatgatgttcccagggacattaaactcctccacccta 3110195


Query: 320     cacgaatcca---gctctttgtcgggcccgggcagcgct-ttcctcttgtggaagatc 373
               ||   |||||   | ||| |||  |   | || || |||  | ||||| |||||||||
Sbjct: 3110194 caaccatccaccgggtctctgtttgttgcagg-agggctccttctcttctggaagatc 3110138


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 191,211
Number of Sequences: 54
Number of extensions: 191211
Number of successful extensions: 2
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 1
Number of HSP's gapped (non-prelim): 1
length of query: 373
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 327
effective length of database: 1,133,627,092
```

```
effective search space: 370696059084
effective search space used: 370696059084
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|50512991|gb|AY644964.1| Andropadus virens clone AviGACA62
microsatellite sequence
         (331 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr4                                                                   81   2e-013

>chr4
          Length = 90634903

 Score = 80.8 bits (50), Expect = 2e-013
 Identities = 67/80 (83%), Gaps = 3/80 (3%)
 Strand = Plus / Plus


Query: 253      atttcaaacaaaattgtagag-aaactcacgccttcagagcaattaaattcctacatgtt 311
                ||||| | |||| ||| |||| ||| |   ||||||| |||||||||||||||||| ||
Sbjct: 15233290 atttccagcaaatttgcagaggaaaatt--gccttcacagcaattaaattcctacaagtc 15233347


Query: 312      ccataaaaaatattaatcca 331
                ||||| ||||||||||||||
Sbjct: 15233348 ccatacaaaatattaatcca 15233367


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 304,706
Number of Sequences: 54
Number of extensions: 304706
Number of successful extensions: 19
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 18
Number of HSP's gapped (non-prelim): 1
length of query: 331
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 285
```

```
effective length of database: 1,133,627,092
effective search space: 323083721220
effective search space used: 323083721220
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|50512990|gb|AY644963.1| Andropadus virens clone AviGTCA85
microsatellite sequence
         (378 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr3                                                                 153   2e-035

>chr3
          Length = 108638738

 Score =  153 bits (96), Expect = 2e-035
 Identities = 160/218 (73%), Gaps = 6/218 (2%)
 Strand = Plus / Plus


Query: 1        attcagcagccttttt-ctcatgcagacttgtaaatctgggagtctgtcagtcagtcagt 59
                || |||  |||||||| ||||| ||  |||||||| ||||||||| |||| |||||||||
Sbjct: 99009810 atgcagtggcctttttgctcat-cacccttgtaaaactgggagtcagtcaatcagtcagt 99009868


Query: 60       cagccagtcaacttttctgttggaaagtccgtcttcataaagccagcatgtctcttgggg 119
                ||| ||||    || |||||||||||||||  |||||||||  ||  ||||| |  | |
Sbjct: 99009869 cagtcagt----ttctctgttggaaagtcccacttcataaaatcaatatgtcccccgaga 99009924


Query: 120      aacctggcattttgttaaaataacaagtgtttaatttttcaggggaaatcctgaaacaat 179
                ||  |||  ||||| | ||||||||||   || ||||||     ||||  ||||||||
Sbjct: 99009925 aaaatggtgttttgctgaaataacaagcaatttatttttacacagaaaagctgaaacagc 99009984


Query: 180      gtattcctttttacccgcctcatgatgtctgcacagag 217
                 | |||||  |||    ||||  |||||||| ||| ||
Sbjct: 99009985 atcttcctcattaatgacctccagatgtctgtacaaag 99010022


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 366,153
Number of Sequences: 54
```

```
Number of extensions: 366153
Number of successful extensions: 11
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 9
Number of HSP's gapped (non-prelim): 1
length of query: 378
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 331
effective length of database: 1,133,627,038
effective search space: 375230549578
effective search space used: 375230549578
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|7621456|gb|AF234986.1|AF234986 Acrocephalus arundinaceus
microsatellite Aar2 sequence
         (454 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr5                                                                  183   2e-044

>chr5
          Length = 56310377

 Score =  183 bits (115), Expect = 2e-044
 Identities = 212/291 (72%), Gaps = 27/291 (9%)
 Strand = Plus / Plus


Query: 168      ctgagctgcacgggctgcacgtattccttacggaaacgcttcaggtcggcgctgatgggc 227
                ||||| ||||| ||||| ||||||||||| || || ||||| ||||| || |||||||||
Sbjct: 54418565 ctgagttgcactggctggacgtattccttgcgaaatcgcttaaggtctgcactgatgggc 54418624


Query: 228      tgctcccccttctcgatggccaacctgtctgcctctgtgggctcaggctcagggatctca 287
                |||||||| |||||||| |||| ||||||||| || || || |||||||| ||||| |||
Sbjct: 54418625 tgctcccctttctcgattgccagcctgtctgcttcagtaggttcaggctctgggatttca 54418684


Query: 288      aacc--tgggggaaaacaccacagagctgatgg-----cagacaaaacacaaaccctctg 340
                ||||  ||   | || || || | | |||||||      ||| |||||||||||||| |
Sbjct: 54418685 aacctatgaatgcaagcaacagaaaactgatggtaattaagataaaacacaaaccctttа 54418744


Query: 341      tgcagcagctgcagcttatag-aaatgtatttatataaattcagtg---------tcagg 390
                || || |    || |  | || || | |||||| | ||||||| ||         ||| |
Sbjct: 54418745 tgtagga----ca-cgaagagcaattttatttaaagaaattcaatgcagcgaaactcaag 54418799


Query: 391      tgct-tccctgcc---atccagtttgcccggaattccctcctcccc-agct 436
                  ||  | |  ||   |||||||  ||| |||| |||||||||||| ||||
Sbjct: 54418800 cactcactcatccagtatccagtccgcctggaactccctcctcccctagct 54418850


  Database: WholeChickenGenome.txt
```

```
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 421,738
Number of Sequences: 54
Number of extensions: 421738
Number of successful extensions: 8
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 7
Number of HSP's gapped (non-prelim): 1
length of query: 454
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 407
effective length of database: 1,133,627,038
effective search space: 461386204466
effective search space used: 461386204466
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|7621458|gb|AF234988.1|AF234988 Acrocephalus arundinaceus
microsatellite Aar4 sequence
         (133 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr5                                                                  100   9e-020

>chr5
          Length = 56310377

 Score = 99.9 bits (62), Expect = 9e-020
 Identities = 78/117 (66%), Gaps = 2/117 (1%)
 Strand = Plus / Minus


Query: 19       gnnnnnnnnnnnnnnnnnnnnnnnnnnngacaggcaaagaa-aaatggcaaaattatatt 77
                |                            || || |||| || ||||||||||||||||||
Sbjct: 29168254 gatgattaaggtctctggtgtgtgtgtggatagacaaacaataaatggcaaaattatatt 29168195


Query: 78       cagcatttatt-tttagcatgactaattgatgcacaaaccatgatagacaattgcta 133
                ||||||||||| |||||||| ||||  |||||||||||| ||| |||| ||| ||||
Sbjct: 29168194 cagcatttattgtttagcataactagatgatgcacaaactatgttagaaaatagcta 29168138
```

```
  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 119,438
Number of Sequences: 54
Number of extensions: 119438
Number of successful extensions: 6
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 0
Number of HSP's successfully gapped in prelim test: 1
Number of HSP's that attempted gapping in prelim test: 5
Number of HSP's gapped (non-prelim): 1
length of query: 133
length of database: 1,133,629,576
effective HSP length: 44
effective length of query: 89
effective length of database: 1,133,627,200
effective search space: 100892820800
effective search space used: 100892820800
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 33 (53.9 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|21745302|gb|AF520899.1| Aphelocoma coerulescens clone ApCo15
microsatellite sequence
         (455 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr3                                                                  226   3e-057

>chr3
          Length = 108638738

 Score =  226 bits (142), Expect = 3e-057
 Identities = 284/460 (61%), Gaps = 31/460 (6%)
 Strand = Plus / Plus


Query: 1        actgtccccatctaagaggcgatcattgttcagtctttttcttacagagacaatctca-- 58
                ||||||| || ||  |||   ||||||| | | ||  |  |||||| |||  ||||||
Sbjct: 82279066 actgtcctcagcttggag---atcattgctgaatccataccttacaaagagcatctcaca 82279122


Query: 59       -----------actacaagaaaagtatcttctgcttttatctttctctgcttaatatttc 107
                           ||||||| |||| ||||| |||  ||  | |||  |||||||||| |||
Sbjct: 82279123 ctgcaacttaaactacaataaaaatatctcctgaattatttttttcctgcttaataattc 82279182
```

```
Query: 108      tgcaaagtgaaa-gtttcttttaactaatttagtaaggaagacaagtgtaaacgatctgc 166
                || |   ||||| |||| |||||||||| | | | || || |  | |||||| |||||||
Sbjct: 82279183 tgtattatgaaaagtttgttttaactaaatcactcagaaacatgaatgtaaatgatctgc 82279242


Query: 167      aaataattttgattattgagaggtggagtggttctgaaatgacagaaagttgaagctgaa 226
                ||  ||| ||     || | || | || ||    ||| | |||| ||  |||||||||||
Sbjct: 82279243 aagcaatgtt-----tttaaagattgactg----tgagaagacaaaa--ttgaagctgaa 82279291


Query: 227      tgtgcctcagtataccatcagtagattaactatttttcattctgtcccatacctctatat 286
                | ||||||||||| |||| ||||||  ||| | ||||| |||| | |  ||  | |||
Sbjct: 82279292 tatgcctcagtatcccataagtagagcaaccagttttctttctattctttatttgtatgc 82279351


Query: 287      tttttgagccaagaccttt-tcttgacatgtaaacaaagtaaagtttcatagcttgattt 345
                | ||  || |||   |||  |||| | ||||| ||||||||| | ||||||| |||||||
Sbjct: 82279352 tcttcaagacaaaggcttcctcttaatatgtagacaaagtaaggcttcatagtttgattt 82279411


Query: 346      gaggaaaaaccctcgtagtagtattgagaattacnnnnnnnnnnnnnnnnnnnnnnnnnn 405
                |||||| | | || | ||||  ||||||||| |
Sbjct: 82279412 gaggaagagcacttgcagtaccattgagaatgatgatgcaagtaagacagaagctctgaa 82279471


Query: 406      nnnnnnnnnnnnnnnnnnnnnnnnnncagctaagacagag 445
                                          | | |||  |||||
Sbjct: 82279472 caaattcaatgcccttgtacagacaactg-taa-tcagag 82279509


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 411,911
Number of Sequences: 54
Number of extensions: 411911
Number of successful extensions: 5
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 3
Number of HSP's gapped (non-prelim): 1
length of query: 455
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 408
effective length of database: 1,133,627,038
effective search space: 462519831504
effective search space used: 462519831504
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.
```

```
Query= gi|21745301|gb|AF520898.1| Aphelocoma coerulescens clone ApCo18
microsatellite sequence
         (378 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr2                                                                  153   2e-035

>chr2
          Length = 147590765

 Score =  153 bits (96), Expect = 2e-035
 Identities = 179/272 (65%), Gaps = 28/272 (10%)
 Strand = Plus / Minus


Query: 6         gtgacatggaggtagggacatggagaagagcaagcctggactaaggcatttgctcttctc 65
                 |||| ||||||||||||  ||||||||||   ||  |||  || ||   ||||| |||||
Sbjct: 100004802 gtgatatggaggtagggggatggagaagaatgaggttggcttaggggcattgcttttctc 100004743


Query: 66        accagtgctgtggaaggtgtggaaaagtacactgtgtactagtgccttggctttcagtga 125
                   || | || |||||||||||||   | |  |||||||||   || |||||| |||||||
Sbjct: 100004742 --cattactctggaaggtgtgga---ggatgctgtgtact---gctttggctctcagtga 100004691


Query: 126       accctgactaaatgactaaaaagaaatcctcagacagcatgcctgtgtgggcatacatat 185
                 ||||   |||| ||||| |||| |||||||  |  |||||         |||| ||
Sbjct: 100004690 acccaagctaagtgactgaaaacaaatcctgtgtaagcat---------ggca-ac---- 100004645


Query: 186       ttnnnnnnnnnnnnnnnnnnnnnnnncatgcatgcatgcacttcagtgcagataagggat 245
                                           || ||| ||||||| |||||||||||||||| ||
Sbjct: 100004644 --tgtatgtccgtgggtgtgtgtatgcaggcaagcatgcatttcagtgcagataaggtat 100004587


Query: 246       ttgtaa----ggtagtcaaattaaagcaattt 273
                 |||| |    ||| | |||||||||||| |||
Sbjct: 100004586 ttgtcaggttggtggccaaattaaagcagttt 100004555


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 304,857
Number of Sequences: 54
Number of extensions: 304857
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 378
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 331
effective length of database: 1,133,627,038
```

```
effective search space: 375230549578
effective search space used: 375230549578
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|21745300|gb|AF520897.1| Aphelocoma coerulescens clone ApCo19
microsatellite sequence
         (322 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr2                                                                 179   4e-043

>chr2
          Length = 147590765

 Score =  179 bits (112), Expect = 4e-043
 Identities = 218/332 (65%), Gaps = 20/332 (6%)
 Strand = Plus / Plus


Query: 3         tacactggatacagaaacagactgcagtcttgctat-agccaaaaggatta----aattg 57
                 || |||| ||| ||||||| | ||||| |||  | | |||  || || ||     | | |
Sbjct: 122058713 tatactgaatagagaaacacagtgcagacttctttttagctgaagggtttgttagactgg 122058772


Query: 58        gcaagattaaagtagaaggccaaattatttacttctgtccatctttaacttttannnnnn 117
                 ||| ||||| || || ||||||||||| |||| |||||| ||||||||  |||
Sbjct: 122058773 gcaggattagaggaggaggccaaattacttacctctgtcaatctttaatctttttttttc 122058832


Query: 118       nnnnnnnnnnnnnnnnnncagtgc-ttg----gttttaaatagtttacatag-ttgggag 171
                                    | ||| |||    ||||||||| |  |  |||  ||  |
Sbjct: 122058833 tttttttcttttttttttaaattgcgttgccctgttttaaatggggttgataccttacgta 122058892


Query: 172       agagccttgtttgtatgaagcatgatagccactgtgcttaaagaatgctgaaattcacct 231
                 |     |||   |  ||  |||||| || |||  |||||  ||| || ||||| ||||
Sbjct: 122058893 a-----ttgagagagtgttgcatgacagacacaatgcttttagagtggtgaaactcac-- 122058945


Query: 232       gagaagtttcacaagctatttttagtgaggctaagcacagtctaatatcgtaaaagcatc 291
                  |||||||||| |||||||||||   ||||||||||||| ||| |||||  || ||||||
Sbjct: 122058946 -agaagtttcagaagctatttttgacgaggctaagcacaatctgatatcagaagagcatc 122059004


Query: 292       caaggctagagccatgaagctgat-caatggt 322
                 ||| |||||   ||||||| || | || ||||
Sbjct: 122059005 caaagctaggaacatgaagttggtccagtggt 122059036


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549
```

```
Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 242,761
Number of Sequences: 54
Number of extensions: 242761
Number of successful extensions: 6
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 4
Number of HSP's gapped (non-prelim): 1
length of query: 322
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 276
effective length of database: 1,133,627,092
effective search space: 312881077392
effective search space used: 312881077392
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|21745296|gb|AF520893.1| Aphelocoma coerulescens clone ApCo28
microsatellite sequence
         (262 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr3                                                                  196   2e-048

>chr3
          Length = 108638738

 Score =  196 bits (123), Expect = 2e-048
 Identities = 155/185 (83%), Gaps = 1/185 (0%)
 Strand = Plus / Plus


Query: 2        tggtgagatcctattaatgtcaacagcggttttactattgactgttttagggccataatt 61
                |||||||||||||||||||||||  || ||||||||| ||||||||||||||| || |||
Sbjct: 38873309 tggtgagatcctattaatgtcaatggcagttttactactgactgttttagggctatgatt 38873368


Query: 62       tcacccagaaattctctgaacttagtcatatcttccacaacgctccctatatggtagtgg 121
                ||||||||||| |||||||||||| || ||||||||||   |||||||||| ||||||||
Sbjct: 38873369 tcacccagaaactctctgaacttaatcgtatcttccactgggctccctatacggtagtgg 38873428


Query: 122      agtccaggctgaaaaccaattcacaattatttgaggactgtgtt-tctcttctcaaagga 180
                ||||||||||||||| |  ||  || || |||||| | ||  || ||||| ||   ||||
Sbjct: 38873429 agtccaggctgaaaaaccttttgcagttgtttgagcagtgcattgtctctccttgtagga 38873488


Query: 181      gaaaa 185
                 ||||
```

```
Sbjct: 38873489 aaaaa 38873493


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 191,336
Number of Sequences: 54
Number of extensions: 191336
Number of successful extensions: 5
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 4
Number of HSP's gapped (non-prelim): 1
length of query: 262
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 216
effective length of database: 1,133,627,092
effective search space: 244863451872
effective search space used: 244863451872
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|21745294|gb|AF520891.1| Aphelocoma coerulescens clone ApCo31
microsatellite sequence
         (226 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr8                                                                   82   3e-014

>chr8
          Length = 30024636

 Score = 82.4 bits (51), Expect = 3e-014
 Identities = 85/179 (47%), Gaps = 3/179 (1%)
 Strand = Plus / Minus


Query: 49       acaaagnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 108
                |||  ||
Sbjct: 26728958 acacaggtggagtgggctggaaataccagtagggccgcgggcaggtatcgcagcaggtgc 26728899


Query: 109      nnnnnnnnagaaaaggaagaatccctttttcagtttgcacagtgatggaacactagtcctg 168
```

```
                         |   | || | || | ||||| |||||    |||||| | ||  |||||||
Sbjct: 26728898 actgacagtggggatgatgcatacattttcggtttggctggtgatgaagcaggagtcctg 26728839


Query: 169      ctgactcagggtga---aacccagatggtgactgggagattctgctgctgcagggcaag 224
                |||||| || ||||     | |||| |||||||| ||||||  ||||||||||||| ||
Sbjct: 26728838 ctgactaagagtgaggcggcacagacggtgactgtgagattgcgctgctgcagggcgag 26728780


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 157,288
Number of Sequences: 54
Number of extensions: 157288
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 0
Number of HSP's successfully gapped in prelim test: 1
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 1
length of query: 226
length of database: 1,133,629,576
effective HSP length: 45
effective length of query: 181
effective length of database: 1,133,627,146
effective search space: 205186513426
effective search space used: 205186513426
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|21745289|gb|AF520886.1| Aphelocoma coerulescens clone ApCo41
microsatellite sequence
         (594 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr4                                                                  290   3e-076

>chr4
          Length = 90634903

 Score =  290 bits (182), Expect = 3e-076
 Identities = 296/404 (73%), Gaps = 8/404 (1%)
 Strand = Plus / Minus
```

```
Query: 168      atcacaaaaataaagggaaattacaagggatgttaatgatttgtacgacatgctgataat 227
                ||||||||   |||||  |    |||||  | || ||||||| ||  |||  ||||||
Sbjct: 80699104 atcacaaactgaaaggagagcagcaaggactcttcatgatttataaaaca--ctgatacc 80699047


Query: 228      ggggagcaacatttaagtgtaaagtgtatttcagttttgtcagctacaaaaaattgatca 287
                   ||| |  ||| |||||||   ||| | | || | |||||||    |||||  |||||
Sbjct: 80699046 atagagaactattaaagtgtactatgtgtattagctatgtcagcagtgaaaaagagatca 80698987


Query: 288      caaaagcatagtggagattgcagtaacattttttgctaattattggtggagagagaatga 347
                ||||| |||| |||    || || |||  ||| |||||||| |||||||||| |||||||
Sbjct: 80698986 caaaatcatactgggttatggagcaactgtttatgctaattcttggtggagacagaatga 80698927


Query: 348      ggaaactggccttccaatacccaccactaatgagactcaatttacgcc---ttttatata 404
                | || |||||||||| ||| | | || | | |||||||||||||||||   | ||| | |
Sbjct: 80698926 gaaagctggccttcctatatctagcaatcacgagactcaatttacgcctgttcttaaaca 80698867


Query: 405      atctacttatgagagcaaagaaaatccccaccctttctgatggatatatactgggataaa 464
                || |||||||||  ||||||| | |||||||||| | |  | || || || | | |||||
Sbjct: 80698866 atgtacttatgattgcaaagagattccccaccctgtttactagacatgtagtagaataaa 80698807


Query: 465      t---ttcccagagagatttgcttcaatcataaaatcaaggagaatgttaagactttgatg 521
                |    ||||| |||||||||| ||||||| | || |||  |||||  | |||||||||||
Sbjct: 80698806 tctcctcccacagagatttgcctcaatcacagaagcaatcagaattcttagactttgatg 80698747


Query: 522      tgaagatggaggcttaagaggaaaatcactccaagaattaaaaa 565
                |||||||| || |  ||||| ||| |||| | |  |||||||||
Sbjct: 80698746 tgaagatgaagaccaaagagtaaagtcacactacaaattaaaaa 80698703


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 506,065
Number of Sequences: 54
Number of extensions: 506065
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 1
Number of HSP's gapped (non-prelim): 1
length of query: 594
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 547
effective length of database: 1,133,627,038
effective search space: 620093989786
effective search space used: 620093989786
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
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Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|21745288|gb|AF520885.1| Aphelocoma coerulescens clone ApCo46
microsatellite sequence
         (459 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr1                                                                  445   e-123

>chr1
          Length = 188239860

 Score =  445 bits (280), Expect = e-123
 Identities = 365/463 (78%), Gaps = 21/463 (4%)
 Strand = Plus / Minus


Query: 1        acaagcagtggatatcctaatgcaatatgtgtaattcctctacctgcaacgacaactaat 60
                ||||||||  |||||||||||||||||||| |||||||||||||| ||  ||||||| ||
Sbjct: 87219694 acaagcagcagatatcctaatgcaatatgtataattcctctaccttcagtgacaactgat 87219635


Query: 61       ttttaaaa-tgcttatactgctcctcattctcaccagctttgctttccatttcttggagc 119
                || ||||| |||||||||| ||| | |||||||| ||||||  |||| || ||||  ||
Sbjct: 87219634 ttataaaaatgcttatactcctcattattctcactagctttaatttctatctctttaagg 87219575


Query: 120      accattaaataccactgaaacacctttaggcaaagtaagacactgactcctctaatggct 179
                  |||||| || |||||||||||||||||||||||  |||||||||||   || |||| |
Sbjct: 87219574 ctcattaagtatcactgaaacacctttaggcaaaggcagacactgactgtgctgatggtt 87219515


Query: 180      ttgctgccagca-ctctgaatgtctggcaacactgttctgtaatcttatttctggctcaa 238
                ||||||||||||  | |   |||||||||||||||||| |||||| |||||| | || ||
Sbjct: 87219514 ttgctgccagcatttttttgtgtctggcaacactgttcagtaatc-tatttcagtctgaa 87219456


Query: 239      cagcacaagtttcatc--nnnnnnnctgtcctcaagggagcctagtatgttaagatgctg 296
                ||| ||||||||| ||         |||||||||||||||||||||||||||||||||||
Sbjct: 87219455 cagtacaagtttcctctttttttttctgtcctcaagggagcctagtatgttaagatgctg 87219396


Query: 297      aaatatgctgccatatgccctggtatttttagcatgaacagcnnnnnnnnnnnnnnnnnn 356
                ||||||||||||||||||||||  ||||||||||  ||||
Sbjct: 87219395 aaatatgctgccatatgccctgccattttagcagaaaca----------------acag 87219352


Query: 357      nnnnnnnnnnnnctgcattcttctgacccctattttgctgaatcacctcacctggaattt 416
                            | ||||||| |||||| |||||||||||||||||||||||||||||||
Sbjct: 87219351 agaaagagagaacggcattctcctgacctctattttgctgaatcacctcacctggaattt 87219292


Query: 417      ccactacttgctcagtaacaccaggtaatcttaaattggaagt 459
                |||| |||||||||||||  ||||| | |||||||||| ||||
Sbjct: 87219291 ccaccacttgctcagtaatgccaggcagtcttaaattgtaagt 87219249


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
```

```
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 377,188
Number of Sequences: 54
Number of extensions: 377188
Number of successful extensions: 7
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 1
length of query: 459
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 412
effective length of database: 1,133,627,038
effective search space: 467054339656
effective search space used: 467054339656
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|21745287|gb|AF520884.1| Aphelocoma coerulescens clone ApCo48
microsatellite sequence
         (232 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr1                                                                  136   2e-030

>chr1
          Length = 188239860

 Score =  136 bits (85), Expect = 2e-030
 Identities = 152/215 (70%), Gaps = 26/215 (12%)
 Strand = Plus / Plus


Query: 7         agcccttccaggactgtggggacccaaacaaaagcataaaacac-tgcaggtgcagccct 65
                 || ||| ||  ||||||||| ||||||||||  ||| | ||| | ||||||||||||  |
Sbjct: 170350794 agtcctccccagactgtggg-acccaaacaa--gcacacaacgcctgcaggtgcagc--t 170350848


Query: 66        gctgggactataaagagccatatcgtcacctccctgcactcttactgggaaaacatgttt 125
                 |||||||| |||||||| | ||||| ||||||||||||| ||||||||||||| ||||||
Sbjct: 170350849 gctgggacaataaagaggcgtatcgccacctccctgcacacttactgggaaaatatgttt 170350908


Query: 126       cttcaaggacggtannnnnnnnnnnnnnnnnnnnnnnctcctcctccaccctctcccta- 184
                 | ||||||||                           | | ||||||||  | |||| |
Sbjct: 170350909 cctcaaggac-------------------agcactctcccttcctccactgtttccccag 170350949


Query: 185       gtgttttaggagcaaaaggcaagtttagtctccca 219
                 |  ||  || ||||||||||| ||  ||| |||||
Sbjct: 170350950 gaattacagaagcaaaaggcaggtccagtgtccca 170350984
```

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  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 178,144
Number of Sequences: 54
Number of extensions: 178144
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 1
length of query: 232
length of database: 1,133,629,576
effective HSP length: 45
effective length of query: 187
effective length of database: 1,133,627,146
effective search space: 211988276302
effective search space used: 211988276302
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|21745281|gb|AF520878.1| Aphelocoma coerulescens clone ApCo81
microsatellite sequence
         (317 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr8                                                                  110   1e-022

>chr8
          Length = 30024636

 Score =  110 bits (69), Expect = 1e-022
 Identities = 135/195 (69%), Gaps = 26/195 (13%)
 Strand = Plus / Plus


Query: 36      aaaatatggtaatatttttagcaatagatccttagcttaaacactattttgcattttgcc 95
               ||||||  ||  |||||| || |||||||  ||||||||||  ||| |||| ||||||
Sbjct: 6429857 aaaatacagttgtattttcagtaatagatttttagcttaaatcctactttgaattttggt 6429916


Query: 96      ttctggcttaaaatacatatcaaaaactaaaaagaggattaggaagaagaatctgaaaga 155
               ||||||||||        || |||     ||||||||||  | ||||||||||| |||||
Sbjct: 6429917 ttctggctta--------ataaaa----taaaagaggatgggaaagaagaatctaaaaga 6429964
```

```
Query: 156     actacaag--------------ataagactgtaaaataagagaaactagaaagagtgtgt 201
                |||||||              | |||||| ||||| ||||||||  | ||  ||| | |
Sbjct: 6429965 gctacaagaacaacagagtagaagaagactataaaacaagagaaatgaaaactagtatat 6430024


Query: 202     ttaagtgctttgttc 216
                 |||||||||| ||
Sbjct: 6430025 caaagtgctttgatc 6430039


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 324,490
Number of Sequences: 54
Number of extensions: 324490
Number of successful extensions: 11
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 9
Number of HSP's gapped (non-prelim): 1
length of query: 317
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 271
effective length of database: 1,133,627,092
effective search space: 307212941932
effective search space used: 307212941932
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|21745278|gb|AF520875.1| Aphelocoma coerulescens clone ApCo88
microsatellite sequence
         (319 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr2                                                                  150   1e-034

>chr2
          Length = 147590765

 Score =  150 bits (94), Expect = 1e-034
 Identities = 210/332 (63%), Gaps = 31/332 (9%)
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 Strand = Plus / Minus


Query: 2        ctgaaaggaatagaaaatatgtattggggtaaggtagaatatggaatcaggaaagccttt 61
                |||||| |||||||||| || || |  |  ||| ||| |||  ||||||  |     | |
Sbjct: 35381628 ctgaaaagaatagaaaaaatataattagaaaag-tagtatacagaatcactagcatttct 35381570


Query: 62       ctgatgggattattattcctttaggaaattcattgttttccagggaataaaaacaactat 121
                |||   | |||  |||||||||||||| ||  |||||| |||| | || |||| ||||||
Sbjct: 35381569 ctgtcagaatttatattcctttaggaagtttcttgtttcccagaggatgaaaataactat 35381510


Query: 122      tacannnnnnnnnnnnnnnnnnnnnnnnnnnngcacagttctctccaatttatgtaatgg 181
                |                               || || ||     | ||||||||| |||
Sbjct: 35381509 t-------ttgttactgttgttgtaaacagttgcccattt---aacgatttatgtagtgg 35381460


Query: 182      tgatttctgagaactccagccaag---attcaa------gacaaataatggcagtgtgtc 232
                ||||||||||||||||||||||||   ||||||       | | ||||   || ||||||
Sbjct: 35381459 tgatttctgagaactccagccaaggccattcaattggtgaatagataaaaccaatgtgtc 35381400


Query: 233      ctttt--------ttcaatcccaatttctcacaatatacaggtcaggctagagggcatca 284
                |||||         ||| | |||| | |||||| ||| || ||||  | ||||   | ||
Sbjct: 35381399 cttttcttgctgcctcact-ccaaatgctcacagtatgcaagtcaaaccagagatgagca 35381341


Query: 285      aagaggcaaaagggatttaagaagg-agaaaa 315
                || || |  ||| ||||| | | || ||||||
Sbjct: 35381340 aaaagac-caagagattttaaagggaagaaaa 35381310


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 286,208
Number of Sequences: 54
Number of extensions: 286208
Number of successful extensions: 7
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 5
Number of HSP's gapped (non-prelim): 1
length of query: 319
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 273
effective length of database: 1,133,627,092
effective search space: 309480196116
effective search space used: 309480196116
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
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programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|21745303|gb|AF520900.1| Aphelocoma coerulescens clone
ApCo104 microsatellite sequence
         (534 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr5                                                                  416   e-114

>chr5
          Length = 56310377

 Score =  416 bits (262), Expect = e-114
 Identities = 405/544 (74%), Gaps = 36/544 (6%)
 Strand = Plus / Minus


Query: 3        tatagactgcaaatttctgttaaaagttaaggtgattt-tgctttt-attttagaaca-t 59
                || |||||| | ||||||| |||||  || ||||  || ||| ||  |    ||   | |
Sbjct: 32392323 tacagactgaagatttctgctaaaatatagggtgcgttctgccttgcaagacagttaagt 32392264


Query: 60       aaattacc--tgtatcaccaaatggaaacctctacagttgtccaatttactttctctctt 117
                || | |||  | |||  | || || |   ||||||| |    ||   || |||||| |||
Sbjct: 32392263 aagtcacccatatatgtcaaactgcag--ctctacaatcccacaccgtattttctcactt 32392206


Query: 118      gattcaaagtgggtgtttttgtgttgcaaactgtaactcccaattccttttggccaactc 177
                ||||  || | ||||||||||||||||| ||||||| || |||||||| ||||||||| |
Sbjct: 32392205 gatttgaaataggtgtttttgtgttgcagactgtaattctcaattcctgttggccaaccc 32392146


Query: 178      catatgcatctgacttgattatttgtttagcagcacctcagcacactgaacagggcaggt 237
                ||||||||||||||   ||||||||||||| |||| ||| ||||||||||||||| ||||
Sbjct: 32392145 catatgcatctgac---attatttgtttagtagca-ctcggcacactgaacagggtaggt 32392090


Query: 238      ttgcctctgctgacgactttattacccatctgccgcaaagcatggctgtgatataattca 297
                 ||  |||||||| |||||||||| ||||||||| ||||||| |||||||||||||||||
Sbjct: 32392089 ctg-ttctgctgaagactttattatccatctgccacaaagcacggctgtgatataattca 32392031


Query: 298      ttctatttaccctaannnnnnnnnnnnnnnnnnnnnnnnnnnnnnntaatcacttctcat 357
                || ||||||||||||                                | |||||||||||
Sbjct: 32392030 ttttatttaccctaaaacaacagaaacaacgacaa------------actcacttctcat 32391983


Query: 358      ggctatgcagtgttacgagagggaa--aaataatttgatgcttcatatttcaatgtcttt 415
                || |||||||||||| ||| || ||  |||||||||||  |||||| ||||||||||||
Sbjct: 32391982 gggtatgcagtgttatgaggggaaaacaaataatttgacacttcatctttcaatgtcttc 32391923


Query: 416      tgccttgtatgcagggaaaaattatgtagatatagtcctttcattagaaacaatg----- 470
                ||||  |||  |||| ||||| |||||||||||| ||||||||||||||||| ||
Sbjct: 32391922 tgcc-agtactcaggaaaaaaatatgtagatataatcctttcattagaaacagtgtattc 32391864


Query: 471      ----caaaaacctaatatttcttctctgaatatacagcaccaaggagacatcccagcatt 526
                     | |||||   ||||||||  ||||| ||| ||||||| |||||||||||||||||
Sbjct: 32391863 tggatataaaccctgtatttctttcctgaacataaagcaccagggagacatcccagcatt 32391804


Query: 527      tgga 530
                | ||
Sbjct: 32391803 ttga 32391800


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
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  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 522,048
Number of Sequences: 54
Number of extensions: 522048
Number of successful extensions: 10
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 4
Number of HSP's gapped (non-prelim): 1
length of query: 534
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 487
effective length of database: 1,133,627,038
effective search space: 552076367506
effective search space used: 552076367506
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|11863533|emb|AJ287384.1|ASE287384 Acrocephalus sechellensis
microsatellite DNA, clone Ase 1 (w2b11)
         (124 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr1                                                                   81   4e-014

>chr1
          Length = 188239860

 Score = 80.8 bits (50), Expect = 4e-014
 Identities = 71/120 (59%), Gaps = 3/120 (2%)
 Strand = Plus / Minus


Query: 2         atcttgaagctatctcaaaaacatattccctgtagaaaaagcagaagcannnnnnnnnnn 61
                  || ||||||||  | ||||| |||||||||||||||| |||||||||||
Sbjct: 103108523 attttgaagctggcacaaaagcatattccctgtagaagaagcagaagca---gtgcacac 103108467


Query: 62        nnnnnnnnnnnnnnnnnnnnnnaatagaagagacttctgagtcatgatgttgtttacagg 121
                                        ||||||||||| || | ||||   || ||||  | |||
Sbjct: 103108466 acaacatataggcacacacaaaaatagaagagatttttaagtccgaattttgtccatagg 103108407


  Database: WholeChickenGenome.txt
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    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 80,367
Number of Sequences: 54
Number of extensions: 80367
Number of successful extensions: 4
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 1
length of query: 124
length of database: 1,133,629,576
effective HSP length: 44
effective length of query: 80
effective length of database: 1,133,627,200
effective search space: 90690176000
effective search space used: 90690176000
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 33 (53.9 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|11140001|emb|AJ287387.1|ASE287387 Acrocephalus sechellensis
microsatellite DNA, clone Ase 4 (SW18C1)
         (491 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr2                                                                  549   e-154

>chr2
          Length = 147590765

 Score =  549 bits (346), Expect = e-154
 Identities = 397/482 (82%), Gaps = 11/482 (2%)
 Strand = Plus / Minus


Query: 4        ctccatcatcaccacaaagctattagtgcnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 63
                |||||||||||||| ||||||||||||||
Sbjct: 32487579 ctccatcatcaccgcaaagctattagtg--------tgtgcacgcacatgcaaaagcaca 32487528


Query: 64       nnnnnnnnnnnnnntgcattggaataactagggcaatggaaaatacattccatctttgct 123
                              ||||| ||||||||| |||||||||||||||| ||||||||| |||
Sbjct: 32487527 ccagcacacacacgtgcataggaataactggggcaatggaaaatacgttccatcttcgct 32487468
```

```
Query: 124      cacttattccatatacaggctaatttctaaaccacaggggagcaaatgttctataaagca 183
                ||||||||||| | ||| |||||||||||||||||||||||||||||||| | ||||||
Sbjct: 32487467 cacttattccacacacaagctaatttctaaaccacaggggagcaaatgttttctaaagcc 32487408


Query: 184      ctcttattctacaactaaatacccttgctaacgaagagttagcagcacagtcatcactat 243
                ||||||| |||||||||||||||||||||||||||||||||||||| ||| | |||||||
Sbjct: 32487407 ctcttatcctacaactaaatacccttgctaacgaagagttagcagcgcagccgtcactat 32487348


Query: 244      caaaagcactaacttttagattagtagcagttggtgactcagtcattcatttttcatttt 303
                |||||||||||||||| ||||||||||||||||| ||||||||||  |||||||||||||
Sbjct: 32487347 caaaagcactaactttgagattagtagcagttggcgactcagtcacccatttttcatttt 32487288


Query: 304      aaggaaacctttttaagactgcactcttgttttcaggaggactataaatgcacttctcat 363
                ||| |||||||||||||||||||||||| ||||||||||||||||||||||||  |||||
Sbjct: 32487287 aagcaaacctttttaagactgcactcttattttcaggaggactataaatgcacagctcat 32487228


Query: 364      gtttttattttatttattctgccctggggatttgggtccctctttgcaagcaataaattt 423
                |||||||||||||||||||| ||| ||||| || | ||||||||  | ||||||||||||
Sbjct: 32487227 gtttttattttatttattctaccccggggactttgttccctcttcactagcaataaattt 32487168


Query: 424      ttctttaaatc---tttttggtaataatatattttaagacaaattggacaaggggagtat 480
                |||||||||||   ||||||||| ||||||||||||| ||||||  |||||||||||||
Sbjct: 32487167 ttctttaaatcttttttttggtactaatatattttaaaacaaatcagacaaggggagtaa 32487108


Query: 481      aa 482
                ||
Sbjct: 32487107 aa 32487106


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 531,151
Number of Sequences: 54
Number of extensions: 531151
Number of successful extensions: 16
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 13
Number of HSP's gapped (non-prelim): 1
length of query: 491
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 444
effective length of database: 1,133,627,038
effective search space: 503330404872
effective search space used: 503330404872
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
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Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|11140002|emb|AJ287388.1|ASE287388 Acrocephalus sechellensis
microsatellite DNA, clone Ase 5 (D61C07)
         (275 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr6                                                                  160   2e-037

>chr6
          Length = 33893787

 Score =  160 bits (100), Expect = 2e-037
 Identities = 188/276 (68%), Gaps = 31/276 (11%)
 Strand = Plus / Plus


Query: 10       gtgttgccacacagggactttgttacagaggatttattccaagtttttgt---tatttct 66
                |||||  ||  ||| | ||||||||||| |||  | ||  | |||||||    | |||||
Sbjct: 19520292 gtgttctcattcagaggctttgttacaggggacatgtttta-gtttttggctctgtttct 19520350


Query: 67       tgccttgaaatatcctgaaacaaaatgg-gatggtcccactgtgctgtgagcttaannnn 125
                 |||||  ||   |||||  |||||||| |||||||||||||||||| ||| ||||
Sbjct: 19520351 cgccttagaaagccctga--caaaatggtgatggtcccactgtgctgagagtttaaatat 19520408


Query: 126      nnnnnnnnnnnnnnnnnnnnnaagtagacaggtaaaagcactaaaagcaatcagttccga 185
                                     |||||||| |||| ||||          |||   || ||
Sbjct: 19520409 acgcatacaaat---------aagtagaccggtagaagcg---------atcgactctga 19520450


Query: 186      gaaaggatttactt---ttacttcagttgcacaagtatatgtgg---gtgtgtttttaaa 239
                ||||||||||| ||   ||||||||  |||| ||||||| |||    ||||||||||||
Sbjct: 19520451 gaaaggatttaattgatttacttcaactgcagaagtatacgtgctgcgtgtgtttttaat 19520510


Query: 240      tagacattagatgtctccactcatcttgctctgatc 275
                |||| || || ||||||||||||||| |||| ||||
Sbjct: 19520511 tagaaatcagttgtctccactcatctagctccgatc 19520546



 Score =  160 bits (100), Expect = 2e-037
 Identities = 188/276 (68%), Gaps = 31/276 (11%)
 Strand = Plus / Plus


Query: 10       gtgttgccacacagggactttgttacagaggatttattccaagtttttgt---tatttct 66
                |||||  ||  ||| | ||||||||||| |||  | ||  | |||||||    | |||||
Sbjct: 19506467 gtgttctcattcagaggctttgttacaggggacatgtttta-gtttttggctctgtttct 19506525


Query: 67       tgccttgaaatatcctgaaacaaaatgg-gatggtcccactgtgctgtgagcttaannnn 125
                 |||||  ||   |||||  |||||||| |||||||||||||||||| ||| ||||
Sbjct: 19506526 cgccttagaaagccctga--caaaatggtgatggtcccactgtgctgagagtttaaatat 19506583


Query: 126      nnnnnnnnnnnnnnnnnnnnnaagtagacaggtaaaagcactaaaagcaatcagttccga 185
                                     |||||||| |||| ||||          |||   || ||
Sbjct: 19506584 acgcatacaaat---------aagtagaccggtagaagcg---------atcgactctga 19506625


Query: 186      gaaaggatttactt---ttacttcagttgcacaagtatatgtgg---gtgtgtttttaaa 239
                ||||||||||| ||   ||||||||  |||| ||||||| |||    ||||||||||||
Sbjct: 19506626 gaaaggatttaattgatttacttcaactgcagaagtatacgtgctgcgtgtgtttttaat 19506685
```

```
Query: 240      tagacattagatgtctccactcatcttgctctgatc 275
                |||| || || ||||||||||||||| |||| ||||
Sbjct: 19506686 tagaaatcagttgtctccactcatctagctccgatc 19506721


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 242,339
Number of Sequences: 54
Number of extensions: 242339
Number of successful extensions: 8
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 4
Number of HSP's gapped (non-prelim): 2
length of query: 275
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 229
effective length of database: 1,133,627,092
effective search space: 259600604068
effective search space used: 259600604068
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|11140004|emb|AJ287390.1|ASE287390 Acrocephalus sechellensis
microsatellite DNA, clone Ase 7 (M59G4)
         (322 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr3                                                                  122   6e-026

>chr3
          Length = 108638738

 Score =  122 bits (76), Expect = 6e-026
 Identities = 116/152 (76%), Gaps = 17/152 (11%)
 Strand = Plus / Plus


Query: 72       agttcaaaagaaactctcctgtcttggaatttcaggattttaactgagcctggagtcatg 131
                ||||||||||||||| | ||||||||||||||||||||||     ||| |||||||||||
Sbjct: 94001336 agttcaaaagaaacttttctgtcttggaatttcaggattt-----gagtctggagtcatg 94001390
```

```
Query: 132      tagtccact------------gaaagtgctacatgtagcatgctgtgttgaaagtaaatg 179
                 ||||||||            || || ||||||||||||||||||||||||||  |||
Sbjct: 94001391 cagtccactaccaattagcctgacagcgctacatgtagcatgctgtgttgaaaacaaaca 94001450


Query: 180      tatacatttttctatgttaataccccttttcc 211
                || |||||| |||| ||| | | ||  | |||
Sbjct: 94001451 tacacatttctctaggtttagaacctctctcc 94001482


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 307,553
Number of Sequences: 54
Number of extensions: 307553
Number of successful extensions: 9
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 7
Number of HSP's gapped (non-prelim): 1
length of query: 322
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 276
effective length of database: 1,133,627,092
effective search space: 312881077392
effective search space used: 312881077392
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|11140006|emb|AJ287392.1|ASE287392 Acrocephalus sechellensis
microsatellite DNA, clone Ase 9 (L16D5)
         (262 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr3                                                                  199   2e-049

>chr3
          Length = 108638738

 Score =  199 bits (125), Expect = 2e-049
 Identities = 190/265 (71%), Gaps = 32/265 (12%)
```

```
 Strand = Plus / Plus


Query: 5        ttttaaaatctcttagaaaatataaataggatagccaagagagaataactgataaaccat 64
                ||||||||||||||| ||||||||||||| ||||||||||||| ||  |||||||||| |
Sbjct: 71270569 ttttaaaatctcttacaaaatataaatagaatagccaagagaggatggctgataaacctt 71270628


Query: 65       gacatgagattctct----tt--ttcttccnnnnnnnnnnctctattcctttcctctcca 118
                ||| | || |||| |    ||  | |||||          || ||||||||| |||||||
Sbjct: 71270629 gacgtaaggttctgtgaggttcatccttccttcttttttcct-tattcctttactctcca 71270687


Query: 119      cttggactgaag-tcctttctggcttcttcaaagagtgtnnnnnnnnnnnnnnnnnnnnn 177
                ||| |||| ||| ||| || |  |||||||||| |
Sbjct: 71270688 cttagactaaagatccattat--cttcttcaaaaa----------------------agt 71270723


Query: 178      nnnnnnnnnccctcacaaattaattccaaaaccatttttctaaatttccaatggacttgt 237
                         | | ||||||||| ||||||||||||||||||||||||||||| |||||||
Sbjct: 71270724 gcacatacacacacacaaattagttccaaaaccatttttctaaatttccaattgacttgt 71270783


Query: 238      attcctggtgtcttttcacatgatc 262
                |||||||||||||||||||||||||
Sbjct: 71270784 attcctggtgtcttttcacatgatc 71270808


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 245,450
Number of Sequences: 54
Number of extensions: 245450
Number of successful extensions: 6
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 4
Number of HSP's gapped (non-prelim): 1
length of query: 262
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 216
effective length of database: 1,133,627,092
effective search space: 244863451872
effective search space used: 244863451872
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|11140007|emb|AJ287393.1|ASE287393 Acrocephalus sechellensis
microsatellite DNA, clone Ase 10 (L11F9)
         (409 letters)
```

```
Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr2                                                                  182   6e-044

>chr2
          Length = 147590765

 Score =  182 bits (114), Expect = 6e-044
 Identities = 179/234 (76%), Gaps = 10/234 (4%)
 Strand = Plus / Plus


Query: 177       ttgaaatgttttcatttcttctccct-tctcgtaaggaattctaccccagtaggtgccac 235
                 |||||||||||||||| ||||||||| ||| || |||||| || ||| | ||||||| ||
Sbjct: 101317172 ttgaaatgttttcattccttctccctgtct-gtgaggaatcctgccctaataggtgctac 101317230


Query: 236       atatactgcaggtcaagcctaggtgagactttatgagaagagaaatgaagaagctgcaca 295
                   |  ||||    | ||   ||| | || |||| || |  |||||  ||    ||||||
Sbjct: 101317231 ccacgctgc----ccag---aggagggattttaagaaagcagaaacaaaagcactgcact 101317283


Query: 296       cactgaaattatgtttgtttttaagacagatttcaagatttggtaagaaaaacatgccac 355
                   | ||||| | |||| |||| |||| ||||||||| ||||||||| ||||||||||
Sbjct: 101317284 tgcagaaataacgtttcttttcaagatagatttcaaaatttggtaataaaaacatgctgt 101317343


Query: 356       actcagaaaagtctaataaacttgcacttctccaaagtgctttgtaaactgatc 409
                 |||||| ||||||| || |||||||| ||||||||| | ||||||||| |||||
Sbjct: 101317344 actcag-aaagtctgatcaacttgcatttctccaaattactttgtaaattgatc 101317396


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 438,623
Number of Sequences: 54
Number of extensions: 438623
Number of successful extensions: 5
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 4
Number of HSP's gapped (non-prelim): 1
length of query: 409
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 362
effective length of database: 1,133,627,038
effective search space: 410372987756
effective search space used: 410372987756
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
```

```
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|11140008|emb|AJ287394.1|ASE287394 Acrocephalus sechellensis
microsatellite DNA, clone Ase 11 (L9W16)
         (280 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr21                                                                  94   2e-017
chrUn                                                                  90   2e-016

>chr21
          Length = 6202554

 Score = 93.5 bits (58), Expect = 2e-017
 Identities = 90/120 (75%), Gaps = 1/120 (0%)
 Strand = Plus / Plus


Query: 1       gatctaaatggagttactcctgaagtgacagaacgaggccaccctttgtgcaagcaagaa 60
               || ||||||  ||||||| ||||||||||||||| ||| ||   |||||   |||||||
Sbjct: 4636364 gaactaaatatagttacttctgaagtgacagaacaaggacaaaatttgtatgagcaagag 4636423


Query: 61      accagagaaatcagaatcaggtgatgccttaccacaaaatgtttatataattttctctc 120
               | |||||  || ||| |||||||  || ||| ||   ||||||| || | |  |||||||
Sbjct: 4636424 a-cagagtgatgagattcaggtggggctttatcaaggaatgtttgtacagtccttctctc 4636482


>chrUn
          Length = 165033910

 Score = 90.3 bits (56), Expect = 2e-016
 Identities = 89/120 (74%), Gaps = 1/120 (0%)
 Strand = Plus / Minus


Query: 1        gatctaaatggagttactcctgaagtgacagaacgaggccaccctttgtgcaagcaagaa 60
                || ||||||  ||||||| ||||||||||||||| ||| ||   |||||   |||||||
Sbjct: 75152863 gaactaaatatagttacttctgaagtgacagaacaaggacaaaatttgtatgagcaagag 75152804


Query: 61       accagagaaatcagaatcaggtgatgccttaccacaaaatgtttatataattttctctc 120
                | |||||  || ||| |||||||  || ||| ||   |||| || || | |  |||||||
Sbjct: 75152803 a-cagagtgatgagattcaggtggggctttatcaaggaatgcttgtacagtccttctctc 75152745


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 212,824
Number of Sequences: 54
```

```
Number of extensions: 212824
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 2
Number of HSP's better than  0.0 without gapping: 2
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 1
Number of HSP's gapped (non-prelim): 2
length of query: 280
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 234
effective length of database: 1,133,627,092
effective search space: 265268739528
effective search space used: 265268739528
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|24940136|emb|AJ287395.2|ASE287395 Acrocephalus sechellensis
microsatellite DNA, clone Ase 12 (SUN4H2)
         (621 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr24                                                                 240   2e-061
chr7                                                                  129   5e-028

>chr24
          Length = 5910111

 Score =  240 bits (151), Expect = 2e-061
 Identities = 267/382 (69%), Gaps = 38/382 (9%)
 Strand = Plus / Plus


Query: 271     aggatctgtcccttgaggcccatatca-gaatgagaaaagggcacattcgttgaatattt 329
               |||| |||||||| |||||| |||||| ||   || ||||||||     | ||| | | |
Sbjct: 2555530 aggaactgtccctggaggcctatatcaagagacaggaaagggcatcgctgctgactgtat 2555589


Query: 330     caggnnnnnnnnnnnnng-------------agaagaggcataaaaatgctcctgccaca 376
               ||||             |             ||||| | |||||||  ||||||| ||||
Sbjct: 2555590 cagggctgggagagacaggggaaaacaagggagaagtgacataaaagcgctcctgtcaca 2555649


Query: 377     aaacctaaactcataaaaattcaggggggaggggagggagatgtgctacacctgagattt 436
               |||||||||| |||||||| |||||| |||  |   ||||||||| |||||||||| |||
Sbjct: 2555650 aaacctaaacacataaaaactcagggaggaaagagaggagatgtgttacacctgaggttt 2555709


Query: 437     ataaaatttatgggtgagcagtaacatttcaggctgggccctgctccagtgcctcagaag 496
               |||||| |||||||||||||| | ||||||||| |  || ||||  ||| | |||  |||
Sbjct: 2555710 ataaaagttatgggtgagcaggagcatttcaggttcagctctgcatcagcgtctccaaag 2555769


Query: 497     actcacaaaggtggaaagcattgggaaaagtatcagggaagctcaggaggggcacag--- 553
               ||||||||||||| || | |  ||| ||||| |||  |||||||||||||| |||||
Sbjct: 2555770 actcacaaaggtgaaaggaaccgggtaaagtgtcaaagaagctcaggagggacacagaca 2555829
```

```
Query: 554     -----agaggcactgcttcatccct---gtg----gac--aaaaattacagcgtgacaca 599
                    |||| |||||||   |||||    ||    |||    |||||||||       ||
Sbjct: 2555830 catacagagacactgctgtgtccctcacctgccccgacctgcaaattacag-------ca 2555882


Query: 600     cccagagctgcttttggtgatc 621
               | ||||||| ||||| ||||||
Sbjct: 2555883 ctcagagctcctttttgtgatc 2555904


>chr7
          Length = 37338262

 Score =  129 bits (81), Expect = 5e-028
 Identities = 180/273 (65%), Gaps = 42/273 (15%)
 Strand = Plus / Plus


Query: 3        tctgagaatgttttacaaactggtatacaaattatccacgcagaaagctattcatccatc 62
                ||||| |||||||||||||||| ||| |||||||| |  |||||||| ||||||||||||
Sbjct: 30054881 tctgaaaatgttttacaaactgatatgcaaattattcctgcagaaagttattcatccatc 30054940


Query: 63       aaggaaacacaactacagcccaaggcaaagcagaacaactatgtgaatnnnnnnnnnnnn 122
                ||||||||||| |||||||||||||||||| | | ||||||| | |||
Sbjct: 30054941 aaggaaacacagctacagcccaaggcaaagaaaagcaactatat-aataa---------- 30054989


Query: 123      nnnnnnnnnnntgaaaaaatctttagtaaatgaaggaagtattctccagtcaaggctgtg 182
                             ||| ||                 |||| |||| |||||| | ||| |
Sbjct: 30054990 -------------aaacaa-----------------aagtcttcttcagtcaggactgag 30055019


Query: 183      aggaaaatattaagtatacaatatgtgagtatgcaagacttaggaagacttttgctttta 242
                ||||| ||||| |  | | |  |||| | ||     || ||| |||||   || | ||||
Sbjct: 30055020 aggaagatattga-aaaatagcatgtaaatacatgggatttatgaagaaccttcccttta 30055078


Query: 243      taatgcaaattcttcaataaaatactgtaggat 275
                 ||| |  |||| |  | | ||||| |||||||
Sbjct: 30055079 aaatcctgattccttcacagaatacagtaggat 30055111


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 571,028
Number of Sequences: 54
Number of extensions: 571028
Number of successful extensions: 4
Number of sequences better than 1.0e-005: 2
Number of HSP's better than  0.0 without gapping: 2
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 2
length of query: 621
length of database: 1,133,629,576
effective HSP length: 48
effective length of query: 573
effective length of database: 1,133,626,984
effective search space: 649568261832
effective search space used: 649568261832
T: 0
A: 0
```

```
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|11140010|emb|AJ287396.1|ASE287396 Acrocephalus sechellensis
microsatellite DNA, clone Ase 13 (W7A11)
         (282 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr5                                                                   68   8e-010

>chr5
          Length = 56310377

 Score = 68.2 bits (42), Expect = 8e-010
 Identities = 59/74 (79%), Gaps = 2/74 (2%)
 Strand = Plus / Plus


Query: 29       gacactccctctgcaacg--tgtgctcctctgctttccaaggtgagaagcagctgagttt 86
                |||  ||||||||| | |  ||||||| |||||  ||||||||||||||||| |   |||
Sbjct: 22294887 gacggtccctctgccatgcatgtgctcttctgccatccaaggtgagaagcagttctcttt 22294946


Query: 87       ttctaaaatagcag 100
                |||| ||| |||||
Sbjct: 22294947 ttctgaaacagcag 22294960


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 240,957
Number of Sequences: 54
Number of extensions: 240957
Number of successful extensions: 4
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 3
Number of HSP's gapped (non-prelim): 1
length of query: 282
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 236
effective length of database: 1,133,627,092
effective search space: 267535993712
effective search space used: 267535993712
T: 0
```

```
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|11863487|emb|AJ276375.1|ASE276375 Acrocephalus sechellensis
microsatellite clone W10F3 (Ase18)
         (189 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr3                                                                   82   3e-014

>chr3
          Length = 108638738

 Score = 82.4 bits (51), Expect = 3e-014
 Identities = 71/89 (79%), Gaps = 3/89 (3%)
 Strand = Plus / Plus


Query: 1        gatccagtcttcgcaaaagcctttagcagaatactaaaccctcttattgcaaaataaact 60
                ||||||||||| ||| ||||| |||||||||  |||| |||||| ||||||||||||||
Sbjct: 19056032 gatccagtctttgcagaagcccttagcagaacgctaacccctctcattgcaaaataaac- 19056090


Query: 61       tttcccagatgagctccacatcagctctg 89
                  |||||     ||  |||| ||||||||
Sbjct: 19056091 --tcccatccatgccacacagcagctctg 19056117


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 132,807
Number of Sequences: 54
Number of extensions: 132807
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 1
length of query: 189
length of database: 1,133,629,576
effective HSP length: 45
effective length of query: 144
effective length of database: 1,133,627,146
effective search space: 163242309024
effective search space used: 163242309024
```

```
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 33 (53.9 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|11863490|emb|AJ276378.1|ASE276378 Acrocephalus sechellensis
microsatellite clone CO1G (Ase21)
         (821 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr5                                                                  648   0.0
chrUn                                                                 588   e-166

>chr5
          Length = 56310377

 Score =  648 bits (408), Expect = 0.0
 Identities = 608/846 (71%), Gaps = 40/846 (4%)
 Strand = Plus / Plus


Query: 1       gatcaaccactccacccacctatattagaaagccaatggcaagaaacctgctgcctcaaa 60
               |||||| || |||| |    ||| ||||||||||||| | ||| ||||||||||||||||
Sbjct: 8846762 gatcaatcagtccatc----tattttagaaagccaataggaagcaacctgctgcctcaaa 8846817


Query: 61      tgatgcttattgtcgtctactgccacctgtgaaacaacagcttgagattttcacatctgc 120
               |||| ||||||| | |  ||||||||||| ||||| |||||| |||| |||||||||||
Sbjct: 8846818 tgatacttattgccattcactgccacctgggaaaccacagctcgagactttcacatctgt 8846877


Query: 121     caagcagctttggcatcataatgcaagcccctgagcttacagtcataaaatattttacac 180
               ||||||||||||||||  |||||||  || |||| |||||||||||||||||||||||||
Sbjct: 8846878 caagcagctttggcattgtaatgcagacctctgatcttacagtcataaaatattttacac 8846937


Query: 181     atccaaagcagatattaatctcccattccatttccagattattctgtatagcttgta--- 237
               | ||||||||||| |  || |||   ||  |||| |  |||| |||||||  |||||
Sbjct: 8846938 acccaaagcagatttgcatgtcctgctctgtttctatcttatcctgtatactttgtatac 8846997


Query: 238     ------cttgcttcagaacatgagtagaaaaccaccacaaagagtgcctgctaaggctac 291
                     ||||||||| |||||||  |||||   | ||||||||| ||||| ||||| ||
Sbjct: 8846998 tctctgcttgcttcataacatgaacagaaaggtagcacaaagagcgcctgttaaggatat 8847057


Query: 292     aaaatattgttg-ttagttaggatttcttagaaccatttg--atagttg--ccacat--- 343
                | || |  ||| || |||| ||||  | |||||  ||||  |||||||   |||||
Sbjct: 8847058 gacatttcattgttttgttacgattagtcagaactgtttgatatagttgtagcacattat 8847117


Query: 344     ------atttatagcnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 397
                     ||||
Sbjct: 8847118 aaggtcatttcattttcttttcttttcttttcttttcttttcttttcttttcttttcttt 8847177


Query: 398     nnnnnnnnnnnnnnnacaatagcaggcagaaataactgttcttattcaggaatctacagt 457
                              ||||||||  |||||||||||||||| ||||||| ||   | ||
Sbjct: 8847178 tttcttttcccttatacaatagcgagcagaaataactgttcctattcagaaactcatagc 8847237
```

```
Query: 458     aattgtttttctttccttttctcttcccca-agaaacccatctgaaataaatgaccccat 516
               ||||||||||||||  ||||||   || || |||| | ||||| |||| ||| ||||| |
Sbjct: 8847238 aattgtttttcttt--ttttcttcccctcagagaagcacatctaaaatgaataacccc-t 8847294


Query: 517     ttgaagtactctgctctttaatttgtaccctggtatgtaatccagcaacatactggatgt 576
                | ||  ||||| |||||||||||| ||  || ||||||||||| |||||   |  | |
Sbjct: 8847295 gtaaaacactctactctttaatttgcactgtgctatgtaatccaacaacaggat--agga 8847352


Query: 577     ttgatgaccacaaaatgtagactgtgctcctggaaaatcatgagacctccatgaagctgc 636
                |||||||||||||| ||| |||||||| ||||||||| | |||||||||| ||||||||
Sbjct: 8847353 ctgatgaccacaaaaagtacactgtgcttctggaaaataaggagacctccacgaagctgc 8847412


Query: 637     aggacacctaactgagctctgctccagacaagaacaagtgcaagatg-agaatgttggtg 695
               | |||||||||| || | | |||| ||||| ||| ||    |||||| ||||||||| ||
Sbjct: 8847413 acgacacctaaccgaacacggctcaagacaggaaaaaacataagatgcagaatgttgttg 8847472


Query: 696     catgaacagtnnnnnnnnncggagctataatttaatttttagagtggaaaatcctgacca 755
                ||||| |||          |||| |||||||||| ||||||||||||||||||  ||||
Sbjct: 8847473 tatgaagagtgtgggg----ggagatataatttaa-ttttagagtggaaaatcccaacca 8847527


Query: 756     ttcttttacagtttaaatatcaataaaaaccaagttgcttagaatgcagaccagattgag 815
               || |||||| ||||||| | ||||||||| ||| ||||| ||||||||||||||||||||
Sbjct: 8847528 ttattttaccgtttaaacaccaataaaaa-caacttgctcagaatgcagaccagattgag 8847586


Query: 816     ctgatc 821
               ||||||
Sbjct: 8847587 ctgatc 8847592


>chrUn
          Length = 165033910

 Score =  588 bits (370), Expect = e-166
 Identities = 607/882 (68%), Gaps = 76/882 (8%)
 Strand = Plus / Minus


Query: 1        gatcaaccactccacccacctatattagaaagccaatggcaagaaacctgctgcctcaaa 60
                |||||| || |||| |    ||| ||||||||||||| | ||| ||||||||||||||||
Sbjct: 91947102 gatcaatcagtccatc----tattttagaaagccaataggaagcaacctgctgcctcaaa 91947047


Query: 61       tgatgcttattgtcgtctactgccacctgtgaaacaacagcttgagattttcacatctgc 120
                |||| ||||||| | |  ||||||||||| ||||| |||||| |||| |||||||||||
Sbjct: 91947046 tgatacttattgccattcactgccacctgggaaaccacagctcgagactttcacatctgt 91946987


Query: 121      caagcagctttggcatcataatgcaagcccctgagcttacagtcataaaatattttacac 180
                ||||||||||||||||  |||||||  || |||| |||||||||||||||||||||||||
Sbjct: 91946986 caagcagctttggcattgtaatgcagacctctgatcttacagtcataaaatattttacac 91946927


Query: 181      atccaaagcagatattaatctcccattccatttccagattattctgtatagcttgta--- 237
                | ||||||||||| |  || |||   ||  |||| |  |||| |||||||  |||||
Sbjct: 91946926 acccaaagcagatttgcatgtcctgctctgtttctatcttatcctgtatactttgtatac 91946867


Query: 238      ------cttgcttcagaacatgagtagaaaaccaccacaaagagtgcctgctaaggctac 291
                      ||||||||| |||||||  ||||    ||||||||||| ||||| ||||| ||
Sbjct: 91946866 tctctgcttgcttcataacatgaacagaatggtaccacaaagagcgcctgttaaggatat 91946807


Query: 292      aaaatattgttgtta-gttaggatttcttagaaccatttgata--gttgc--cacata-- 344
                 | || |  |||||  |||| ||||  | |||||  |||||||  ||||   |||||
Sbjct: 91946806 gacatttcattgttttgttacgattagtcagaactgtttgatatagttgtagcacattat 91946747


Query: 345      -------------------------------------------tttatagcnnnnnnnnn 361
                                                           ||| |
```

```
Sbjct: 91946746 aaggtcatttcattttcttttcttttcttttcttttcttttcttttcttttcttttcttt 91946687


Query: 362      nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnacaatagca 421
                                                                   ||||||||
Sbjct: 91946686 tcttttcttttcttttcttttcttttttttttttcttttcttttcccttatacaatagcg 91946627


Query: 422      ggcagaaataactgttcttattcaggaatctacagtaattgtttttctttccttttctct 481
                 |||||||||||||||| ||||||| ||   | || ||||||||||||||  ||||||
Sbjct: 91946626 agcagaaataactgttcctattcagaaactcatagcaattgtttttcttt--ttttcttc 91946569


Query: 482      tcccca-agaaacccatctgaaataaatgaccccatttgaagtactctgctctttaattt 540
                 || || |||| | ||||| |||| ||| ||||| | | ||  ||||| |||||||||||
Sbjct: 91946568 ccctcagagaagcacatctaaaatgaataacccc-tgtaaaacactctactctttaattt 91946510


Query: 541      gtaccctggtatgtaatccagcaacatactggatgtttgatgaccacaaaatgtagactg 600
                | ||  || ||||||||||| |||||   | |  |  |||||||||||||| ||| ||||
Sbjct: 91946509 gcactgtgctatgtaatccaacaacaggatag--gactgatgaccacaaaaagtacactg 91946452


Query: 601      tgctcctggaaaatcatgagacctccatgaagctgcaggacacctaactgagctctgctc 660
                |||| ||||||||| | |||||||||| ||||||||| |||||||||| || | | ||||
Sbjct: 91946451 tgcttctggaaaataaggagacctccacgaagctgcacgacacctaaccgaacacggctc 91946392


Query: 661      cagacaagaacaagtgcaagatg-agaatgttggtgcatgaacagtnnnnnnnnncggag 719
                 ||||| ||| ||    |||||| ||||||||| || ||||| |||          ||||
Sbjct: 91946391 aagacaggaaaaaacataagatgcagaatgttgttgtatgaagagtgtgggg----ggag 91946336


Query: 720      ctataatttaatttttagagtggaaaatcctgaccattcttttacagtttaaatatcaat 779
                 |||||||||| ||||||||||||||||||  |||||| |||||| ||||||| | ||||
Sbjct: 91946335 atataatttaa-ttttagagtggaaaatcccaaccattattttaccgtttaaacaccaat 91946277


Query: 780      aaaaaccaagttgcttagaatgcagaccagattgagctgatc 821
                ||||| ||| ||||| ||||||||||||| ||||||||||||
Sbjct: 91946276 aaaaa-caacttgctcagaatgcagaccaaattgagctgatc 91946236


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 766,108
Number of Sequences: 54
Number of extensions: 766108
Number of successful extensions: 18
Number of sequences better than 1.0e-005: 2
Number of HSP's better than  0.0 without gapping: 2
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 5
Number of HSP's gapped (non-prelim): 3
length of query: 821
length of database: 1,133,629,576
effective HSP length: 48
effective length of query: 773
effective length of database: 1,133,626,984
effective search space: 876293658632
effective search space used: 876293658632
T: 0
A: 0
```

```
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|11863493|emb|AJ276381.1|ASE276381 Acrocephalus sechellensis
microsatellite clone D51C07 (Ase24)
         (383 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr5                                                                  179   5e-043

>chr5
          Length = 56310377

 Score =  179 bits (112), Expect = 5e-043
 Identities = 253/411 (61%), Gaps = 50/411 (12%)
 Strand = Plus / Plus


Query: 1        gatcctgttgcaagataaacaacacgatgtgatgtaacataattttgtgcatgtgtgtgc 60
                |||||||||||||||||||||||  ||||  ||||||||||||||||||| ||||||||
Sbjct: 29845988 gatcctgttgcaagataaacaacgtgatgcaatgtaacataattttgtgcgtgtgtgtg- 29846046


Query: 61       atttgtgagagact-----ggggcgggaacacnnnnnnnnnnnnnnnnnnnnnnnnnnnn 115
                    ||||||||||     ||||||||  |
Sbjct: 29846047 ---agtgagagacttgaagggggcgggggcgagtgctgagagaaaggaagagagaaagca 29846103


Query: 116      nnnntgtacggcagcatttgcaa-gggaaaaatatacatggcctgagtagttttgagtcc 174
                     |  || ||||||| |||| || ||||||| | ||| ||  || |||| | |||||
Sbjct: 29846104 agcacg--cgtcagcattcgcaatggaaaaaatacatatgtccacaggagttctcagtcc 29846161


Query: 175      ggtgctcactaaaaagcagaa-ggagaaacacgtaagcaatgacag--cttcagacaaca 231
                 |  ||  ||| ||   |||| |||||| || | ||  ||  | ||  |||    |||||
Sbjct: 29846162 agcacttgctataatttagaatggagaagca-gaaaaaaaaaaaagaacttagtgcaaca 29846220


Query: 232      gaaataat----ctttcttctattattc---nnnnnnncatacattataacagcttcaca 284
                 ||||| |    ||   || |||| |||          |||| || | ||||| |   ||
Sbjct: 29846221 aaaatactgatgctgctttatattgttcaaaatacaatcataaatcaaaacaggtcagca 29846280


Query: 285      gaatagccactttctttatcaag-------------------------ctggctaagtct 319
                 ||  ||||||||||||||||||                          | |||| |||
Sbjct: 29846281 aaagggccactttctttatcaagttcgctttatcaatattcgtccagaatagctatgtca 29846340


Query: 320      gtatttattttttgaaccaaaacctagtagtca--atacacactgtacttt 368
                |||||||  ||||| |||||||| |||||||||  ||| ||||| ||||||
Sbjct: 29846341 gtatttaaattttggaccaaaacttagtagtcaatatatacactatacttt 29846391


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549
```

```
Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 358,469
Number of Sequences: 54
Number of extensions: 358469
Number of successful extensions: 7
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 4
Number of HSP's gapped (non-prelim): 2
length of query: 383
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 336
effective length of database: 1,133,627,038
effective search space: 380898684768
effective search space used: 380898684768
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|11863496|emb|AJ276384.1|ASE276384 Acrocephalus sechellensis
microsatellite clone 0805E (Ase27)
         (408 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chrUn                                                                  97   3e-018
chr1                                                                   94   3e-017

>chrUn
          Length = 165033910

 Score = 96.7 bits (60), Expect = 3e-018
 Identities = 90/200 (45%)
 Strand = Plus / Plus


Query: 79        gnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 138
                 |
Sbjct: 141687269 gttgctattaattaaaaacaaaatattataatgttgcatgccctatgtttacatgcttct 141687328


Query: 139       nnnnnnnnnnnnnnnnnnnnnattgccatgttcactgctttcttttatctctcaatcaaa 198
                                      ||| ||||||||||| |  ||| | || | |||| | ||
Sbjct: 141687329 gtcttcacttttctctttattattcccatgttcacttccctctgtcatttgtcaaactaa 141687388


Query: 199       gaacgacattcaaaagcatgactatactataacagattgaaagcctatctagcctgtacc 258
                 |||   |||| ||||| || | |||||||||||||||  |     ||||||||||||| |
Sbjct: 141687389 gaattgcattgaaaagaataattatactataacagatccattcggtatctagcctgtatc 141687448
```

```
Query: 259       ttgactccaacagtaccaag 278
                 ||| ||||| || || | ||
Sbjct: 141687449 ttggctccagcaatatctag 141687468


>chr1
          Length = 188239860

 Score = 93.5 bits (58), Expect = 3e-017
 Identities = 88/118 (74%)
 Strand = Plus / Minus


Query: 161      ttgccatgttcactgctttcttttatctctcaatcaaagaacgacattcaaaagcatgac 220
                || ||||||||||| |  ||| | || | |||| | |||||   |||| ||||| || |
Sbjct: 16626117 ttcccatgttcacttccctctgtcatttgtcaaactaagaattgcattgaaaagaataat 16626058


Query: 221      tatactataacagattgaaagcctatctagcctgtaccttgactccaacagtaccaag 278
                |||||||||||||||  |     ||||||||||||| |||| ||||| || || | ||
Sbjct: 16626057 tatactataacagatccattcggtatctagcctgtatcttggctccagcaatatctag 16626000


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 231,246
Number of Sequences: 54
Number of extensions: 231246
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 2
Number of HSP's better than  0.0 without gapping: 2
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 1
Number of HSP's gapped (non-prelim): 2
length of query: 408
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 361
effective length of database: 1,133,627,038
effective search space: 409239360718
effective search space used: 409239360718
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|11863498|emb|AJ276386.1|ASE276386 Acrocephalus sechellensis
microsatellite clone M3C2 (Ase29)
         (243 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters
```

```
                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr14                                                                 166   2e-039

>chr14
          Length = 20603938

 Score =  166 bits (104), Expect = 2e-039
 Identities = 169/256 (66%), Gaps = 21/256 (8%)
 Strand = Plus / Plus


Query: 1       gatcagtttggagacgttttcttactaatcattgtaaacctt-aaaggacaatgtaattg 59
               |||||||| | |||  ||||| ||||||| ||||||||| || ||| ||||||| |||||
Sbjct: 9416707 gatcagttagcagagattttcctactaataattgtaaacatttaaaagacaatgcaattg 9416766


Query: 60      gtgctnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnaaaatacacaaatgttaccaccca 119
               |||||                                    ||||| |  ||||  ||||
Sbjct: 9416767 gtgctacacacacacacacacacacacacac--------acacacaccttacagccca 9416818


Query: 120     gaaacacaagtatttgggtgtactttgtttcagaatcagtgtcagc------------cc 167
                |||  |||  || ||||  ||  ||||||||||||||||| ||||            ||
Sbjct: 9416819 caaatgcaaacatctgggcctatattgtttcagaatcagtgacagcatcagtggcagccc 9416878


Query: 168     tagttgactgtattatactgcacattccttatggctctgtgacataatctattatgtaat 227
                || ||||||| | | |||||||||||||||  || |||  ||||| ||||||| ||||
Sbjct: 9416879 cagctgactgtctcacactgcacattccttacagcactgcaacatattctattaggtaag 9416938


Query: 228     aacagcctaggagatc 243
               ||||||||||||||||
Sbjct: 9416939 aacagcctaggagatc 9416954


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 147,857
Number of Sequences: 54
Number of extensions: 147857
Number of successful extensions: 4
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 1
length of query: 243
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 197
effective length of database: 1,133,627,092
effective search space: 223324537124
effective search space used: 223324537124
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
```

```
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|11863507|emb|AJ276641.1|ASE276641 Acrocephalus Sechellensis
microsatellite DNA, clone L1I14 (Ase39)
         (378 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr1                                                                 158   7e-037

>chr1
          Length = 188239860

 Score =  158 bits (99), Expect = 7e-037
 Identities = 220/330 (66%), Gaps = 16/330 (4%)
 Strand = Plus / Minus


Query: 55       aaattagnnnnnnntctttcggaaagcaccacctatatttcaaattg-agctgaaaagca 113
                ||||||        | ||| | ||||  |||  || ||||||||| | |  ||||| |||
Sbjct: 40771335 aaattaaagagtatt-tttggtaaagg-ccagatacatttcaaataggaagtgaaatgca 40771278


Query: 114      atgtttcaatacttcagttcaacaacacacattggcatggagtattaacttagttatttt 173
                |||| |   ||| || ||||||| | | | ||    |   |   ||||    |||  |||||
Sbjct: 40771277 atgtctttgtacatctgttcaaccaaaaaaataatgaaaaa-tatttttgtaggcatttt 40771219


Query: 174      tcttggatacttgcattttaaaaatacaactg--tctgacctgta--aagtagcagagaa 229
                |||  |  | |||  ||| |||||||  |||   ||||||||||   || | |  || ||
Sbjct: 40771218 tctcaggcatttgtcttt-aaaaatatgactaaatctgacctgttttaaatggtggaaaa 40771160


Query: 230      attcacatgccgctcattaacaaatgagactttccttcactgtcatgctcatagctacct 289
                |  || |||  |||| | ||  | ||  | ||||||| | ||||| ||| | ||| ||||
Sbjct: 40771159 aaacatatgttgctcttcaatcagtgttagtttcctttattgtcacgctaacagcaacct 40771100


Query: 290      gcacttttgctgaactgctatctgtgttgatattttctcca----aat---ttttaaata 342
                | |||| |||||||||||| |||| |   ||||||||| ||    |||   |||   |
Sbjct: 40771099 gaacttatgctgaactgctgtctgggccaatattttctgcaaggtaatttgtttctgact 40771040


Query: 343      tgttttccaaatatttaatttttataaatg 372
                || |||||| | ||||||||  ||||||||
Sbjct: 40771039 tgctttccacacatttaattaatataaatg 40771010


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 412,624
```

```
Number of Sequences: 54
Number of extensions: 412624
Number of successful extensions: 16
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 15
Number of HSP's gapped (non-prelim): 1
length of query: 378
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 331
effective length of database: 1,133,627,038
effective search space: 375230549578
effective search space used: 375230549578
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|11863514|emb|AJ276775.1|ASE276775 Acrocephalus sechellensis
microsatellite DNA, clone M7G9 (Ase 46)
         (380 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr14                                                                 316   1e-084

>chr14
          Length = 20603938

 Score =  316 bits (199), Expect = 1e-084
 Identities = 205/211 (97%)
 Strand = Plus / Minus


Query: 170    taagcaagccagccaaattccatcttcatggacagttcaatggaaagttagctagaaaat 229
              ||||||||||||| ||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct: 939420 taagcaagccagctaaattccatcttcatggacagttcaatggaaagttagcttgaaaat 939361


Query: 230    gcagtatatcatatttcatgaatttaataggtttttcatgattttacaaagtgcttcaac 289
              ||||||||||| ||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct: 939360 gcagtatatcaaatttcatgaatttaatagggttttcatgattttacaaagtgcttcaac 939301


Query: 290    cagacagtcatggctggaggctgcacagcaggagacctaaaacactgcatctgtgttttt 349
              |||||| ||| |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 939300 cagacactcacggctggaggctgcacagcaggagacctaaaacactgcatctgtgttttt 939241


Query: 350    caactcttgccagaatccattgaatttgatc 380
              |||||||||||||||||||||||||||||||
Sbjct: 939240 caactcttgccagaatccattgaatttgatc 939210


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54
```

```
Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 333,707
Number of Sequences: 54
Number of extensions: 333707
Number of successful extensions: 2
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 1
Number of HSP's gapped (non-prelim): 1
length of query: 380
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 333
effective length of database: 1,133,627,038
effective search space: 377497803654
effective search space used: 377497803654
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|11863515|emb|AJ276776.1|ASE276776 Acrocephalus sechellensis
microsatellite DNA, clone W10B7 (Ase 47)
         (317 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chrW                                                                  141   1e-031

>chrW
          Length = 4916845

 Score =  141 bits (88), Expect = 1e-031
 Identities = 181/264 (68%), Gaps = 28/264 (10%)
 Strand = Plus / Minus


Query: 75      atacatatatgtatttgtatgcatatatatt----gcccattctgacacagagcaaataa 130
               ||||||  | |||| ||||||  | | ||||    ||||  | | | | || ||| ||||
Sbjct: 2513104 atacatggaagtatatgtatgtttgtgtattctttgccctctttaatatagggcatataa 2513045


Query: 131     acattttaggcca------------------ttcagcctaaataaatacactgacaagca 172
               ||| ||||| | |                  |||||||| | ||| ||  || ||||  |
Sbjct: 2513044 acactttagacaactgttgagttttccctctttcagcctcagtaattaagctaacaacta 2512985


Query: 173     tacactagcatccttagttcacttgctagcatttattgttattatccatttgcattgtgg 232
               | ||||   ||| ||| |||   ||||| ||| |||| ||||||||||||||||||||||
Sbjct: 2512984 tgcactgatatcattatttcctgtgctaccatatattattattatccatttgcattgtgg 2512925
```

```
Query: 233     tagcaatcatatagcagtgccttgccctaaagagtttgcaatctggaaggatgctctaat 292
               | ||||||| ||   ||||||||  ||| |||||||||||  || ||  ||  || ||| 
Sbjct: 2512924 tggcaatcacatgttagtgccttatcctgaagagtttgcagcctaga--gagtct-taac 2512868


Query: 293     gggaagagacagaagagtaatgat 316
                ||||||   ||||||| ||||||
Sbjct: 2512867 aggaaga---agaagaggaatgat 2512847


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 256,057
Number of Sequences: 54
Number of extensions: 256057
Number of successful extensions: 86
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 85
Number of HSP's gapped (non-prelim): 1
length of query: 317
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 271
effective length of database: 1,133,627,092
effective search space: 307212941932
effective search space used: 307212941932
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|11863516|emb|AJ276777.1|ASE276777 Acrocephalus sechellensis
microsatellite DNA, clone AO8B (Ase 48)
         (896 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr5                                                                   84   5e-014

>chr5
          Length = 56310377

 Score = 84.0 bits (52), Expect = 5e-014
 Identities = 70/86 (81%), Gaps = 1/86 (1%)
 Strand = Plus / Minus
```

```
Query: 812      aagataataccaatt-agaagcccagtagcccaatgttctctaatgactcaccaacctac 870
                |||||| ||||| |  ||  |||||| |||||||| ||  || || |||||| |||||||
Sbjct: 30387107 aagatagtaccagtccaggggcccagcagcccaatatttgctcattactcacaaacctac 30387048


Query: 871      ctctgcaatatctgtgcaacttgatc 896
                ||||||||||||  || |||||||||
Sbjct: 30387047 ctctgcaatatcaatgtaacttgatc 30387022


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 589,929
Number of Sequences: 54
Number of extensions: 589929
Number of successful extensions: 4
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 3
Number of HSP's gapped (non-prelim): 1
length of query: 896
length of database: 1,133,629,576
effective HSP length: 48
effective length of query: 848
effective length of database: 1,133,626,984
effective search space: 961315682432
effective search space used: 961315682432
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|11863518|emb|AJ276779.1|ASE276779 Acrocephalus sechellensis
microsatellite DNA, clone M60A9 (Ase 50)
         (434 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chrZ                                                                  358   6e-097

>chrZ
          Length = 33651169

 Score =  358 bits (225), Expect = 6e-097
 Identities = 327/436 (75%), Gaps = 27/436 (6%)
```

```
 Strand = Plus / Plus


Query: 1        gatctatcctgacaagggaagtttcttcc-acacatctcctgtagctcagtctttgacaa 59
                ||||||| | ||||| | | | ||||||| || |||||  ||  || ||| ||| || |
Sbjct: 26965745 gatctattcagacaaag-atgattcttcccacccatcttttgatgcccagccttggatag 26965803


Query: 60       tattacttcattctttcaagcaggtagtggaggaatgcaactcatgc-taaatgtacaaa 118
                |||  |||||  |||||| ||||||| |||||||||||||||||| | ||||||| ||||
Sbjct: 26965804 tatctcttcaccctttca-gcaggtactggaggaatgcaactcattcctaaatgtgcaaa 26965862


Query: 119      taaaaggggggaaggagaaattaccttctgctgtggaatgctgtctggcatgctgactcc 178
                 | | ||| |||||||| ||||| | |||||| |||||||||||||||||||||||||||
Sbjct: 26965863 caga-gggaggaaggaggaattatcgtctgctatggaatgctgtctggcatgctgactcc 26965921


Query: 179      tgtgcacgnnnnnnnnnnnnnnnnnnnnnnnntacatttcatttatggacacacaaagag 238
                |||||| |                         ||   ||||||||| ||||||||||||
Sbjct: 26965922 tgtgcatgcatgcacgcgcacacacacacac--ac---tcatttatgtacacacaaagag 26965976


Query: 239      acccagaaggaggtgagaagggaaagtttttcagcctcacactaagcctcacagagggag 298
                |||||||||                 ||| |||||||||| |||||||||||||| ||||
Sbjct: 26965977 acccagaag-----------------tttctcagcctcacgctaagcctcacagaaggag 26966019


Query: 299      caactgagttctccaagcgagcggcaaagacttggaggagaatccaactgcagcttgtgt 358
                  | ||| ||||   || ||     || || |||  |||||||||||| ||| |  ||||
Sbjct: 26966020 tgagtgaattctgtgagagaataataatgatttgatggagaatccaacagcaccccgtgt 26966079


Query: 359      ttcatatttgcgttggatgctcaggtttccaaattaaatctgcaagttagacgggagtcc 418
                ||||||||||| |||||| |||||||||||||||||||| |||||||||||| |||||||
Sbjct: 26966080 ttcatatttgcattggatactcaggtttccaaattaaatttgcaagttagacaggagtcc 26966139


Query: 419      atgttgtctgctgatc 434
                ||||||||||||||||
Sbjct: 26966140 atgttgtctgctgatc 26966155


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 361,321
Number of Sequences: 54
Number of extensions: 361321
Number of successful extensions: 6
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 3
Number of HSP's gapped (non-prelim): 1
length of query: 434
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 387
effective length of database: 1,133,627,038
effective search space: 438713663706
effective search space used: 438713663706
T: 0
A: 0
```

```
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|11863520|emb|AJ276781.1|ASE276781 Acrocephalus sechellensis
microsatellite DNA, clone M10G6 (Ase 52)
         (491 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr3                                                                  328   9e-088

>chr3
          Length = 108638738

 Score =  328 bits (206), Expect = 9e-088
 Identities = 348/492 (70%), Gaps = 27/492 (5%)
 Strand = Plus / Minus


Query: 2        atcttagcctgcactcatttcagtaaactcatggtttttctaacacatctgaaaaccagc 61
                || ||| || |||||||| | |    | ||||| |||||||  |||||   ||||||| |
Sbjct: 48100672 attttaacccgcactcatataaaggcattcatgatttttctgtcacattcaaaaaccatc 48100613


Query: 62       tactgaaaaaatccaaaatttccattttctttcatgacacttaggagccttcaaaaagcc 121
                |||| ||      |||||| |  ||||||||||| | || ||   |||| || |||||||
Sbjct: 48100612 tact-aactgtgacaaaatgtgtattttctttcaaggcatttgaaagccatccaaaagcc 48100554


Query: 122      cttaggtaccaaattagcgctcacgnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnntgc 181
                |||| |||||| ||| || | ||||                                  |
Sbjct: 48100553 cttaagtaccagatttgcacacacgcacatatacata----------------------c 48100516


Query: 182      ttttactgaatacacaaagagacaaaatcttcagcacattcagaaataaatgacaccata 241
                | ||| ||||||||||||   ||||   ||||||||  ||   ||| ||   |||| |||
Sbjct: 48100515 tcttaatgaatacacaaaattacaactccttcagcatgtttgaaaaaaagctacactata 48100456


Query: 242      atatgcatcaagaaaaggcctatgaacttacggtgactgcttcacatgtttaggct-gca 300
                ||| ||||||| ||||||||||| ||||||| ||||||||||||||  || ||| | |||
Sbjct: 48100455 atacgcatcaataaaaggcctattaacttacagtgactgcttcacacattcaggtttgca 48100396


Query: 301      cagttttcaaggaatcgtctcaaacatt--ggtagcatgtagctttaggattg-aaactg 357
                |||||||||||||||| |||| |||||   |||||||| || | ||||  ||  ||||||
Sbjct: 48100395 cagttttcaaggaatcttctccaacatgtaggtagcatctatcattagatttctaaactg 48100336


Query: 358      ctcgtatcctcagatatgtacatgaaattattatagacaccgttatgtacattcactaaa 417
                  ||||||||||| ||||||||||| | | |||| ||||   || |||||| ||||||||
Sbjct: 48100335 tgcgtatcctcaggtatgtacatgagactgttatggacattattgtgtacactcactaaa 48100276


Query: 418      gaattgaattcttgacttgaagcacaaacctgtcctatgccttgctgccttcacaactgc 477
                |||||| || |||||     |||||||||   ||||||||||   |  |||||||| |||
Sbjct: 48100275 gaattggatccttgatgaagagcacaaacacatcctatgcctcattctcttcacaattgc 48100216


Query: 478      tgtgaaacttga 489
                | || |||| ||
```

```
Sbjct: 48100215 tttgtaactgga 48100204



 Score =  172 bits (108), Expect = 5e-041
 Identities = 167/220 (75%), Gaps = 4/220 (1%)
 Strand = Plus / Minus


Query: 274      gtgactgcttcacatgtttaggct-gcacagttttcaaggaatcgtctcaaacatt--gg 330
                |||||||| |||||  || ||| | ||||||||||||||||||| |||| | |||   ||
Sbjct: 48105202 gtgactgcgtcacacattcaggtttgcacagttttcaaggaatcttctccagcatgtagg 48105143


Query: 331      tagcatgtagctttaggattg-aaactgctcgtatcctcagatatgtacatgaaattatt 389
                |||||| || | ||||  ||  ||||||  ||||||||||||||||||||||  | | ||
Sbjct: 48105142 tagcatctatcattagacttctaaactgtgcgtatcctcagatatgtacatggcactgtt 48105083


Query: 390      atagacaccgttatgtacattcactaaagaattgaattcttgacttgaagcacaaacctg 449
                || ||||   || |||| | | |||||||| ||| || |||||     |||||||||
Sbjct: 48105082 atggacattattgtgtatactaactaaagacttggatccttgatgcagagcacaaactca 48105023


Query: 450      tcctatgccttgctgccttcacaactgctgtgaaacttga 489
                ||||||||||   |  |||||||| |||| || |||| ||
Sbjct: 48105022 tcctatgcctcattctcttcacaattgctttgtaactgga 48104983


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 422,772
Number of Sequences: 54
Number of extensions: 422772
Number of successful extensions: 9
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 3
Number of HSP's gapped (non-prelim): 2
length of query: 491
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 444
effective length of database: 1,133,627,038
effective search space: 503330404872
effective search space used: 503330404872
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|11863522|emb|AJ276783.1|ASE276783 Acrocephalus sechellensis
microsatellite DNA, clone M6H10 (Ase 54)
```

```
         (295 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



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

  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 191,009
Number of Sequences: 54
Number of extensions: 191009
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 0
Number of HSP's better than  0.0 without gapping: 0
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 3
Number of HSP's gapped (non-prelim): 0
length of query: 295
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 249
effective length of database: 1,133,627,092
effective search space: 282273145908
effective search space used: 282273145908
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|11863523|emb|AJ276784.1|ASE276784 Acrocephalus sechellensis
microsatellite DNA, clone M37E11 (Ase 55)
         (343 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                  Score    E
Sequences producing significant alignments:                      (bits) Value

chr3                                                                  285   4e-075

>chr3
          Length = 108638738

 Score =  285 bits (179), Expect = 4e-075
 Identities = 267/357 (74%), Gaps = 29/357 (8%)
 Strand = Plus / Plus
```

```
Query: 1        gatctcttccagctggattggcatcgtgctgtatgtgtggactctggtggctccactggt 60
                ||| |||||||||||||||||||| ||| ||||||||||||||||||| ||||| |||||
Sbjct: 59761328 gatatcttccagctggattggcattgtgttgtatgtgtggactctggttgctccgctggt 59761387


Query: 61       tcttaccaaccgcgactttgact----gagctgtgctgctctggagggaggctg-tgtta 115
                |||||| || || ||||||||||    |||||| | |||||   ||||| | || |||||
Sbjct: 59761388 tcttacaaatcgtgactttgactaagggagctgcgttgctccccagggaagatggtgtta 59761447


Query: 116      g---cacc-------tgaaacaaacagtattccgggtaatggtgtgggtgtaaatacann 165
                |   ||||       ||||||||||||||||| || | || |||| | ||||||||
Sbjct: 59761448 ggtccaccatgtctttgaaacaaacagtattcaggattatagtgtagttgtaaata---- 59761503


Query: 166      nnnnnnnnnnnnnnnnctgtccaggtagtattccctgctttatcctgcatgattaccttg 225
                                ||||  ||    ||| ||||||||||  ||||||||| ||||||
Sbjct: 59761504 tgtgtgcgcgtgctatctgtgtagca--tataccctgctttactctgcatgatcaccttg 59761561


Query: 226      aatcacgtcattt--------cattaaatgactttttctagctgagctcaatggtaattg 277
                ||||| ||| |||        || |||||| || |||||||||||||||| ||  |||||
Sbjct: 59761562 aatcatgtctttttgtcacttcactaaatggctctttctagctgagctcagtgagaattg 59761621


Query: 278      ctgtaatgatggttttcataggattactcctagtttgagtgctttgggagcatgaga 334
                ||  |||||| ||||||||||||||| |||||| |  |||||||||||||||| |||
Sbjct: 59761622 ctacaatgatagttttcataggattattcctagatcaagtgctttgggagcattaga 59761678



 Score =  272 bits (171), Expect = 3e-071
 Identities = 263/357 (73%), Gaps = 29/357 (8%)
 Strand = Plus / Plus


Query: 1        gatctcttccagctggattggcatcgtgctgtatgtgtggactctggtggctccactggt 60
                ||| |||||||||||||||||||| ||| |||||||||||||| |||| ||||| |||||
Sbjct: 59774962 gatatcttccagctggattggcattgtgttgtatgtgtggactttggttgctccgctggt 59775021


Query: 61       tcttaccaaccgcgactttgact----gagctgtgctgctctggagggaggctg-tgtta 115
                |||||| || || || || || |    |||||| | |||||   ||||| | || |||||
Sbjct: 59775022 tcttacaaatcgtgatttggaataagggagctgcgttgctccccagggaagatggtgtta 59775081


Query: 116      g---cacc-------tgaaacaaacagtattccgggtaatggtgtgggtgtaaatacann 165
                |   ||||       ||||||||||||||||| || | || |||| | ||||||||
Sbjct: 59775082 ggtccaccatgtctttgaaacaaacagtattcaggattatagtgtagttgtaaata---- 59775137


Query: 166      nnnnnnnnnnnnnnnnctgtccaggtagtattccctgctttatcctgcatgattaccttg 225
                                ||||  ||    ||| ||||||||||  ||||||||| ||||||
Sbjct: 59775138 tgtgtgcgcgtgctatctgtgtagca--tataccctgctttactctgcatgatcaccttg 59775195


Query: 226      aatcacgtcattt--------cattaaatgactttttctagctgagctcaatggtaattg 277
                ||||| ||| |||        || |||||| || |||||||||||||||| ||  |||||
Sbjct: 59775196 aatcatgtctttttgtcacttcactaaatggctctttctagctgagctcagtgagaattg 59775255


Query: 278      ctgtaatgatggttttcataggattactcctagtttgagtgctttgggagcatgaga 334
                ||  |||||| ||||||||||||||| |||||| |  |||||||||||||||| |||
Sbjct: 59775256 ctacaatgatagttttcataggattattcctagatcaagtgctttgggagcattaga 59775312


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
```

```
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 242,267
Number of Sequences: 54
Number of extensions: 242267
Number of successful extensions: 10
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 2
length of query: 343
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 297
effective length of database: 1,133,627,092
effective search space: 336687246324
effective search space used: 336687246324
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|11863527|emb|AJ276788.1|ASE276788 Acrocephalus sechellensis
microsatellite DNA, clone M61F1 (Ase 59)
         (319 letters)

Database: WholeChickenGenome.txt
          54 sequences; 1,133,629,576 total letters



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

  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 300,577
Number of Sequences: 54
Number of extensions: 300577
Number of successful extensions: 4
Number of sequences better than 1.0e-005: 0
Number of HSP's better than  0.0 without gapping: 0
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 4
Number of HSP's gapped (non-prelim): 0
length of query: 319
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 273
effective length of database: 1,133,627,092
effective search space: 309480196116
```

```
effective search space used: 309480196116
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|11863528|emb|AJ276789.1|ASE276789 Acrocephalus sechellensis
microsatellite DNA, clone M21B5 (Ase 60)
         (440 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr3                                                                  261   8e-068

>chr3
          Length = 108638738

 Score =  261 bits (164), Expect = 8e-068
 Identities = 306/446 (68%), Gaps = 63/446 (14%)
 Strand = Plus / Plus


Query: 1        gatcttgaacagtgttagcagcatttgcaacagaaaacaaatcaagaccaaacatgaaaa 60
                |||||| | |||  |||| |||||||   ||||||||||||||||||  || ||||||||
Sbjct: 50234303 gatcttaagcagcattaggagcatttatgacagaaaacaaatcaagagtaagcatgaaaa 50234362


Query: 61       ggaactctccagcttatgtggtggggcttttttccttggcttgcttttattgtatcatgc 120
                ||||| |||| ||||||| | |     || |||||| | |||| |||||||||||    |
Sbjct: 50234363 ggaacgctcctgcttatgcgttattt-ttctttcctag-cttgtttttattgtattgcac 50234420


Query: 121      tcaagaaagacacagttaaggaaagagtgattctgtctacagccttctgaactaattagt 180
                ||||||| |||||| ||||  | | ||||||||||||| |||| |||||||||||||| |
Sbjct: 50234421 tcaagaaggacacatttaacaacacagtgattctgtctgcagcattctgaactaattact 50234480


Query: 181      ttccccctactcagaaaaatcctggaacaggtagctgcagtaaaacaacagtgannnnnn 240
                ||||| |  ||||| ||||  ||| || |||||||| |||||||||
Sbjct: 50234481 ttcccaccgctcagcaaaaagctgaaataggtagctccagtaaaac-------------- 50234526


Query: 241      nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnagaatattagtaaacattt 300
                                                         ||||||||||||||||| |
Sbjct: 50234527 ---------------------------gaaaataagttgggagaatattagtaaacatat 50234559


Query: 301      ctaatatgccagtcctgcatccgctagccatttattggaagcctttgatgtccagtattc 360
                ||||| ||| || | | |||| ||| ||   ||||| ||||||||||||||||||  ||
Sbjct: 50234560 ctaatctgctag-catccatcagct-gc---ttattagaagcctttgatgtccagcgttt 50234614


Query: 361      cccaaattactaatgtaaaa-----gaagcg----------cagtagaacagagatggaa 405
                 |||||||| | ||||||||     |||  |          |||| ||||||||||||||
Sbjct: 50234615 tccaaattatttatgtaaaacgtttgaaaggaaaaggacaacagttgaacagagatggaa 50234674


Query: 406      agtacaaattatgaaacaaaagtata 431
                ||| |||||||||| ||| |||||||
Sbjct: 50234675 agtgcaaattatgacacagaagtata 50234700
```

```
  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 409,271
Number of Sequences: 54
Number of extensions: 409271
Number of successful extensions: 13
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 7
Number of HSP's gapped (non-prelim): 3
length of query: 440
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 393
effective length of database: 1,133,627,038
effective search space: 445515425934
effective search space used: 445515425934
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|31071460|dbj|AB091045.1| Lonchura striata gene, repeat
sequence, microsatellite BF02
         (520 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chrZ                                                                  172   5e-041

>chrZ
          Length = 33651169

 Score =  172 bits (108), Expect = 5e-041
 Identities = 112/116 (96%)
 Strand = Plus / Minus


Query: 405      tgttatccagtatccattctgcaatgcaaaggtgagaaactaaatctacaaaaaggctgt 464
                ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct: 11273614 tgttatccagtatccattctgcaatgcaaaggtgagaaactaaatctataaaaaggctgt 11273555


Query: 465      tatggctttattttgttttgcagattaataatgcagcacttgaaaaatggaaaggt 520
                |||||||| |||||||||||| ||||||| ||||||||||||||||||||||||||
Sbjct: 11273554 tatggcttaattttgttttgcggattaattatgcagcacttgaaaaatggaaaggt 11273499
```

```
  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 299,709
Number of Sequences: 54
Number of extensions: 299709
Number of successful extensions: 6
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 5
Number of HSP's gapped (non-prelim): 1
length of query: 520
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 473
effective length of database: 1,133,627,038
effective search space: 536205588974
effective search space used: 536205588974
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|31071463|dbj|AB091048.1| Lonchura striata gene, repeat
sequence, microsatellite BF05
         (469 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr1                                                                  497   e-139

>chr1
          Length = 188239860

 Score =  497 bits (313), Expect = e-139
 Identities = 386/476 (81%), Gaps = 16/476 (3%)
 Strand = Plus / Minus


Query: 1         gatcaactgcttctt--cattccttgaagagctagggaccagctattccacattatggaa 58
                 ||||||||  || ||  | | ||||||||||  ||| | |||||| ||||||||||||||
Sbjct: 160041915 gatcaactctttttttccttcccttgaagagtgaggaaacagctactccacattatggaa 160041856


Query: 59        gatttatttgtctgctttcatgagtattgtgtcacaatggagctttgttatctttaatag 118
                 ||||||||  |||| || | ||||| ||| |||| ||| |||||||||||||||||||||
```

```
Sbjct: 160041855 gatttattcatctgtttacctgagttttgggtcataatagagctttgttatctttaatag 160041796


Query: 119       attcatgtactc-ttccctagtgctttgtcaaataataatacttacaaggcaataaaagg 177
                 |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 160041795 attcatgtactccttccctagtgctttgtcaaataataatacttacaaggcaataaaagg 160041736


Query: 178       gaaaagaatgcacaaaataaagaaccaccccctgtaccataagtcctgggtaggtgaann 237
                  ||| ||  | | ||||  | ||||||||||||||  |||||||       | |||||
Sbjct: 160041735 aaaaggaggggataaaa--aggaaccaccccctgtgtcataagt-------aagtgaacg 160041685


Query: 238       nnnnnnnnnnnnnnnnnnnnnnnnnnna--ggagaggggttgtttattgcaccgtccggt 295
                                            |  |||||| ||| ||||||||||| |||||||
Sbjct: 160041684 cgtgtgtgcattttcgtgtgcgtatgtataggagagaggtagtttattgcactgtccggt 160041625


Query: 296       gcagaattaaataatttatgtaccatctacatgcaaatgtatccttcatttaggtaataa 355
                 ||||||| ||||||||||||||||||||||||||||||  ||| ||||||| ||||||||
Sbjct: 160041624 gcagaatgaaataatttatgtaccatctacatgcaaatacatctttcatttcggtaataa 160041565


Query: 356       actgcacccttgtataatttacccaaacaaaggagctgcgaggacaccgccactaatctt 415
                 |||||| |||||| ||||||| |||||||| | ||||||||||||||||| |||||||||
Sbjct: 160041564 actgcagccttgtgtaatttagccaaacaatgaagctgcgaggacaccgctactaatctt 160041505


Query: 416       c--aaaaaatcaactgtgccttttcaaaagggattttgtctttctgtgaattgatc 469
                 |  |||||||||||||||||||||||||| ||||||||||||||| ||||||||||
Sbjct: 160041504 caaaaaaaatcaactgtgccttttcaaaatggattttgtctttctatgaattgatc 160041449


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 420,300
Number of Sequences: 54
Number of extensions: 420300
Number of successful extensions: 12
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 8
Number of HSP's gapped (non-prelim): 1
length of query: 469
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 422
effective length of database: 1,133,627,038
effective search space: 478390610036
effective search space used: 478390610036
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
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programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|31071464|dbj|AB091049.1| Lonchura striata gene, repeat
sequence, microsatellite BF08
         (210 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr2                                                                  122   3e-026

>chr2
          Length = 147590765

 Score =  122 bits (76), Expect = 3e-026
 Identities = 137/209 (65%), Gaps = 20/209 (9%)
 Strand = Plus / Plus


Query: 1        gatctctaaaaagttatcacgg-tatttattactgctattatgnnnnnnnnactgaccac 59
                |||||||||  | |||| |    ||||||||    || |||||        ||  |  ||
Sbjct: 46648816 gatctctaattaattatgaaatatatttattgtcactgttatggttttat-accaattac 46648874


Query: 60       tgttcatgctgaacttcagaaattcttcagagagaaagaagnnnnnnnnnnnnnnnnnnn 119
                ||||  || || ||||| ||| || |||   |||||
Sbjct: 46648875 tgtttttgttgcacttcggaagtttttctaggagaa------------------gacaca 46648916


Query: 120      nnnntacttatcttacctgctttggttgtcactttcagcaaataaccatccaaatcgatc 179
                     | ||  | ||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct: 46648917 cacacagttgccctacctgctttggtggtcactttcagcaaataaccatccaaatcgatc 46648976


Query: 180      tgaaattgcggtgtctcacaaggtagtga 208
                |||||||| |||||||| || ||||||||
Sbjct: 46648977 tgaaattgtggtgtctcgcagggtagtga 46649005


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 145,126
Number of Sequences: 54
Number of extensions: 145126
Number of successful extensions: 5
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 4
Number of HSP's gapped (non-prelim): 1
length of query: 210
length of database: 1,133,629,576
effective HSP length: 45
effective length of query: 165
effective length of database: 1,133,627,146
effective search space: 187048479090
effective search space used: 187048479090
T: 0
```

```
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|31071467|dbj|AB091052.1| Lonchura striata gene, repeat
sequence, microsatellite BF18
         (413 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr1                                                                  152   7e-035

>chr1
          Length = 188239860

 Score =  152 bits (95), Expect = 7e-035
 Identities = 250/428 (58%), Gaps = 74/428 (17%)
 Strand = Plus / Plus


Query: 1         gatcaatcggtgttatttatgtaatagtaaaagcagggtggaagggaggcagnnnnnnnt 60
                 ||||||||| ||||||||||||||||||||||| | || ||  |||||| ||
Sbjct: 183562545 gatcaatcgctgttatttatgtaatagtaaaaggatgggggggggaggaagagaaaaag 183562604


Query: 61        ag------------------aatgagaaaaaagtgccttgttatttgtcagcc-caccag 101
                 ||                  ||| | ||  |||| | | | ||||| |||||  ||| |
Sbjct: 183562605 agggaaaaaataaaaataaaaataaaaaggaagtccttcggtatttctcagctgcacaaa 183562664


Query: 102       gctccttcggctctgtctgaaccc----cccatactcatgtcctgctgcagggtggtgcg 157
                  || |||  |||||||||||||||    ||  | | |||||||||| |||||||  || |
Sbjct: 183562665 actgcttttgctctgtctgaacccttgccctgtccccatgtcctgcggcagggtactgtg 183562724


Query: 158       tggtgagagtatannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnatgtttac 217
                 | ||| |||| |                                         |||||||
Sbjct: 183562725 ttgtgggagtgtgtg--------------------------------------tgtttac 183562746


Query: 218       atttgcatccgtgctagaatccggggtgagaatggggttgcccattttccagggaaaggt 277
                 ||||| ||| ||||| || || ||| || | | |||||  ||||||||||||||   |||
Sbjct: 183562747 atttggatctgtgctggagtcagggatggggaaggggtctcccattttccaggg--gggt 183562804


Query: 278       gggtttgcctccaacnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnntgtgcaagtt 337
                 |  ||||||| |||                                      ||||| ||
Sbjct: 183562805 gactttgccttcaagacaaattatgagggaatgtgcttggc-----------tgcaactt 183562853


Query: 338       gagtgacaagtctgtttcttaggcattaaaggttaaagcccttcttccagccatgcccta 397
                    |||||| ||||| ||| |||| ||||| || ||||| || ||||  ||||||||||
Sbjct: 183562854 agctgacaattctgtgtctcaggcgttaaatgtgaaagctctgcttctggccatgccctg 183562913


Query: 398       ccaggatt 405
                 | || |||
Sbjct: 183562914 ctagtatt 183562921


  Database: WholeChickenGenome.txt
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    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 226,117
Number of Sequences: 54
Number of extensions: 226117
Number of successful extensions: 6
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 4
Number of HSP's gapped (non-prelim): 2
length of query: 413
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 366
effective length of database: 1,133,627,038
effective search space: 414907495908
effective search space used: 414907495908
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|2352499|gb|AF005375.1| Manorina melanophrys microsatellite
sequence BMC-2
          (285 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr6                                                                   92   6e-017

>chr6
          Length = 33893787

 Score = 91.9 bits (57), Expect = 6e-017
 Identities = 109/153 (71%), Gaps = 9/153 (5%)
 Strand = Plus / Minus


Query: 1        tcctgaattaacaaaaagtccaagccgctctct-gagagccttggaaatgccaagggacc 59
                 ||||||| | |||| ||| ||| || || || | |||||| |  |||| ||| ||||| |
Sbjct: 10766139 tcctgaactgacaacaagcccatgctgccctgttgagagc-tcagaaacgccgagggagc 10766081


Query: 60       aacaactcactgcactgccttgcaattaaaaattcccactaaagagcagtgatatcacag 119
                 || || ||||  || ||||||||||||||||  |||||   ||||||||   ||   |||
Sbjct: 10766080 aaaaattcaccacagtgccttgcaattaaaagctcccagcgaagagcagcattactgcag 10766021
```

```
Query: 120      gataaaatggataaaatggatgcacgcacgcac 152
                ||       || | |  || ||||| |||||||
Sbjct: 10766020 ga------agacacagcgg-tgcacacacgcac 10765995


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 204,195
Number of Sequences: 54
Number of extensions: 204195
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 1
length of query: 285
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 239
effective length of database: 1,133,627,092
effective search space: 270936874988
effective search space used: 270936874988
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|2352500|gb|AF005376.1| Manorina melanophrys microsatellite
sequence BMC-3
          (183 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr15                                                                  90   1e-016

>chr15
          Length = 12438626

 Score = 90.3 bits (56), Expect = 1e-016
 Identities = 79/98 (80%), Gaps = 4/98 (4%)
 Strand = Plus / Plus


Query: 86      cttcaagggcacccagaagctgcaattcagctcagctggggcaggag---agggcaaagc 142
               ||||||||||||  |||||||  |||||||  ||||||| |||||||   ||||||||||
Sbjct: 8572464 cttcaagggcactgagaagctctaattcagaccagctggtgcaggagacaagggcaaagc 8572523
```

```
Query: 143     aggaga-ggacttacctgtgaacacagctctgtccagc 179
               |||||| || | ||||| | || |||||||| | | ||
Sbjct: 8572524 aggagaggggcctacctataaaaacagctctctgctgc 8572561


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 131,835
Number of Sequences: 54
Number of extensions: 131835
Number of successful extensions: 2
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 1
Number of HSP's gapped (non-prelim): 1
length of query: 183
length of database: 1,133,629,576
effective HSP length: 45
effective length of query: 138
effective length of database: 1,133,627,146
effective search space: 156440546148
effective search space used: 156440546148
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 33 (53.9 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|2352501|gb|AF005377.1| Manorina melanophrys microsatellite
sequence BMC-4
         (287 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr1                                                                  191   5e-047

>chr1
          Length = 188239860

 Score =  191 bits (120), Expect = 5e-047
 Identities = 206/291 (70%), Gaps = 45/291 (15%)
 Strand = Plus / Minus


Query: 4         gcctgataggagactgagagactgtccccacagctttcccaaaggacaaatcttgaatag 63
                 || |||||||||| ||||||||| |||| ||||| |||||||||||  || ||||| |||
Sbjct: 157589931 gcttgataggagattgagagactatccctacagccttcccaaaggatgaaacttgagtag 157589872
```

```
Query: 64        ataatgnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnntgcatgca 123
                 | |||                                                |||||||
Sbjct: 157589871 aaaatagacacacacac------------------------------------gcatgca 157589848


Query: 124       aattctctctccaactcaccttctgccaactgctctgcctctgagcacagggtctgtagc 183
                 ||| ||||| |||||||||||| | |||||||  || ||| |||||||||  |||| |||
Sbjct: 157589847 aatgctctc-ccaactcacctttt-ccaactgtgctacctatgagcacagactctgcagc 157589790


Query: 184       taacccttcagaaactcccatgttagctgctctgtttgctgggct--gctgtttcattca 241
                 || ||||||| |||||||| |||||||||||||||||||  ||||  |||||||||||||
Sbjct: 157589789 tagcccttcaaaaactcccttgttagctgctctgtttgccaggctcagctgtttcattca 157589730


Query: 242       gctttt--attccgagtaaagttatttcaa---ctaaacagaaggaatcat 287
                 | ||||  |||| |||||||||||||||||   |||| |||||||||| ||
Sbjct: 157589729 gttttttgattctgagtaaagttatttcaatggctaagcagaaggaatgat 157589679


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 232,506
Number of Sequences: 54
Number of extensions: 232506
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 1
Number of HSP's gapped (non-prelim): 2
length of query: 287
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 241
effective length of database: 1,133,627,092
effective search space: 273204129172
effective search space used: 273204129172
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|28881866|dbj|AB089172.1| Cettia diphone DNA, microsatellite
locus Cdi31
         (631 letters)

Database: WholeChickenGenome.txt
          54 sequences; 1,133,629,576 total letters
```

```
                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr7                                                                  530   e-148

>chr7
          Length = 37338262

 Score =  530 bits (334), Expect = e-148
 Identities = 484/633 (76%), Gaps = 33/633 (5%)
 Strand = Plus / Plus


Query: 8        aggaaatgagaccctgccccatattcacctgaggac------tcctcttttccccttgcc 61
                |||||   ||| || ||||  ||| || ||||| ||      ||||||| ||||  ||||
Sbjct: 28498059 aggaagcaagatcccgccctgtatccatctgagaaccccttttcctcttctccctgtgcc 28498118


Query: 62       ctccctatggtcacttctgataaaagact-aggtccacatgaagcagcagatacaataga 120
                 |||||  |||  | ||||  || ||  | | ||||||||| | | | || |    | |
Sbjct: 28498119 ttccctgaggttgcctctggcaatagctttaagtccacatgtaactgtagctgtggtggg 28498178


Query: 121      ga--acttctgcatttgttcctctcactaggcactcttggacagtactgaagtcatgttt 178
                 |  ||| |||    ||||| ||| || || ||||||||||||| |  ||||| ||||||
Sbjct: 28498179 aatgactgctgtggctgttcttcttaccag-cactcttggacagcaaagaagtgatgttt 28498237


Query: 179      tatttcagcagnnnnnnnnnnnnnnnnnnnnnnngccttcccttgtactgtttctctccc 238
                   |   ||||                                ||| | | |||||||||
Sbjct: 28498238 acat---gcagtgggctccagcac-------------------tgtgcagcttctctccc 28498275


Query: 239      tggagacccagctcactcattcagcacgctctcaggatttcagtaacttttcttgcaagg 298
                 |  | ||| |||| ||||||| ||||||||||||| |||||| ||||| ||||||| ||
Sbjct: 28498276 agcgg-cccggctctctcattctgcacgctctcagggtttcaggaacttctcttgcaggg 28498334


Query: 299      tctctggggaccatgcgcctctgtgctgtttctccaggcttttggttttatctcactctt 358
                ||||| | |||| ||||||||||||||| ||||||||||||| || ||| |||||  ||
Sbjct: 28498335 tctcttgagaccgtgcgcctctgtgctgcttctccaggctttgggctttctctcagcctg 28498394


Query: 359      tgaaactttcccagaactgcagtgacttttctttgacctccaggaactacagctcttgag 418
                ||||||||||||||||||||||||||||||   |||||||| |||||    ||||| |||
Sbjct: 28498395 tgaaactttcccagaactgcagtgactttttgctgacctccgggaaccggcgctctcgag 28498454


Query: 419      ccctgacacgccgactggcacaacgaagacctggagactgctttgggatgtcagctttcc 478
                ||||||| | ||| |||||||||| |||||||||||||| ||||||||||||||||||||
Sbjct: 28498455 ccctgacgctccggctggcacaaccaagacctggagactactttgggatgtcagctttcc 28498514


Query: 479      cagcacatgttggatggaagctgcatctgagcaacaccagctaaaataaaagctattca 538
                ||||||||| |||||| ||||  |||||||||||||||||||||||||||||||||||||
Sbjct: 28498515 cagcacatgctggatgaaagcctcatctgagcaacaccagctaaaataaaagctattca 28498574


Query: 539      actgaagctaatggcaggttgccacaagttattgctcattaaagtgaattgacagatgct 598
                || | |||||||||| |  |||||  |||||||||||||||||| |||||| ||||||||
Sbjct: 28498575 accggagctaatggcggcctgccatgagttattgctcattaaagggaattgtcagatgct 28498634


Query: 599      taacttcagctaatcattccctgctgcgagatc 631
                |||||||||||||||||| ||||||||||||||
Sbjct: 28498635 taacttcagctaatcatttcctgctgcgagatc 28498667


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549
```

```
Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 585,587
Number of Sequences: 54
Number of extensions: 585587
Number of successful extensions: 4
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 2
length of query: 631
length of database: 1,133,629,576
effective HSP length: 48
effective length of query: 583
effective length of database: 1,133,626,984
effective search space: 660904531672
effective search space used: 660904531672
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|28881869|dbj|AB089175.1| Cettia diphone DNA, microsatellite
locus Cdi38
         (290 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr19                                                                 163   2e-038

>chr19
          Length = 9463882

 Score =  163 bits (102), Expect = 2e-038
 Identities = 205/309 (66%), Gaps = 35/309 (11%)
 Strand = Plus / Minus


Query: 1       gatctcagccagacctttcacctgctgctttttgtagccaaaatgcccctacaaatctct 60
               ||||  |  |||||||||||||| ||||||   |||| |||| ||||||||  ||  |||
Sbjct: 7744209 gatccaaagcagacctttcacctactgcttg--gtaggcaaa-tgcccctattaaaatct 7744153


Query: 61      cctcgttctggacatcttcggcacggctcgctccannnnnnnnnnnnnnnnnnnnnnnnn 120
                 || || |||||| |||| ||| || ||  | ||
Sbjct: 7744152 tttcattttggacagcttcagcatggttcatttcactctctctctctccaag-------- 7744101


Query: 121     agaatttgtgtctctacataaaaataaacttccaccacttccagctcctcagc-accagc 179
                   ||||| ||||| | || ||| ||| |||||  | ||||| ||    ||  | ||||
Sbjct: 7744100 ----tttgtatctctgcgtataaacaaaattccaatatttccaacttaagagtgatcagc 7744045


Query: 180     atttcaacagcacca-------------gagcaatccacatttccagaaaagtgtcaatg 226
               |||| ||||||| ||             || ||||| | | ||||| |||||  ||||||
```

```
Sbjct: 7744044 atttaaacagcatcatacatctttcaaagaccaatcaatacttcca-aaaagcatcaatg 7743986


Query: 227     catgcaaatatca--catacagaa---catcgagagtgctgggagatggtaccaaggata 281
               |||||||||||||  |||||| ||   || | |||||||||||||||| |||||||||||
Sbjct: 7743985 catgcaaatatcaaacatacaaaaaaccaacaagagtgctgggagatgataccaaggata 7743926


Query: 282     gaggtgatc 290
                ||||| ||
Sbjct: 7743925 aaggtggtc 7743917


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 248,277
Number of Sequences: 54
Number of extensions: 248277
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 0
Number of HSP's successfully gapped in prelim test: 1
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 1
length of query: 290
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 244
effective length of database: 1,133,627,092
effective search space: 276605010448
effective search space used: 276605010448
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|28881871|dbj|AB089177.1| Cettia diphone DNA, microsatellite
locus Cdi41
         (253 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr1                                                                   89   4e-016

>chr1
          Length = 188239860

 Score = 88.8 bits (55), Expect = 4e-016
```

```
 Identities = 93/152 (61%), Gaps = 7/152 (4%)
 Strand = Plus / Minus


Query: 4        cttgcccttttgggaattgtttatgtaagcatgaagttccttcagatttccaggtc--at 61
                ||| | ||||||||||   ||| |||||| | || ||||||||| ||||||| ||   ||
Sbjct: 22543694 ctttctcttttgggaaccttttgtgtaagtacgaggttccttcatatttccaagtgctat 22543635


Query: 62       ag----gctggcaggaaagtaggaattcttctgcatgaaacatttaaaattagctgaaan 117
                ||    ||||||||||||||  |||||| ||||| | || || |||| ||    |||||
Sbjct: 22543634 agaagagctggcaggaaagtgagaattcctctgcgtaaagca-ttaagatcttttgaaac 22543576


Query: 118      nnnnnnnnnnnnnnnnnnnnnnnnnnctcaag 149
                                           | |||
Sbjct: 22543575 ttctttttgctccccatgagaattaaattaag 22543544


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 183,125
Number of Sequences: 54
Number of extensions: 183125
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 0
Number of HSP's successfully gapped in prelim test: 1
Number of HSP's that attempted gapping in prelim test: 3
Number of HSP's gapped (non-prelim): 1
length of query: 253
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 207
effective length of database: 1,133,627,092
effective search space: 234660808044
effective search space used: 234660808044
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|44894265|gb|AY539735.1| Calocitta formosa clone CfAAAG64
microsatellite sequence
         (390 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value
```

```
chr12                                                                226   2e-057

>chr12
          Length = 19821895

 Score =  226 bits (142), Expect = 2e-057
 Identities = 203/258 (78%), Gaps = 13/258 (5%)
 Strand = Plus / Minus


Query: 143      agaggaggattttgtaagtttgtctggcacttccagatgttgagcagccccgcctgacca 202
                ||||||||||| ||||| |||||| |||||||||||||||  || ||||| | |||||||
Sbjct: 16673152 agaggaggattctgtaaatttgtccggcacttccagatgtcaaggagccctgtctgacca 16673093


Query: 203      catatggatcaactctgccatgcacctgtaaggagagcagtgcccctgggactgccaggc 262
                ||  ||||||| |||| |||  ||||||||| |||  ||||||| ||||||||||||| |
Sbjct: 16673092 cacgtggatcagctctaccacacacctgtaatgagtacagtgcctctgggactgccagtc 16673033


Query: 263      c-gtgatggatgcacgaggaaacggatcctgatggatttatggatcacatgcaaatcatc 321
                | |||||| | | | ||| ||| |||| ||||||||||||| || ||| |||||     |
Sbjct: 16673032 cggtgatgtacgtatgagtaaatggatactgatggatttattgagcacgtgcaa---tgc 16672976


Query: 322      tctgcagcacactgtatatc---------acatttacatgagtatcagttctgggctgtg 372
                ||| |||||| |||||||||         |||||||||  || ||||||||||   |  |
Sbjct: 16672975 tctacagcacgctgtatatcacaagtctaacatttacagaagcatcagttctgctatacg 16672916


Query: 373      ttcactcctgaaatgaac 390
                |||||| |||||||||||
Sbjct: 16672915 ttcactactgaaatgaac 16672898


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 292,126
Number of Sequences: 54
Number of extensions: 292126
Number of successful extensions: 4
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 1
Number of HSP's gapped (non-prelim): 1
length of query: 390
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 343
effective length of database: 1,133,627,038
effective search space: 388834074034
effective search space used: 388834074034
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
```

```
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|2570887|gb|AF026332.1|AF026332 Corvus kubaryi GT
dinucleotide repeat Ck.1B5D
         (261 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr2                                                                  218   4e-055

>chr2
          Length = 147590765

 Score =  218 bits (137), Expect = 4e-055
 Identities = 199/266 (74%), Gaps = 33/266 (12%)
 Strand = Plus / Plus


Query: 1        gatcatgctgacctagatgctatcagaggttagcaaaaatgactggtcagacctgtcagg 60
                |||||   ||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct: 91296347 gatcactatgacctagatgctatcagaggttagcaaaaatgacaggtcagacctgtcagg 91296406


Query: 61       actaaacagctgcatcaagcaatnnnnnnnagc-----tctaggggaaggagggcgcccg 115
                |  ||||||||||||||||||||        ||     ||| |||| |||||||| ||||
Sbjct: 91296407 atgaaacagctgcatcaagcaatggggtggggcaggtgtct-gggggaggagggcacccg 91296465


Query: 116      agttgcgaatagagagacagaggagcaggaggaaaagatggaaactgcgtgtcctgaata 175
                ||||||  | | |||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct: 91296466 agttgc--aaacagagacagagaagcaggaggaaaagatggaaactgcgtgtcctgaata 91296523


Query: 176      cgcatgaannnnnnnnnnnnnnnnnnnnnnnnnnnnnnntctctgcagctgaagctctgg 235
                 | || ||                               | | |||||||| ||||| ||
Sbjct: 91296524 tgtataaa-------------------------tgcgtgtgtgtgcagctgcagctcagg 91296558


Query: 236      tcttgtcatttgcatatacacagatc 261
                |||| ||||||||||| |||||||||
Sbjct: 91296559 tcttatcatttgcatacacacagatc 91296584


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 167,907
Number of Sequences: 54
Number of extensions: 167907
Number of successful extensions: 5
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 2
length of query: 261
```

```
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 215
effective length of database: 1,133,627,092
effective search space: 243729824780
effective search space used: 243729824780
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|2570888|gb|AF026333.1|AF026333 Corvus kubaryi GT
dinucleotide repeat Ck.1B6G
         (247 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr4                                                                  153   1e-035

>chr4
          Length = 90634903

 Score =  153 bits (96), Expect = 1e-035
 Identities = 121/146 (82%)
 Strand = Plus / Plus


Query: 102      tgggaactcttcaattcctcccttaattagcaggtgaactggtagtactagattactgat 161
                ||| |  ||| || ||||    || ||||  |||||||||||||||| ||||||| | ||
Sbjct: 20481148 tggtagatctccagttcccagttttattaataggtgaactggtagtaatagattagtaat 20481207


Query: 162      atttgataccatgccatattcaggtttttgttttaacccatgcaggtatttaaccaggag 221
                |||||||   |||||||| ||| | |||||||||||||| |  |||||||||||||||||
Sbjct: 20481208 atttgatgtgatgccatagtcaagcttttgttttaacccctataggtatttaaccaggag 20481267


Query: 222      ggagaattcatgctgaagtttggatc 247
                ||||||||||| ||||||||||||||
Sbjct: 20481268 ggagaattcatactgaagtttggatc 20481293


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 200,070
Number of Sequences: 54
Number of extensions: 200070
Number of successful extensions: 4
```

```
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 2
length of query: 247
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 201
effective length of database: 1,133,627,092
effective search space: 227859045492
effective search space used: 227859045492
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|2570890|gb|AF026335.1|AF026335 Corvus kubaryi GT
dinucleotide repeat Ck.4A3G
         (255 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr1                                                                   71   8e-011

>chr1
          Length = 188239860

 Score = 71.3 bits (44), Expect = 8e-011
 Identities = 85/118 (72%), Gaps = 7/118 (5%)
 Strand = Plus / Plus


Query: 22       agggaatggcttgggattaaggggg-gattgtggctttctgagggccagctctgtgtgcg 80
                || |||  || ||||   ||||||| ||  || | | ||  |||||||||||      ||
Sbjct: 20862538 agtgaagtgcctgggtgcaagggggtga--gtagatgtcccagggccagctccaa---cg 20862592


Query: 81       agagagcatctgtggctctctaagagtgagagaacagagatgtcatctatggaaccag 138
                 |||||||||||||  |||| | ||||||||| ||| ||  ||   ||||||||||||
Sbjct: 20862593 tgagagcatctgtgtatctccaggagtgagagcaca-aggggttggctatggaaccag 20862649


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 170,313
Number of Sequences: 54
Number of extensions: 170313
```

```
Number of successful extensions: 2
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 0
Number of HSP's successfully gapped in prelim test: 1
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 1
length of query: 255
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 209
effective length of database: 1,133,627,092
effective search space: 236928062228
effective search space used: 236928062228
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|2570895|gb|AF026340.1|AF026340 Corvus kubaryi GT
dinucleotide repeat Ck.4B6D
         (321 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr1                                                                  133   2e-029

>chr1
          Length = 188239860

 Score =  133 bits (83), Expect = 2e-029
 Identities = 173/291 (59%), Gaps = 28/291 (9%)
 Strand = Plus / Plus


Query: 6        tttgcatccctgatttatggcattattttctctcatctgaatctttccgatatatccatt 65
                |||| ||  ||| |||||||||||||||||||  |||||| ||||    ||  || ||||
Sbjct: 49370872 tttgtatatctgttttatggcattattttctcctatctgagtctt---catgcattcatt 49370928


Query: 66       atgcgnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnncacatgcatgt 125
                |  |                                             ||| | ||
Sbjct: 49370929 a--cacatgtataagcacagatgcacatgtgtgggaagagttgttaatacaccttca--- 49370983


Query: 126      ytcacccacctgactctggattgcttcctagttggata-actgaagcatccagaatggaa 184
                              |||| ||| ||||  |||||  || |||| | |||||||||||| |
Sbjct: 49370984 --------------tctgaatttcttcaaagttgagtatactgta-catccagaatggca 49371028


Query: 185      ttccaggt-agagaattctgttctgat--agactgctcagcagaatgcacagatttttct 241
                || ||||| ||| ||||||||||  ||  || |||||   ||  ||   || ||||||||
Sbjct: 49371029 tttcaggtgaga-aattctgttcgaatggagtctgcttgacatgatttccaaatttttct 49371087


Query: 242      agttcctatgtagatgtgtttcagagtgctgagggaacagcacaaaaactt 292
                 ||||| || ||||||||||||||||| |||||  ||   || |||| |||
Sbjct: 49371088 ggttcccatatagatgtgtttcagagtactgagacaattccataaaatctt 49371138


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
```

```
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.334    0.551

Gapped
Lambda     K      H
    1.10    0.334    0.551


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 230,115
Number of Sequences: 54
Number of extensions: 230115
Number of successful extensions: 4
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 1
Number of HSP's gapped (non-prelim): 2
length of query: 321
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 275
effective length of database: 1,133,627,092
effective search space: 311747450300
effective search space used: 311747450300
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.6 bits)
S1: 14 (23.8 bits)
S2: 34 (55.6 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|2570891|gb|AF026336.1|AF026336 Corvus kubaryi GT
dinucleotide repeat Ck.5A4B
         (258 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr2                                                                   97   2e-018

>chr2
          Length = 147590765

 Score = 96.7 bits (60), Expect = 2e-018
 Identities = 143/243 (58%), Gaps = 21/243 (8%)
 Strand = Plus / Minus


Query: 17       gccttttttggtcagccttgctcctttagaagtgattttaaacacaatgtgataaagctt 76
                |||| || | ||||||||  || | | |||||||| |  |||  |||    | |||||||
Sbjct: 47550206 gcctcttcttgtcagcctcccttcctcagaagtgact--aaatccaacaaaacaaagctt 47550149


Query: 77       cccctttttattcaagatgctgagtgcaatttgcacaaaaaacaacaagataataacatt 136
                |   || ||  ||||||  |||  ||  ||    |  || |||| ||||| | |||||||
Sbjct: 47550148 cttgttctttctcaagacactgcatgagatgcaaaggaagaacagcaagacagtaacatt 47550089


Query: 137      tactcaattagaaaattgtgtctcnnnnnnnnnnnnnnnnnnnnnnnnnnnnnttacagc 196
```

```
                | ||||| |||||||||||||                               |||| |
Sbjct: 47550088 ttctcaaatagaaaattgtgt---gtgcgtgtatttacagcacagtttcttaactaca-c 47550033


Query: 197      agactgtttcttaagtacgttagtggttgcttccagca-aaccaaccctcccaaaacaag 255
                |         ||||     ||||||| ||| ||||||| || |||||| ||  |||   |
Sbjct: 47550032 a---------ttaa-----ttagtggctgcctccagcagaagcaacccgcctgaaatgtg 47549987


Query: 256      atc 258
                |||
Sbjct: 47549986 atc 47549984


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 243,692
Number of Sequences: 54
Number of extensions: 243692
Number of successful extensions: 2
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 1
Number of HSP's gapped (non-prelim): 1
length of query: 258
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 212
effective length of database: 1,133,627,092
effective search space: 240328943504
effective search space used: 240328943504
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|2570893|gb|AF026338.1|AF026338 Corvus kubaryi GT
dinucleotide repeat Ck.5A5F
         (323 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr2                                                                   98   8e-019

>chr2
          Length = 147590765
```

```
 Score = 98.3 bits (61), Expect = 8e-019
 Identities = 154/238 (64%), Gaps = 39/238 (16%)
 Strand = Plus / Plus


Query: 93       aacataaccgatagacttaatagatggatatgtggttataccagaggtcctagagaccaa 152
                ||| |||    |||||||||  ||  | | ||||||||| |||| |||  ||| ||| ||
Sbjct: 11781206 aacttaaaaagtagacttaag-gactgctgtgtggttattccagtggttttagggacaaa 11781264


Query: 153      ataaatccatatatannnnnnnnnnnnnnnnnnnnnnnnnnnnnntaaacactcttccctt 212
                |||||||| | ||||                             ||||| ||||||||||
Sbjct: 11781265 ataaatccttgtatatcagt------------------------taaac-ctcttccctt 11781299


Query: 213      cccccgt--gaagaaaaaagtaaataaaa-----agtattaaacaggtgtcttgagagaa 265
                 | || |  ||| |||| | ||||| |||     |  |||||||| || |||||||||||
Sbjct: 11781300 tctccatctgaataaaatattaaatgaaatcaaaaacattaaacaagtatcttgagagaa 11781359


Query: 266      caaaaagatatctgataatgttcctttttgtctctttaaacctgatagatagcagatc 323
                 ||||  |||||||  |||      |||  | ||||||||||| ||| | ||||||||
Sbjct: 11781360 taaaa--atatctggaaat----actttcatttctttaaacctaatacacagcagatc 11781411


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 268,371
Number of Sequences: 54
Number of extensions: 268371
Number of successful extensions: 8
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 0
Number of HSP's successfully gapped in prelim test: 1
Number of HSP's that attempted gapping in prelim test: 8
Number of HSP's gapped (non-prelim): 1
length of query: 323
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 277
effective length of database: 1,133,627,092
effective search space: 314014704484
effective search space used: 314014704484
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|2570894|gb|AF026339.1|AF026339 Corvus kubaryi GT
dinucleotide repeat Ck.5A5G
          (254 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters
```

```
                                                                  Score    E
Sequences producing significant alignments:                       (bits) Value

chr2                                                                   100   2e-019

>chr2
          Length = 147590765

 Score = 99.9 bits (62), Expect = 2e-019
 Identities = 154/237 (64%), Gaps = 44/237 (18%)
 Strand = Plus / Minus


Query: 21       ttgtgttcagactgccttctgcacttagagaaagtttgagttctgcatgcattttcag-a 79
                |||| ||   ||||||||||| ||||  |||||| |  |||||||||| ||||||||| |
Sbjct: 92405864 ttgtatttcaactgccttctggacttccagaaagctccagttctgcattcattttcagca 92405805


Query: 80       ttc-agttttcannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnatacaaggtaa 138
                ||| | ||||||                                      ||||||||||
Sbjct: 92405804 ttctacttttcatgc-----------------------------------tacaaggtaa 92405780


Query: 139      tcagtgatggctc--tattttaagtgtgtgcaacaaattttctgctctccttcccattcc 196
                |||| |||| |||  |||||||||| |||| || |||||   || ||||  |  |||||
Sbjct: 92405779 tcagcgatgactcagtattttaagtttgtgaaagaaattgagtgttctc--tgtcattct 92405722


Query: 197      agctcactgaggatagaagca---ttagacccagactgtcagtttgaagctcaggct 250
                ||||   |||||| || ||||   | | | ||| ||||| || ||||||||||| ||
Sbjct: 92405721 agcttgatgaggacagcagcagagtcacatccaaactgttaggttgaagctcagact 92405665


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 209,465
Number of Sequences: 54
Number of extensions: 209465
Number of successful extensions: 6
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 4
Number of HSP's gapped (non-prelim): 2
length of query: 254
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 208
effective length of database: 1,133,627,092
effective search space: 235794435136
effective search space used: 235794435136
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]
```

```
Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|44894272|gb|AY539742.1| Psilorhinus morio clone CmAAAG25
microsatellite sequence
         (422 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr2                                                                  117   2e-024

>chr2
          Length = 147590765

 Score =  117 bits (73), Expect = 2e-024
 Identities = 108/139 (77%), Gaps = 6/139 (4%)
 Strand = Plus / Minus


Query: 284      tttgacttatttcaaagattttgtcttagtaatgacagaattacaagttaaccattattt 343
                ||||   | ||||||||| ||||  ||| ||||||||||||||||||||| | |||| ||
Sbjct: 11747216 tttgttatttttcaaagaatttggtttattaatgacagaattacaagttagctattactt 11747157


Query: 344      cagggtctagggagcaatgacacattattgacactgtgcttgttctcacagaaataagca 403
                |  |||||||| || ||||| |||||||| ||   |||   ||||||| || ||||| |
Sbjct: 11747156 ccaggtctaggcagtaatgatacattattaac---gtg---gttctcagaggaataacct 11747103


Query: 404      acaatgagtcaataattag 422
                 || ||| ||| |||||||
Sbjct: 11747102 gcattgaatcagtaattag 11747084


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 283,469
Number of Sequences: 54
Number of extensions: 283469
Number of successful extensions: 5
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 4
Number of HSP's gapped (non-prelim): 1
length of query: 422
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 375
effective length of database: 1,133,627,038
effective search space: 425110139250
effective search space used: 425110139250
T: 0
A: 0
X1: 7 (11.1 bits)
```

```
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|44894275|gb|AY539745.1| Psilorhinus morio clone CmAAAG35
microsatellite sequence
         (308 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr3                                                                   76   4e-012

>chr3
          Length = 108638738

 Score = 76.1 bits (47), Expect = 4e-012
 Identities = 83/137 (60%), Gaps = 6/137 (4%)
 Strand = Plus / Plus


Query: 171      tgttttgaaagcaatgtgtta-gcattgtgttattgaaacagtgaaacatgttaaagtat 229
                |||||||| || ||||| |   |  || |||||||||||||||||| |||| ||| ||||
Sbjct: 39524426 tgttttgacagtaatgtatagtgttttctgttattgaaacagtgaagcatgctaatgtat 39524485


Query: 230      ctacctaatttaannnnnnnnnnnnnnnnnnnnnnnnnnaagaacactactaagtataca 289
                 |||||||| |||                           | ||| ||   ||  || ||
Sbjct: 39524486 ttacctaatgtaaaaacaaaaaacaagccacaaac-----aaaaccctcaaaaacatgca 39524540


Query: 290      gatctaaattatgggaa 306
                 ||| || || ||| ||
Sbjct: 39524541 aatcaaatttgtggaaa 39524557


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 226,764
Number of Sequences: 54
Number of extensions: 226764
Number of successful extensions: 1
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 308
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 262
```

```
effective length of database: 1,133,627,092
effective search space: 297010298104
effective search space used: 297010298104
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|32483447|gb|AY330729.1| Corcorax melanorhamphos
microsatellite CmeH2 sequence
         (150 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr1                                                                  114   5e-024

>chr1
          Length = 188239860

 Score =  114 bits (71), Expect = 5e-024
 Identities = 91/152 (59%), Gaps = 8/152 (5%)
 Strand = Plus / Minus


Query: 1        aagctttgggtcatatgtgtatgtnggcctgcatcannnnnnnnnnnnnnnnnnnnnnnn 60
                |||||||||||||| |||||||||  | ||||||||
Sbjct: 60031241 aagctttgggtcatttgtgtatgtgtgtctgcatcactctctccctctctctctctctct 60031182


Query: 61       nnnnnnnnnnnnnnnnnnnnnnnnnngagtcataagccggggctgcaataca--cacaca 118
                                          ||||||||||| ||||||||||| ||  ||||||
Sbjct: 60031181 ctccctctctctctctctct------gagtcataagctggggctgcaatccatacacaca 60031128


Query: 119      tctctgcactgcaactttcactcaagctgcag 150
                || |||||||||||||||| ||| ||||||||
Sbjct: 60031127 tccctgcactgcaactttcgctcgagctgcag 60031096


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 65,525
Number of Sequences: 54
Number of extensions: 65525
Number of successful extensions: 4
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
```

```
Number of HSP's that attempted gapping in prelim test: 1
Number of HSP's gapped (non-prelim): 1
length of query: 150
length of database: 1,133,629,576
effective HSP length: 44
effective length of query: 106
effective length of database: 1,133,627,200
effective search space: 120164483200
effective search space used: 120164483200
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 33 (53.9 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|10505193|gb|AF286731.1|AF286731 Cyphorhinus phaeocephalus
clone AAT54 microsatellite sequence
         (235 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr8                                                                  137   7e-031

>chr8
          Length = 30024636

 Score =  137 bits (86), Expect = 7e-031
 Identities = 118/148 (79%), Gaps = 1/148 (0%)
 Strand = Plus / Minus


Query: 3       tctcactttttaaataaaga-gagtattaacttgctaacagctgcttcacagtgaagtga 61
               |||||| || ||| |||| | ||  ||||| |   |||||||||||||||||  || |||
Sbjct: 6376092 tctcacgttgtaagtaaaaaagaacattaaatcagtaacagctgcttcacagcaaattga 6376033


Query: 62      tgtgcaggtagcattttggaagcagtgatgattctgtgcagttaattgcattcccctgag 121
               | ||| | |||| |||||||| |||| |||||| ||||||||| |||||| ||  |||||
Sbjct: 6376032 tctgctgatagcgttttggaaacagtaatgattatgtgcagttgattgcagtctactgag 6375973


Query: 122     gatgaagttgggcagttccagcattagt 149
                ||||||| | | | |||||||||||||
Sbjct: 6375972 aatgaagtagtgtatttccagcattagt 6375945


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 182,415
```

```
Number of Sequences: 54
Number of extensions: 182415
Number of successful extensions: 2
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 2
length of query: 235
length of database: 1,133,629,576
effective HSP length: 45
effective length of query: 190
effective length of database: 1,133,627,146
effective search space: 215389157740
effective search space used: 215389157740
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|4836462|gb|AF122890.1|AF122890 Catharus ustulatus
microsatellite Cu02 sequence
          (413 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr24                                                                 164   1e-038

>chr24
          Length = 5910111

 Score =  164 bits (103), Expect = 1e-038
 Identities = 269/427 (62%), Gaps = 50/427 (11%)
 Strand = Plus / Minus


Query: 1       ctgccagataatttccgtgcgaaccacctgttcccaggcactcgcgcgttcc--acccag 58
               |||||| |||||||| ||| |||||||||||| ||||||||||| |  || |  |  | |
Sbjct: 4938287 ctgccaaataatttcagtgagaaccacctgtttccaggcactcgtggatttctgaagctg 4938228


Query: 59      ccacccttttgggcagcgtcttccagccttggattgcttccaaatgcaaacgtgg-tgc- 116
                |||||||||||| ||| ||||||||||||||| ||||||      ||| ||||| ||| 
Sbjct: 4938227 tcacccttttgggaagcatcttccagccttggagtgcttc------caagcgtggatgca 4938174


Query: 117     ctgtgcctgcatannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnctggagcaaaatccctc 176
                ||||  ||||||                              | |||||||||||||||
Sbjct: 4938173 gtgtgtgtgcata----tgcatgcgtgtgtgcgtgtttgtgtgccggagcaaaatccctc 4938118


Query: 177     caggcgttgcaacggaatgagaggattcatatgaaag----agt--ctg------cagga 224
               ||||| ||  || ||||| | | ||||||  ||||||    |||   ||      |||||
Sbjct: 4938117 caggcattttaatggaattaaaagattcacgtgaaaggctaagttgatgcatacacagga 4938058


Query: 225     aatt-gggagcgt-----gtttgccccagggagg-tgcgtgcatccttcccaaatgcttg 277
               |||| ||||||||     || |    | |||||| | ||||  |||    || | ||   
Sbjct: 4938057 aattggggagcgtggcgggtgtttatctgggaggatacgtg--tccgcttcagaggcaca 4938000
```

```
Query: 278     catgcagcagggagatggtgatccatctcctcacctttcctttcaccttcccgatgctga 337
                ||||||||   | | ||||  ||  |  |  | |||   |  || ||||      |||
Sbjct: 4937999 catgcagcccagtg-tggt-ctcactgccagcccct---cgctctcctt-----ggcttt 4937950


Query: 338     caaggaagtttctgtgtccccttgtgcttcagttttggttctgagccgcgctgtgctgcc 397
                |     |  |||| |||     ||||||| | |||||| | ||||| | ||||  ||||
Sbjct: 4937949 c-----accttctttgttgtgctgtgcttgaattttggctgtgagctgggctgcactgcg 4937895


Query: 398     aagtcac 404
                 ||||||
Sbjct: 4937894 cagtcac 4937888


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 292,064
Number of Sequences: 54
Number of extensions: 292064
Number of successful extensions: 6
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 3
Number of HSP's gapped (non-prelim): 1
length of query: 413
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 366
effective length of database: 1,133,627,038
effective search space: 414907495908
effective search space used: 414907495908
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|4836463|gb|AF122891.1|AF122891 Catharus ustulatus
microsatellite Cu04 sequence
         (291 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr5                                                                  240   8e-062

>chr5
          Length = 56310377
```

```
 Score =  240 bits (151), Expect = 8e-062
 Identities = 212/291 (72%), Gaps = 20/291 (6%)
 Strand = Plus / Minus


Query: 1        ctaaatattactactagcatggcaaatgaagagattttctacaggcaagaacaaagcaaa 60
                ||||||||||||||| | ||||||||||| ||||||||||||  ||||| ||||||||||
Sbjct: 27829473 ctaaatattactacttgaatggcaaatgaggagattttctacgtgcaagcacaaagcaaa 27829414


Query: 61       atcctattctaagcatttcagaatataagaagtatctgcatccaaatcagaattgcataa 120
                ||||  |||||||||||||| ||| || |  |||||||  |||| ||||||||||| |||
Sbjct: 27829413 atccctttctaagcatttcaaaatctatgccgtatctgtttccagatcagaattgcgtaa 27829354


Query: 121      atgtgatccacattcttaattcactgtatctaaatcccaaaatctgatgannnnnnnnnn 180
                |||||||||||||||||||||||||  ||| ||||||||||||||| ||
Sbjct: 27829353 atgtgatccacattcttaattcactaaatccaaatcccaaaatctgctggttgtgtgtgt 27829294


Query: 181      nnnnnnnnnnnnnnnnnnnnnntatgttaatgggagaggaggaattctaccacatttcat 240
                                              |||| |||||||||||||||||  ||||||
Sbjct: 27829293 gtcacgtggg--------------------tgggggaggaggaattctaccatgtttcat 27829254


Query: 241      ttctgtattttccctcttgagtccacctgagatttaggaaatgctttaggg 291
                 ||  | ||||    |||||||| |  |||| ||||||||||  |||||||
Sbjct: 27829253 ctccctgttttgttgcttgagtcaatttgaggtttaggaaatattttaggg 27829203


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 280,708
Number of Sequences: 54
Number of extensions: 280708
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 1
Number of HSP's gapped (non-prelim): 2
length of query: 291
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 245
effective length of database: 1,133,627,092
effective search space: 277738637540
effective search space used: 277738637540
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.
```

```
Query= gi|4836464|gb|AF122892.1|AF122892 Catharus ustulatus
microsatellite Cu05 sequence
         (411 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr1                                                                  120   2e-025

>chr1
          Length = 188239860

 Score =  120 bits (75), Expect = 2e-025
 Identities = 195/302 (64%), Gaps = 26/302 (8%)
 Strand = Plus / Minus


Query: 116       attatatgtgctaggtaaagaataccacagtgataatgcacattaaannnnnnngctgct 175
                 |||| ||||   ||||||| |||  |||| || |  | |  |   |         ||| |
Sbjct: 128999999 attaaatgtaacaggtaaaaaat--cacaatggt--ttcttaaagagaaattcttctgat 128999944


Query: 176       catatgatcattaagatgatacttttagcagaactgtagactgtcacatcttttgaattg 235
                  |||||||| ||| | |||||||| |||     ||||| || | |||| |      | |
Sbjct: 128999943 tatatgatctttatgctgatacttatagg----ctgta-acag-caca-cggagacagta 128999891


Query: 236       catgaatagttctcatgt-caaaggtgagtatctgagacaggcactccttttagtctgaa 294
                 | |   || ||   |||| |||||||  || |||||| |   || || ||||||||  |
Sbjct: 128999890 cttacttatttt--atgttcaaaggtaggtttctgagtctatcattctttttagtccaac 128999833


Query: 295       ttcctaaggaaaaaggggcatgctcctcaagtaaatgtgacaacagtcttttttaaaaat 354
                 ||||||| ||||   |  |||  |||| |  || ||||||| |||| |||| ||  | ||
Sbjct: 128999832 ttcctaatgaaatccgtacattttccttagttacatgtgactacagcctttcttttatat 128999773


Query: 355       ccatcttcccatttca--caaa----------acagatagatgtctcagacatgatcatt 402
                 ||||    ||||||||  ||||          |||||| |||||||||||||| || |||
Sbjct: 128999772 ccattaaaccatttcaaccaaatttcacagggacagatggatgtctcagacataataatt 128999713


Query: 403       ac 404
                 ||
Sbjct: 128999712 ac 128999711



 Score = 60.2 bits (37), Expect = 3e-007
 Identities = 66/116 (56%), Gaps = 1/116 (0%)
 Strand = Plus / Minus


Query: 2         cctctaaatacctgtgagtgcatgcatgcacaccagcacagtgttagacttgttttaaat 61
                 ||||||||||  |||   |  ||||||||| |||||||  || ||  | |||||||||||
Sbjct: 129000263 cctctaaatatgtgtacttatatgcatgcaaaccagcagtgttttgaatttgttttaaat 129000204


Query: 62        actcaaatgcaaatgactgg-gggagagtgcnnnnnnnnnnnnnnnnnnnnnnnaa 116
                 |  |  ||  |||    ||| ||||| |||                        ||
Sbjct: 129000203 atccctattgaaacccgtggagggagtgtgtgcatgtgtgtatgtagcatcctcaa 129000148


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549
```

```
Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 361,505
Number of Sequences: 54
Number of extensions: 361505
Number of successful extensions: 4
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 0
Number of HSP's successfully gapped in prelim test: 1
Number of HSP's that attempted gapping in prelim test: 3
Number of HSP's gapped (non-prelim): 2
length of query: 411
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 364
effective length of database: 1,133,627,038
effective search space: 412640241832
effective search space used: 412640241832
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|4836465|gb|AF122893.1|AF122893 Catharus ustulatus
microsatellite Cu10 sequence
         (352 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr2                                                                  128   8e-028

>chr2
          Length = 147590765

 Score =  128 bits (80), Expect = 8e-028
 Identities = 202/325 (62%), Gaps = 40/325 (12%)
 Strand = Plus / Plus


Query: 3        gaaagacgtctctaaacagagaccagtgtgaccccagtgtcctttactctccccacaagt 62
                ||| ||  ||| ||||||||||| ||  ||||    ||||||| | ||||| |  ||  |
Sbjct: 60521587 gaaggaaatctgtaaacagagactagcatgactttggtgtcctctgctctctctgcatat 60521646


Query: 63       ctcagaggtgagacatgatacactccagagatggaaaatgaggagaatactaggcatgan 122
                ||  || ||||||  ||||||  ||||||||  |||||||| || |     || ||||
Sbjct: 60521647 cttggaagtgagatgtgatacgttccagagactgaaaatgaagaca----cagacatg-- 60521700


Query: 123      nnnnnnnnnnnnnnnnnnnngaattcatcatgcaggaaactttgctggtatgtagtgttt 182
                                    | ||| |   || ||||||||||||||| ||  || ||||
Sbjct: 60521701 -------gacacatacacatgcattaactgtggaggaaactttgctggcatacagagttt 60521753


Query: 183      tctatggttaaaaagtgtagaggtcaacgtaggtgaatttaggactgaaataagttttga 242
                ||||    ||||   ||  |||| ||| || ||| |||||||                 |
```

```
Sbjct: 60521754 tctacaaataaatcatg--gaggacaatgttggtaaatttag----------------aa 60521795


Query: 243      tttcaaaacaacacaca-ctgatttctaaatagaatgcccaactccgtgcagagaacagg 301
                |||| ||  || |  || |||        | | ||  |||| || ||||| |||||  ||
Sbjct: 60521796 tttctaattaagatgcagctg--------agaaaactcccagctacgtgctgagaagggg 60521847


Query: 302      ttcctgtctaaatagggatgaacag 326
                |||||| |||||||||| |||||||
Sbjct: 60521848 ttcctgcctaaatagggctgaacag 60521872


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 246,457
Number of Sequences: 54
Number of extensions: 246457
Number of successful extensions: 5
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 3
Number of HSP's gapped (non-prelim): 1
length of query: 352
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 306
effective length of database: 1,133,627,092
effective search space: 346889890152
effective search space used: 346889890152
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|4836466|gb|AF122894.1|AF122894 Catharus ustulatus
microsatellite Cu28 sequence
         (356 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                  Score    E
Sequences producing significant alignments:                      (bits) Value

chr7                                                                  185   5e-045

>chr7
          Length = 37338262

 Score =  185 bits (116), Expect = 5e-045
```

```
 Identities = 179/236 (75%), Gaps = 4/236 (1%)
 Strand = Plus / Plus


Query: 15       aaggttgacaatttatgaagcaattaactctccacttttcaatagcactccttgagcatg 74
                ||| |||  | | |||||| || |||||||||| ||| ||  || || || | ||||||
Sbjct: 28094942 aagtttgt-agtctatgaaccagttaactctcctcttctctgtaccaatcttggagcatc 28095000


Query: 75       tcagaacactgta--aactagaacaaggcttccttgccactcttgtgaggcaaaga-gta 131
                |||||||||| ||  |||  | ||||||  || ||||   |||| ||||||| | | |||
Sbjct: 28095001 tcagaacactttataaacaggtacaagggatctttgctgttcttttgaggcagataagta 28095060


Query: 132      tcactatacccattttacagaagtgtaaaagagaggcacagaaatgtgaattgcttgagg 191
                |||||||| ||||||||||||||   ||| ||||| ||||||  ||||||| || |||||
Sbjct: 28095061 tcactataaccattttacagaaggacaaatgagagacacagatctgtgaatagcctgagg 28095120


Query: 192      ttgttttgcagacccatagcagaattgttagaagatccagagatacctgtgtgtat 247
                |  |||| || | ||| ||||||| ||||| |||| |||||||   | |||  |||
Sbjct: 28095121 tcattttacaaatccagagcagaactgttacaagagccagagactgcagtgcatat 28095176


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 269,697
Number of Sequences: 54
Number of extensions: 269697
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 1
length of query: 356
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 310
effective length of database: 1,133,627,092
effective search space: 351424398520
effective search space used: 351424398520
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|54645926|gb|AY769673.1| Dendroica kirtlandii clone DkiB102
microsatellite sequence
         (684 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters
```

```
                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr15                                                                 267   2e-069

>chr15
          Length = 12438626

 Score =  267 bits (168), Expect = 2e-069
 Identities = 291/403 (72%), Gaps = 10/403 (2%)
 Strand = Plus / Minus


Query: 12     caaatacagttttgccttgnttg-gcacttgctttgtggtataactttgccttttgaggt 70
              |||||    |||| ||||| | | |||  ||  ||||||| | |||||||  | |||||
Sbjct: 639709 caaatgtgattttaccttgttggtgcaactg--ttgtggtgttactttgc--tctgaggc 639654


Query: 71     atttggcatatcctgctggattaagtgtccctggttatctctggtt--tttgtggcatga 128
              |||||||||||||  | || ||| || ||| || | ||||||||||  ||| |||||
Sbjct: 639653 atttggcatatcccacagggttacgtctccttgttcatctctggttcgtttatggcacag 639594


Query: 129    taactcccaaacaggcttttaataggctgccatttctgtcagcaagctgctctcagctcc 188
              ||||| |||   |  ||| ||||||  ||   ||  | |    |   |||| ||| |||
Sbjct: 639593 taacttccatctacacttctaatagt-tgttgttcttttgtttagattgctttcaactct 639535


Query: 189    tgtagtcagctggaattcttacagcttgagccttttcaggaaaaaagtcacttgccaacc 248
                || ||||||| | |||||| |  |   || |||  | ||||||   || || ||||||
Sbjct: 639534 cctactcagctgtatttcttataattactgcttttagaagaaaaataccatttaccaacc 639475


Query: 249    agaagaattatggtggttctggtgttactgcattcccttgaatgtaaaacaattcactag 308
               ||||  | ||||   |  |||  ||||||  |||   ||| ||| |||||||||| |
Sbjct: 639474 tgaagggtcatggatctgttggcattactgtgttctgctgactgtgaaacaattcagtg- 639416


Query: 309    ttgctgtttgttctctaattccaggaaagccaatattttcagtggacattcacccagatg 368
               || |  ||||||||| ||| |||||||||| ||||||||||||||||||||||||||||
Sbjct: 639415 -tgtttcttgttctctgatttcaggaaagcccatattttcagtggacattcacccagatg 639357


Query: 369    ggaccaagtttgcaacaggaggacaaggtaagtctgtgtactg 411
              |||||||||||||||||||||||||||||| |  | ||  |||
Sbjct: 639356 ggaccaagtttgcaacaggaggacaaggtatgcttatgccctg 639314


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 576,971
Number of Sequences: 54
Number of extensions: 576971
Number of successful extensions: 4
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 1
length of query: 684
length of database: 1,133,629,576
```

```
effective HSP length: 48
effective length of query: 636
effective length of database: 1,133,626,984
effective search space: 720986761824
effective search space used: 720986761824
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|54645929|gb|AY769676.1| Dendroica kirtlandii clone DkiB118
microsatellite sequence
         (586 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr7                                                                  104   2e-020

>chr7
          Length = 37338262

 Score =  104 bits (65), Expect = 2e-020
 Identities = 210/342 (61%), Gaps = 22/342 (6%)
 Strand = Plus / Minus


Query: 249      gtgtctggacagtcatttttaaacaag--gact-tgct---gctggtgctgtcctgattt 302
                ||||||| |||| |||||||||| |||  |||| ||||   |||  ||||||||| ||||
Sbjct: 32739738 gtgtctgcacagccatttttaaa-aagctgactatgctaatgctcttgctgtcctaattt 32739680


Query: 303      gctctgagcctgggctgagctctaggacaaaagttaaaccccccaagctccacactgctt 362
                 |||     |||  || ||||||| | ||| |||   ||         |||      | |
Sbjct: 32739679 actcctttgctgtacttagctctacgccaatagtctgactgttt----tcc------cgt 32739630


Query: 363      tagcctgcagctcctcaggctgcaagtcagacacaatttcagggatcttctttatttcta 422
                ||||||| |  |  | || ||| ||  ||| ||||||||||| | |||||||| |||||
Sbjct: 32739629 tagcctgaattttgttagactggaaaccaggcacaatttcagagttcttcttt-tttctt 32739571


Query: 423      cctttattgcccttcaatcattgagcaattaatgaaaactttcccccttcctcccccact 482
                   || ||   || |||    ||| || |||||||     ||         |     |
Sbjct: 32739570 ttatttttcttctacaagttctgaacatttaatgattttcttgtgttaggattttggaaa 32739511


Query: 483      ccctcccnnnnnnntcctattttcaaagtgattttttaatattgtcgctttt-caactaa 541
                   |  |        |  ||||||||  |   |||||| | || |   |||| |||  ||
Sbjct: 32739510 aaatatctttaaaaactgattttcaatttttatttttattttttttatttttgcaa--aa 32739453


Query: 542      gggaaaaggttatttattaagtggaaggagcaatagagtctg 583
                 |||||||||  ||||||||||   | ||| || | ||||||
Sbjct: 32739452 aggaaaaggtggtttattaagt-ttatgagaaaaatagtctg 32739412


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54
```

```
Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 503,233
Number of Sequences: 54
Number of extensions: 503233
Number of successful extensions: 7
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 0
Number of HSP's successfully gapped in prelim test: 1
Number of HSP's that attempted gapping in prelim test: 7
Number of HSP's gapped (non-prelim): 1
length of query: 586
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 539
effective length of database: 1,133,627,038
effective search space: 611024973482
effective search space used: 611024973482
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|54645930|gb|AY769677.1| Dendroica kirtlandii clone DkiB119
microsatellite sequence
         (603 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr18                                                                 478   e-133

>chr18
          Length = 8919268

 Score =  478 bits (301), Expect = e-133
 Identities = 410/563 (72%), Gaps = 40/563 (7%)
 Strand = Plus / Minus


Query: 49      gccttcctccctgggcaa-cagctc-agcagttgagctgcaggtcttgctc-atcaattc 105
               ||||  | ||||  | |  |||||| |  || ||| ||| || || |  || || |||||
Sbjct: 7799466 gcctcgcaccctatgaaggcagctcgaagagctgaactg-agatccttgtctataaattc 7799408


Query: 106     cttttaggatgcacattaaatatattccacaacagggacacttctcctctgctctcccct 165
                ||||||||||||||||||||||  |||||||||  |||||||||| |||    || | |
Sbjct: 7799407 tttttaggatgcacattaaatattatccacaacacagacacttctcttctt---tctctt 7799351


Query: 166     ctcctcagacacctcta-ccccagcaaagccctacaagtgctgcttgctgtggcctcatt 224
                ||||| | ||||| |  ||||||||||||||||  | |  |||||||||||||||||||
Sbjct: 7799350 ttcctctggcacctttttccccagcaaagccctaggactattgcttgctgtggcctcatt 7799291
```

```
Query: 225     ttgnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnccaccaccacgcactcatcctc 284
               | |                                    || |||||| || ||||||||
Sbjct: 7799290 tagcatcaccat---------------------------catcaccacacattcatcctc 7799258


Query: 285     atataaaacagaaatctattccatcaagcacttaacataaatattaaaataatggaaggg 344
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 7799257 atataaaacagaaatctattccatcaagcacttaacataaatattaaaataatggaaggg 7799198


Query: 345     acaaaatataaatctacatacaacttcatgactaccatagcacctattaccatgacaaag 404
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 7799197 acaaaatataaatctacatacaacttcatgactaccatagcacctattaccatgacaaag 7799138


Query: 405     caaattttggttcnnnnnnnnnnnnnnnnnnatgaggagcaagttaggaagaggaacctc 464
               ||||||   ||||                  | |||||| |||||||||||||| |
Sbjct: 7799137 caaattcctgttcaggaggaagggaaagggaacgaggagaaagttaggaagagggattct 7799078


Query: 465     gactgtcattaaatatgtaaatcactc----attcnnnnnnnnnnnnnnnnnnnnnnnnn 520
               |||||||||||||||||||||||||||    |||
Sbjct: 7799077 gactgtcattaaatatgtaaatcactcttagattttgttgttgttgttgttgttgttttg 7799018


Query: 521     nnnnnnnnnnaaggttaccaaccttattaaaattcatttccactaaccagctcgttctat 580
                         ||||||||||||||||||| ||||||||| ||||||||||||||||||||
Sbjct: 7799017 cttctgtttcaaggttaccaaccttattagaattcattt-cactaaccagctcgttctat 7798959


Query: 581     gtcactatggataccaaagaacc 603
               |||||||||||||||||||||||
Sbjct: 7798958 gtcactatggataccaaagaacc 7798936


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 477,197
Number of Sequences: 54
Number of extensions: 477197
Number of successful extensions: 5
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 2
length of query: 603
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 556
effective length of database: 1,133,627,038
effective search space: 630296633128
effective search space used: 630296633128
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]
```

```
Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|54645931|gb|AY769678.1| Dendroica kirtlandii clone DkiB124
microsatellite sequence
         (653 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr5                                                                  78   3e-012

>chr5
          Length = 56310377

 Score = 77.7 bits (48), Expect = 3e-012
 Identities = 200/367 (54%), Gaps = 30/367 (8%)
 Strand = Plus / Plus


Query: 220      acctttgccatggaagtagtccctgtagtaggtggcgcccaggtcggcgtgctccacgct 279
                ||||||   || |||  | |  | ||| ||    || || |||||  | || || ||  |
Sbjct: 24295774 acctttctgatagaaaaattttcggtaataatatgcaccaaggtctacatgttcaacaat 24295833


Query: 280      gtaactccgaaccctctccgggttcc---tctgctcctccttaggaaactccaaaatgga 336
                ||| ||    || || ||  | |      ||   | |||||| ||||  || | ||  |
Sbjct: 24295834 gtatcttttcactctgtctagatgtaaaatcaaattctccttgggaacttctagaactgc 24295893


Query: 337      aactccagcatttgtcaccttcaaaaaattcccagattccaccaaaattccagaagaagg 396
                 ||||||||||| || ||  | | ||    | |||| |  ||  |||            |
Sbjct: 24295894 cactccagcattcgt-acaatgagaa----ctcagagttgactcaaac-----------g 24295937


Query: 397      aggagaannnnnnnnnnnnnnnnnnnnnnnnnnnnnaaacgcagatttggaaaaactgac 456
                |||   |                             |      ||||||||||  || |
Sbjct: 24295938 aggc--actttcacatccactgaaggaacctgaatta------gatttggaaaggcttat 24295989


Query: 457      gtcgcgttcgcctcgaccgccgccgatctcgttgcggaaatgagggcagctcaacaataa 516
                 |  |  || |||    | || || ||||| || || |||| ||||||||||| ||  |
Sbjct: 24295990 cttcctctcccctt---ccccaccaatctcattacgaaaataagggcagctcatcacaag 24296046


Query: 517      atcgttgctggtgttatcccctaaatcctgctccaaattttctttggaatttaaattttc 576
                 ||||||||  | | ||||||    |||   |  | | || |||| ||||| | || |||
Sbjct: 24296047 ttcgttgcttttatcatccccctggtccatattgagacttccttttgaattcagatcttc 24296106


Query: 577      catgctg 583
                  |||||
Sbjct: 24296107 agtgctg 24296113


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
```

```
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 311,336
Number of Sequences: 54
Number of extensions: 311336
Number of successful extensions: 1
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 653
length of database: 1,133,629,576
effective HSP length: 48
effective length of query: 605
effective length of database: 1,133,626,984
effective search space: 685844325320
effective search space used: 685844325320
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|54645932|gb|AY769679.1| Dendroica kirtlandii clone DkiC105
microsatellite sequence
         (469 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr1                                                                  110   2e-022

>chr1
          Length = 188239860

 Score =  110 bits (69), Expect = 2e-022
 Identities = 166/258 (64%), Gaps = 11/258 (4%)
 Strand = Plus / Plus


Query: 110      gctcgggtatctggctttaagtaattgctgtccggaaaaacgctannnnnnnatcaggta 169
                ||| | ||| |||| ||||||| | | | ||  | |  || | ||       ||||||||
Sbjct: 24579699 gcttgagtagctggttttaagttagtacagttggaagtaaggttaactttttatcaggta 24579758


Query: 170      ttacacttgttgaatatttattg-ttttacataaggcactagtacgcaaaagataagtaa 228
                ||| ||||||||| | ||  ||| | ||| | |||    | |||    | |||  | |
Sbjct: 24579759 ttatacttgttgagtgttacttgctattatacaagatgttggta---tagagactaatct 24579815


Query: 229      tcctcttcccatgttcttttcagacaaatttcatgagatagttatgactgaactgtgtaa 288
                || |||| |  ||||  || |  ||||||||||| |  |   | ||| ||||||||||||
Sbjct: 24579816 tcatctttctgtgtt-gttcctaacaaatttcataacgtgaatttgattgaactgtgtaa 24579874


Query: 289      accagagattataaggacagctctccaggcacaacaagttcagtg---tttagtactaca 345
                | |  ||||||      ||| |  ||| | |  |||| || ||||    ||||| || ||
Sbjct: 24579875 atctcagattactgaaccagtttcccacg-agcacaactttagtgcatcttagtgctcca 24579933


Query: 346      tttcactttattattttg 363
                |||  |||  || |||||
Sbjct: 24579934 ttttcctt--ttcttttg 24579949
```

```
  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 360,927
Number of Sequences: 54
Number of extensions: 360927
Number of successful extensions: 11
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 8
Number of HSP's gapped (non-prelim): 2
length of query: 469
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 422
effective length of database: 1,133,627,038
effective search space: 478390610036
effective search space used: 478390610036
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|54645933|gb|AY769680.1| Dendroica kirtlandii clone DkiC116
microsatellite sequence
         (767 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr2                                                                  275   8e-072
chrUn                                                                  70   8e-010

>chr2
          Length = 147590765

 Score =  275 bits (173), Expect = 8e-072
 Identities = 412/681 (60%), Gaps = 49/681 (7%)
 Strand = Plus / Minus


Query: 3        ttcacacaattag-tccctatttctcttggcctctccagggn--ctgttgcat-tttatg 58
                ||||||||||| | | || ||| || ||  |||||  ||||   |||     | |||||
Sbjct: 70815761 ttcacacaattggcttcccattcctattatcctctagagggctactgaacagtgtttata 70815702


Query: 59       g--gattgcccaatacttttgctaggcaccaaaatattgatgacattaaataatacccag 116
```

```
                |  |  ||  ||   |||||  ||| |||||| | | || |||||||||||  ||  ||
Sbjct: 70815701 gatgcatgggcag--cttttcttagtcaccaagacaatggtgacattaaatggtatacaa 70815644


Query: 117      agcaacccagacatcctttgatatttacatctgtcagaaagnnnnnnnnnnnnnnnttac 176
                ||| ||||||||||||||| | ||||||||  |||||||||               | |
Sbjct: 70815643 agctacccagacatcctttcacatttacat--gtcagaaagaaaagaacaattgcctgaa 70815586


Query: 177      ctacagcaagcagacttctcattccttctggagcaatccacgaggaaagggttatggctt 236
                 || |   | |   |||||   ||||  || |  |||  |   ||||| |  |||| |||
Sbjct: 70815585 gtaaac--atctctcttcttgctcctggtgaacaaataaatacggaaaagtatatgactt 70815528


Query: 237      gcactgcacctaaaggtcagcagtacttctaattattggtggaagaattcagtcaaattc 296
                ||| ||||||| || ||  ||| ||  ||| |||||||||||||| |||   | ||||||
Sbjct: 70815527 gcagtgcacctgaaagtttgcactagatctgattattggtggaagtatttgattaaattc 70815468


Query: 297      ctcatacaggacaactggctactgctcacaacatcttagatggtaggaattttcatgaca 356
                |||  |||||||| | || |||||| |||  || ||||| ||   ||  |||| |||  |
Sbjct: 70815467 ctcccacaggacacccggttactgcccacggcaacttaggtg--tggggtttttatgtta 70815410


Query: 357      agtgcatctgtggtcactgctgccagggtacaactgga-gagact-gacattctgggaat 414
                | ||||| | | ||| |||||| | | ||   | |||| |||||| ||   |||||   |
Sbjct: 70815409 actgcatgtcttgtccctgctg-ctgtgtcacagtggaggagactggaaggtctggaggt 70815351


Query: 415      ttctcagtccaaactagtccagggagaacaaagttctcaccact-cagaagcaaaagggt 473
                || ||||            || |||         | | |||| | |||||  || || ||
Sbjct: 70815350 ttgtcag------------catgga---------tatgaccagtccagaaataagagagt 70815312


Query: 474      gcctattgaacagttagaccaaaacacttcaattattcctgtgtaaagaggtaataactc 533
                 |  | ||     || |         |  | ||  |||||||  | ||||    || || | |
Sbjct: 70815311 tctcactg----cttgg------atgcatctgttattcccatataaattcctagtagcac 70815262


Query: 534      tgtgacttgatggtaatccttaaataattttgaagtgtagcctttggtaaaggactttgt 593
                ||||| |      ||| || |||||||  |||||||||| |||||||||||||||| ||
Sbjct: 70815261 tgtgaatcagcactaacccctaaataaccttgaagtgtaacctttggtaaaggactatgc 70815202


Query: 594      caccatgctgaggaaatgtaattaccaatgcaagnnnnnnnnnnnnnnnnnnnnnnnnnn 653
                |||||| |||| ||| |||||||||  |||| ||
Sbjct: 70815201 caccatactgaagaactgtaattactgatgccagaagtatctgtatctagtgggaggaaa 70815142


Query: 654      nnnnnnnnnnnnnnnnnnnnt 674
                                    |
Sbjct: 70815141 ctgcagcagctgatacaggtt 70815121


>chrUn
          Length = 165033910

 Score = 69.7 bits (43), Expect = 8e-010
 Identities = 107/160 (66%), Gaps = 10/160 (6%)
 Strand = Plus / Plus


Query: 3        ttcacacaattag-tccctatttctcttggcctctccagggn--ctgttgcat-tttatg 58
                ||||||||||| | | || ||| || ||  |||||  ||||   |||     | |||||
Sbjct: 38120669 ttcacacaattggcttcccattcctattatcctctagagggctactgaacagtgtttata 38120728


Query: 59       g--gattgcccaatacttttgctaggcaccaaaatattgatgacattaaataatacccag 116
                |  |  ||  ||   |||||  ||| |||||| | | || |||||||||||  ||  ||
Sbjct: 38120729 gatgcatgggcag--cttttcttagtcaccaagacaatggtgacattaaatggtatacaa 38120786


Query: 117      agcaacccagacatcctttgatatttacatctgtcagaaa 156
                ||| ||||  |  ||||||    ||||||  ||||| |||
Sbjct: 38120787 agctaccccaaactcctttttcctttaca--tgtcaaaaa 38120824
```

```
  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 658,083
Number of Sequences: 54
Number of extensions: 658083
Number of successful extensions: 6
Number of sequences better than 1.0e-005: 2
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 1
Number of HSP's that attempted gapping in prelim test: 3
Number of HSP's gapped (non-prelim): 3
length of query: 767
length of database: 1,133,629,576
effective HSP length: 48
effective length of query: 719
effective length of database: 1,133,626,984
effective search space: 815077801496
effective search space used: 815077801496
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|54645934|gb|AY769681.1| Dendroica kirtlandii clone DkiC118
microsatellite sequence
         (554 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr7                                                                  242   6e-062

>chr7
          Length = 37338262

 Score =  242 bits (152), Expect = 6e-062
 Identities = 179/267 (67%)
 Strand = Plus / Plus


Query: 286      ccnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 345
                ||
Sbjct: 23740641 cccagtttcagggagaagtggcaccagtgaagccctgtctcgtgcacatggccatgccaa 23740700


Query: 346      nnnacgtattaccctttataaatagctaccagcagatgttcagccagcaagtggctgtgc 405
                   ||  |||| ||| ||||||||||| ||||||||||||||||| |||||||||||||
Sbjct: 23740701 tgtaccaattatcctctataaatagctgccagcagatgttcagccggcaagtggctgtgt 23740760
```

```
Query: 406      tggttgaagccattacatcttgcagatgcttggcacagccctccagccaaagattacctc 465
                  ||||||| ||||||| ||||||||||||||||  ||||||||||||||| ||||||||
Sbjct: 23740761 cagttgaagacattacagcttgcagatgcttggcgaagccctccagccaaaaattacctc 23740820


Query: 466      tcctggagctctgctggcagtcagctctgctgcaagcaaaagtcgtctggattagctcat 525
                |||   |||||| |||||| ||||||||||| |||||| |||||  ||||||||||||||
Sbjct: 23740821 tcccacagctctactggcaatcagctctgcttcaagcagaagtcagctggattagctcat 23740880


Query: 526      agcacctgggtcagctgcttgagcagt 552
                | ||||||| |||||||||  ||||||
Sbjct: 23740881 accacctggatcagctgctcaagcagt 23740907


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 431,824
Number of Sequences: 54
Number of extensions: 431824
Number of successful extensions: 2
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 1
Number of HSP's gapped (non-prelim): 1
length of query: 554
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 507
effective length of database: 1,133,627,038
effective search space: 574748908266
effective search space used: 574748908266
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|54645936|gb|AY769683.1| Dendroica kirtlandii clone DkiD10
microsatellite sequence
         (620 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr4                                                                  118   1e-024
```

```
>chr4
          Length = 90634903

 Score =  118 bits (74), Expect = 1e-024
 Identities = 127/170 (74%), Gaps = 7/170 (4%)
 Strand = Plus / Minus


Query: 4        cagactcgataaagtgataattacctattaaattttta--acagagtttagtacctttaa 61
                ||| || ||||  |||||||||||||||  || |||||  ||||||||||| ||| | ||
Sbjct: 47615668 caggcttgatacggtgataattacctatcgaagttttagcacagagtttagcacc-tcaa 47615610


Query: 62       aaaatatg-tctagataatccatttatgcaggtaagattagaaggatggaataaatgagt 120
                |||||||| | ||| ||||| |||||| || ||||||||||    ||  ||| |||    |
Sbjct: 47615609 aaaatatgatatagctaatcgatttatccaagtaagattaggcagacagaacaaacacat 47615550


Query: 121      ttggatagtgcactgatttctaagcatggatgcttca-aatagtgaggaa 169
                   ||||||   |||||||||||    |  |||||||   ||||||||||
Sbjct: 47615549 acagatagt--tctgatttctaaaatcgcgtgcttcaggctagtgaggaa 47615502


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 553,092
Number of Sequences: 54
Number of extensions: 553092
Number of successful extensions: 4
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 1
length of query: 620
length of database: 1,133,629,576
effective HSP length: 48
effective length of query: 572
effective length of database: 1,133,626,984
effective search space: 648434634848
effective search space used: 648434634848
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|54645937|gb|AY769684.1| Dendroica kirtlandii clone DkiD12
microsatellite sequence
          (418 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters
```

```
                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr9                                                                  148   6e-034
chr3                                                                   59   9e-007

>chr9
          Length = 23409228

 Score =  148 bits (93), Expect = 6e-034
 Identities = 159/272 (58%), Gaps = 17/272 (6%)
 Strand = Plus / Minus


Query: 3       actaataaacatacttcaaggcttgctttgaaaacccttttatttcttagcaaga----- 57
               |||||| |||| |||||| | ||| ||| |||| |||| |||| ||||  |||||
Sbjct: 5308675 actaattaacaaacttcaggtcttacttagaaagccctgttatctctttccaagatattt 5308616


Query: 58      -atatt-tctggcc------tttattttcctgcctgcacttgaactctaatcatgctaat 109
                ||||| |||  ||      ||||||||||||||| |||||  | ||||||| |||||||
Sbjct: 5308615 catattatctttccagtctctttattttcctgcctacacttctattctaatcctgctaat 5308556


Query: 110     gatcttcattttctgtgccttctgtcagggttttttgtgacctctctaggtctctagggc 169
               ||||||||  ||||||   ||||| ||   ||||   ||||||||||  |||||||||||
Sbjct: 5308555 gatcttcaacttctgt---ttctgcca-cattttaaatgacctctctcagtctctagggc 5308500


Query: 170     ttggcaattaaaaactcaactctgggtaaggtgnnnnnnnnnnnnnnnnnnnnnnnnnnn 229
               |  ||| ||||  | ||   ||||  |||||||
Sbjct: 5308499 tcagcagttaagcagtcggttctgattaaggtgaactttgttacatatatatgaatatat 5308440


Query: 230     nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnta 261
                                             ||
Sbjct: 5308439 acacatttcaatttctctatataaagcacata 5308408


>chr3
          Length = 108638738

 Score = 58.6 bits (36), Expect = 9e-007
 Identities = 40/44 (90%)
 Strand = Plus / Minus


Query: 268      tcatatgtataaagcacctaccatcatattggtaaacattcttt 311
                |||||| |||||||||||||| ||||||| | ||||||||||||
Sbjct: 31670371 tcatatatataaagcacctacaatcatatagctaaacattcttt 31670328


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 377,359
Number of Sequences: 54
Number of extensions: 377359
Number of successful extensions: 11
Number of sequences better than 1.0e-005: 2
Number of HSP's better than  0.0 without gapping: 2
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 7
```

```
Number of HSP's gapped (non-prelim): 3
length of query: 418
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 371
effective length of database: 1,133,627,038
effective search space: 420575631098
effective search space used: 420575631098
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|54645940|gb|AY769687.1| Dendroica kirtlandii clone DkiD109
microsatellite sequence
         (472 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr3                                                                  95   1e-017

>chr3
          Length = 108638738

 Score = 95.1 bits (59), Expect = 1e-017
 Identities = 120/181 (66%), Gaps = 12/181 (6%)
 Strand = Plus / Plus


Query: 3        actgactcaattttttgag-atgttcactgtaaagagtgtctgagatggtggg-----at 56
                ||||||||| |||   | | || || ||  ||||   | |||  | | |||       ||
Sbjct: 97493274 actgactcattttgggggggatcttgaccataaatgctatctagggtagtgaagcaaaat 97493333


Query: 57       tgaaattgnnnnnnnncataaaaaggagtgttctcacattaagtgtttgtgtttgtatgc 116
                 |||||||           ||||||||||||| ||| ||||    | | | |||||||||
Sbjct: 97493334 ggaaattgaagccata---aaaaaggagtgttttcatattatagatgtatatttgtatgc 97493390


Query: 117      ttggatgactgaaaaagtgcatttcct---agaacctggacagactttctatacaccact 173
                |||||| |||||||||   ||||||||   | || |   |||||||||||  |||||| |
Sbjct: 97493391 ttggataactgaaaaaacacatttcctataataatccaaacagactttctgaacaccagt 97493450


Query: 174      a 174
                |
Sbjct: 97493451 a 97493451


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549
```

```
Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 288,436
Number of Sequences: 54
Number of extensions: 288436
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 1
length of query: 472
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 425
effective length of database: 1,133,627,038
effective search space: 481791491150
effective search space used: 481791491150
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|54645941|gb|AY769688.1| Dendroica kirtlandii clone DkiD117
microsatellite sequence
         (580 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr1                                                                  280   2e-073

>chr1
          Length = 188239860

 Score =  280 bits (176), Expect = 2e-073
 Identities = 283/379 (74%), Gaps = 15/379 (3%)
 Strand = Plus / Plus


Query: 4        aagactcaatgtgagagt-tctaattgaattttcattttcttttaagacgtagaattnga 62
                ||||||||||||||  |  ||||||| || || |||||| ||||||    ||||  | ||
Sbjct: 93463113 aagactcaatgtgatggcatctaattaaaattacattttattttaaagattaga--ttga 93463170


Query: 63       ttttagccaagttt-ggtttaaatggatttttggaaacaaatctcccagac-tttcatgt 120
                ||  |||||| ||| ||  |||| || ||||||||||||| ||| |||  | ||| |||
Sbjct: 93463171 ttc-agccaacttttggactaaacgggtttttggaaacaattctgccaaccctttaatgg 93463229


Query: 121      gaggtaatttgttatgaagtaatagacaatcagtggcagaacaaatctttgggaaaatgt 180
                |||||||||||||| |||| |||||||||||  ||||| || ||||||||||||||||||
Sbjct: 93463230 gaggtaatttgttaagaaggaatagacaatctatggcaaaataaatctttgggaaaatgt 93463289


Query: 181      atgtcatgttaatgtaggtgatggttttcttgttcagatcttcttcagcaatgactggaa 240
                |    ||||||||||||||||||||  | || | ||||||||||||||||||| |||| |
Sbjct: 93463290 acaaaatgttaatgtaggtgatggtaat-ttctccagatcttcttcagcaatgtctggta 93463348


Query: 241      aaataaatt--aagttttctttgcttaagaagcaactgaagagnnnnnnnnttttattct 298
```

```
                ||| |  ||  | ||  ||||||||||||||| | ||||| |         |||| |||
Sbjct: 93463349 aaaaactttccaggtcctctttgcttaagaagaagctgaa-ataaattctatttgttc- 93463406


Query: 299      atgcattttgaaggaagaatgtgtttgccacaaaatagccagtggcactaatttgaggaa 358
                     |||  || | || || |  |||| |||||||||| |   ||| |||| ||| ||
Sbjct: 93463407 ---actttaaaatgcaggatattattgcaacaaaatagcta-aagcattaatgtgaagac 93463462


Query: 359      tgaatctgtgtcttcagac 377
                ||||| || |  |||| ||
Sbjct: 93463463 tgaatttgggctttcatac 93463481


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 496,178
Number of Sequences: 54
Number of extensions: 496178
Number of successful extensions: 10
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 8
Number of HSP's gapped (non-prelim): 1
length of query: 580
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 533
effective length of database: 1,133,627,038
effective search space: 604223211254
effective search space used: 604223211254
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|54645942|gb|AY769689.1| Dendroica kirtlandii clone DkiD120
microsatellite sequence
         (653 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr2                                                                  223   4e-056

>chr2
          Length = 147590765
```

```
 Score =  223 bits (140), Expect = 4e-056
 Identities = 221/292 (75%), Gaps = 17/292 (5%)
 Strand = Plus / Plus


Query: 366       ttct-tctcctttacttttcctctttgtggggcagatcagagaaagcagaaggttaagga 424
                 |||| |||| || | | ||||||||| ||||  ||| ||||| |||||| || ||||||
Sbjct: 134263233 ttctctctctttcattattcctctttctgggtaagaccagaggaagcaggagattaaggg 134263292


Query: 425       caattacatccccagtgaagaagtttagtgcctctacatagacatacaacgtgtaactgg 484
                  | || ||| |||||||||| | ||| |||||  | |  |           ||||||||
Sbjct: 134263293 tagttccatacccagtgaaggattttggtgcccgttctca-----------tgtaactga 134263341


Query: 485       aaaatctggaagtcaagccaagatttgagcaaagtgtgggaatccaaacagttctgcaaa 544
                 |||||||| ||| |||||||||| ||||||| | ||   |||||||||||||||||||||
Sbjct: 134263342 aaaatctgaaagccaagccaagacttgagcagaatgcatgaatccaaacagttctgcaaa 134263401


Query: 545       agtgtgggtttctttcaaatgtgactggctgaaagctgaaacagattcag---tttatac 601
                 ||||| || ||| |||| || || |||||| ||||||||||||| |||||   || ||||
Sbjct: 134263402 agtgtaggcttcattcagatttggctggctaaaagctgaaacagcttcagttcttcatac 134263461


Query: 602       tgtcact-tcaagtgcatctcccaacctctctgcatggaaataggtttcttt 652
                 ||||||| |||||||| |||||| | |||  |   ||| |    ||||||||
Sbjct: 134263462 tgtcactatcaagtgcttctccc-agctcgttatgtgggagccagtttcttt 134263512



 Score =  152 bits (95), Expect = 1e-034
 Identities = 154/215 (71%), Gaps = 4/215 (1%)
 Strand = Plus / Plus


Query: 10        cactgctagaacagaattgcagaattttagcagcgcttttgtttagggttc-nnnnnnnn 68
                 ||||||||||| || |||||||| |||||| |  |||||||||| || |||
Sbjct: 134262993 cactgctagaataggattgcagagttttagtattgcttttgttt-ggtttcttctgcttt 134263051


Query: 69        atgttgggaagaagtgtctacttaaggaaatgtaactctgttagagcagtgcaggagatg 128
                 ||  |||| ||||||||| | | ||  ||||  ||  |||| || |||  ||| | ||
Sbjct: 134263052 attctggggagaagtgtccagtcaaaaaaatagaa--ctgtgagggcaaagcaagtgacc 134263109


Query: 129       aaattttgttgggattagaatgaaataagggagtaaatacaagaatgtatcacttctgat 188
                 |  ||||| ||| || ||||| ||||| | ||||| |||| |||    |||||||||| |
Sbjct: 134263110 aggttttgctggaatcagaataaaatatgagagtagatactagatgcaatcacttctggt 134263169


Query: 189       gccacacagagatgtgggtattgattgctatagta 223
                  ||||||| | |||||| |  |||||  || ||||
Sbjct: 134263170 accacacacaaatgtggatgctgatttataaagta 134263204


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 521,806
Number of Sequences: 54
Number of extensions: 521806
Number of successful extensions: 7
Number of sequences better than 1.0e-005: 1
```

```
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 5
Number of HSP's gapped (non-prelim): 2
length of query: 653
length of database: 1,133,629,576
effective HSP length: 48
effective length of query: 605
effective length of database: 1,133,626,984
effective search space: 685844325320
effective search space used: 685844325320
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|54645943|gb|AY769690.1| Dendroica kirtlandii clone DkiD123
microsatellite sequence
         (632 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr1                                                                  210   2e-052

>chr1
          Length = 188239860

 Score =  210 bits (132), Expect = 2e-052
 Identities = 243/348 (69%), Gaps = 13/348 (3%)
 Strand = Plus / Minus


Query: 2         attcactctttccaaatcaaatgtagggaaacctttggactacttaccagtggtcttgnn 61
                 ||| | | | || |  || |||  || |||   |||| |||  ||||||||||||||
Sbjct: 175296661 atttagtatgtctagctccaatacagagaattatttgaacttgttaccagtggtcttttt 175296602


Query: 62        nnnnngtcttgggtttatgcagcacaatacagaactctgtgcagaatatatcacaggttg 121
                       |||||  |   ||  |||||||||||||||| |||||||||  || | |  ||
Sbjct: 175296601 gt----tcttg--tcactggggcacaatacagaactcagtgcagaatgcataagatatta 175296548


Query: 122       atgaaatttagttgcagtaagtagtatggaaaatatcaaagcattaatgccctgcactga 181
                 ||| ||| || |||   |  || || ||||||  |  ||    ||||  |||  |||  |
Sbjct: 175296547 atgtaatatatttgtgatgggtggtgtggaaagaaataatatgttaacaccccacacgca 175296488


Query: 182       cctcttgcttctgcatgagtgaaacagtggagagagagaacatgatatgagttatttcta 241
                 | ||||  |||||||||||||       || |||||||||||||| ||||| |||||||||
Sbjct: 175296487 catcttatttctgcatgagtg-----ctgcagagagagaacatgctatgaattatttcta 175296433


Query: 242       tacaacaaagaacaacatcttgtgcccaca-caaatttt-gatgagaattcagacaatac 299
                 || || || ||||||||||||||||   || |||||||| ||||||| |||| |  |||
Sbjct: 175296432 tataataaggaacaacatcttgtgcatgcagcaaattttagatgagagttcacaggatag 175296373


Query: 300       agtttagaaggagcctcacagtattagaaggccttgtgagaggttctc 347
                 |  | |  || | |||  ||||| | ||| |||| || ||||| ||||
Sbjct: 175296372 aaataaagagtaacctatcagtactggaaagcctggtaagaggctctc 175296325
```

```
  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 630,147
Number of Sequences: 54
Number of extensions: 630147
Number of successful extensions: 2
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 632
length of database: 1,133,629,576
effective HSP length: 48
effective length of query: 584
effective length of database: 1,133,626,984
effective search space: 662038158656
effective search space used: 662038158656
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|444017|emb|X77081.1|ESCU4 E.schoeniclus DNA repeat region
(Escu4 locus)
         (338 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr2                                                                  188   6e-046

>chr2
          Length = 147590765

 Score =  188 bits (118), Expect = 6e-046
 Identities = 220/342 (64%), Gaps = 33/342 (9%)
 Strand = Plus / Minus


Query: 1        gtacatatcctatgacnnnnnnnccttgtcccatccattagccttcactgttgtttctgc 60
                ||| ||  || |||||        |||||||||||  | ||| |||| ||| | ||||||
Sbjct: 58831301 gtatatgccccatgacttcgt---cttgtcccatctgtcagctttcaatgtagcttctgc 58831245


Query: 61       acctggatgctggagggaaggaggtggggcaggatgagggggaaacagatgatgcatgcc 120
                ||||||| |||| ||||  ||||| ||    ||||  |||   ||||||  |||| ||||
Sbjct: 58831244 acctggaagctgaaggg-gggaggggg----ggat--gggcagaacagacaatgcgtgcc 58831192
```

```
Query: 121      agaagaaaaagtaattgtgctggtaagaagttttagcaatttggagaaa-catcctttcc 179
                |  |||| || |||||||| || |||| | ||| ||||| |||||||||  |||||||||
Sbjct: 58831191 a-tagaataattaattgtggtgataaggattttcagcaacttggagaaagaatcctttcc 58831133


Query: 180      ctcacaattttc---cgacttttggctttcttgttagcctttcagtgttattnnnnnnnn 236
                |||||| |||||   | ||||||||||||| ||||||||| |||   || ||
Sbjct: 58831132 ctcacagttttctaaccacttttggctttcatgttagcctctca---ttctttgtgtgta 58831076


Query: 237      nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnncgcatattaaacacatcattat 296
                                                       ||||||||| |||||  || |
Sbjct: 58831075 caaacatgcacacacataggtatgtgt------------gcatattaagcacattgttct 58831028


Query: 297      atgtaaagaggatggttcact---tcagcacataaaggagag 335
                |||||||||||  |||||  |   ||| || |  ||| ||||
Sbjct: 58831027 atgtaaagagggaggttctttctgtcaacatagcaagaagag 58830986


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 269,415
Number of Sequences: 54
Number of extensions: 269415
Number of successful extensions: 9
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 6
Number of HSP's gapped (non-prelim): 1
length of query: 338
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 292
effective length of database: 1,133,627,092
effective search space: 331019110864
effective search space used: 331019110864
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|444019|emb|X77082.1|ESCU6 E.schoeniclus DNA repeat region
(Escu6 locus)
         (243 letters)

Database: WholeChickenGenome.txt
          54 sequences; 1,133,629,576 total letters
```

```
                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr1                                                                   87   1e-015

>chr1
          Length = 188239860

 Score = 87.2 bits (54), Expect = 1e-015
 Identities = 75/98 (76%)
 Strand = Plus / Minus


Query: 1         agctcttactgactgacatggacttcttaggagtcaccttcaagangganagaaatgcct 60
                 |||||||| |||||||||||||| ||||  |||| |||||||  |   | || |||||||
Sbjct: 132684842 agctcttaatgactgacatggacctcttcagagtgaccttcagaaataaaaggaatgcct 132684783


Query: 61        aggtggtagaatatgggggcttaagtatttggtgtcca 98
                 | ||   ||| |   | || ||| ||||||||||||||
Sbjct: 132684782 atgtatcagatttcagtggtttaggtatttggtgtcca 132684745


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 77,146
Number of Sequences: 54
Number of extensions: 77146
Number of successful extensions: 1
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 243
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 197
effective length of database: 1,133,627,092
effective search space: 223324537124
effective search space used: 223324537124
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|1143448|emb|X84361.1|FHDNAFHU2 F.hypoleuca microsatellite
DNA (ID:FhU2)
         (138 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters
```

```
                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr9                                                                   78   4e-013

>chr9
          Length = 23409228

 Score = 77.7 bits (48), Expect = 4e-013
 Identities = 64/78 (82%), Gaps = 1/78 (1%)
 Strand = Plus / Plus


Query: 61       gcaaacaacttgaccttacagtaatggcatcaattcctctgcctgtcttgctgtggccca 120
                 ||||||| ||| | |||||||  || |||||||||  |||||||||||  || ||| |||
Sbjct: 13751385 gcaaacagcttcatcttacagccatagcatcaattattctgcctgtctctctttgg-cca 13751443


Query: 121      gcaaatatttacctgtgc 138
                 || ||||||||||| |||
Sbjct: 13751444 gcgaatatttacctatgc 13751461


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 87,727
Number of Sequences: 54
Number of extensions: 87727
Number of successful extensions: 1
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 138
length of database: 1,133,629,576
effective HSP length: 44
effective length of query: 94
effective length of database: 1,133,627,200
effective search space: 106560956800
effective search space used: 106560956800
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 33 (53.9 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|1143449|emb|X84362.1|FHDNAFHU3 F.hypoleuca microsatellite
DNA (ID:FhU3)
         (174 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters
```

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

  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 62,436
Number of Sequences: 54
Number of extensions: 62436
Number of successful extensions: 1
Number of sequences better than 1.0e-005: 0
Number of HSP's better than  0.0 without gapping: 0
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 1
Number of HSP's gapped (non-prelim): 0
length of query: 174
length of database: 1,133,629,576
effective HSP length: 45
effective length of query: 129
effective length of database: 1,133,627,146
effective search space: 146237901834
effective search space used: 146237901834
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 33 (53.9 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|37622152|gb|AY366077.1| Garrulax canorus microsatellite
GC-GATA-11 sequence
         (250 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr1                                                                   95   5e-018

>chr1
          Length = 188239860

 Score = 95.1 bits (59), Expect = 5e-018
 Identities = 113/161 (70%), Gaps = 7/161 (4%)
 Strand = Plus / Plus


Query: 1        cctttttctgcactcaacaggatgttttctgcatctca-aatgttttgaactacttacca 59
                |||||||| |       || |||||||||||||||||| ||   |   ||  |||||||
Sbjct: 35007078 cctttttccggttggggcaagatgttttctgcatctcacaaaccatcaaaacacttacct 35007137
```

```
Query: 60       gatatcatccagccctgctgaaataaggactacccagcaggagcaaattgatacttaaat 119
                |  || |||||       ||||||||   ||||||  |||||| |||| ||   ||||
Sbjct: 35007138 ggcattatccacg-----tgaaataaat-ctaccccacaggagtaaatggaattttaaga 35007191


Query: 120      aaacaggttttgtattcatggtgtgggagagtaagaaatgc 160
                ||| |  ||||||  || |||||||||||||||| ||||||
Sbjct: 35007192 aaatattttttgtcctcctggtgtgggagagtaaaaaatgc 35007232


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 192,730
Number of Sequences: 54
Number of extensions: 192730
Number of successful extensions: 2
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 1
Number of HSP's gapped (non-prelim): 1
length of query: 250
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 204
effective length of database: 1,133,627,092
effective search space: 231259926768
effective search space used: 231259926768
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|37622155|gb|AY366080.1| Garrulax canorus microsatellite
GC-GATA-15 sequence
         (211 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr1                                                                   78   8e-013

>chr1
          Length = 188239860

 Score = 77.7 bits (48), Expect = 8e-013
 Identities = 66/82 (80%), Gaps = 2/82 (2%)
 Strand = Plus / Plus
```

```
Query: 10       tgccctgcatacataaattaggcagagactatggaaaatcaatcaaggtgacag--tatt 67
                |||| || || | | ||||| || ||||||||| |||||||||||||||||| |  ||||
Sbjct: 90477171 tgccttgtatgcttcaattaagccgagactatgtaaaatcaatcaaggtgacggtctatt 90477230


Query: 68       tgtatgtgaaatgctcacacag 89
                  ||||| |||||| |||| ||
Sbjct: 90477231 catatgtaaaatgcccacatag 90477252


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 100,445
Number of Sequences: 54
Number of extensions: 100445
Number of successful extensions: 1
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 211
length of database: 1,133,629,576
effective HSP length: 45
effective length of query: 166
effective length of database: 1,133,627,146
effective search space: 188182106236
effective search space used: 188182106236
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|37622156|gb|AY366081.1| Garrulax canorus microsatellite
GC-GATA-22 sequence
         (264 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr3                                                                   90   2e-016
chr5                                                                   55   5e-006

>chr3
          Length = 108638738

 Score = 90.3 bits (56), Expect = 2e-016
 Identities = 136/252 (53%), Gaps = 13/252 (5%)
```

```
 Strand = Plus / Plus


Query: 7        cacacaggctggaaaagatattgagaccagaatccaccctga----cagcctgggggtag 62
                ||||||| ||| |||| |||||| |||    |||||||||||    |||||| |||| |
Sbjct: 49621916 cacacagactgcaaaatatattgggactgagatccaccctgagagccagcctaggggaaa 49621975


Query: 63       cacagttaccctgcaatgtctcatgcttgcaaataaccctgattaattcctctgtct-ca 121
                 ||   | | || |||||  |  |||| | ||| |||||||||||| ||| |  ||| ||
Sbjct: 49621976 tacttctgctctccaatgcattttgctcgtaaacaaccctgattaactccaccatctcca 49622035


Query: 122      ttcccattttctaaaagaattaannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 181
                || |    |||||| ||||  |
Sbjct: 49622036 ttac----ttctaagagaacga--ttccaccttccccagatacctccctatctctatgca 49622089


Query: 182      nnnnnnnnnnnnatcttagatacctctccatccctgtgtgctca-tgtccttcttcacac 240
                            || || |     | | | ||| | | ||| || ||  ||||  |||||
Sbjct: 49622090 cttatgtccctcatatt-gccttttattcctccttctctgcacactgctcttccgcacac 49622148


Query: 241      tggcttttattc 252
                |  ||  | |||
Sbjct: 49622149 tatctcctgttc 49622160


>chr5
          Length = 56310377

 Score = 55.5 bits (34), Expect = 5e-006
 Identities = 61/131 (46%), Gaps = 4/131 (3%)
 Strand = Plus / Plus


Query: 117      tctcattcccattttctaaaagaattaannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 176
                ||||||||||||||| ||||| ||| ||
Sbjct: 46558536 tctcattcccattttttaaaaaaataaaaacatttctagttagtatttcacgctttacgt 46558595


Query: 177      nnnnnnnnnnnnnnnnnatcttagatacctctccatccctgt--gtgctcatgtccttct 234
                                  | ||| | |||| || |||||| |   | ||  | ||||||
Sbjct: 46558596 tttctataagaccgcatctgttacagacctttcaatcccttttattactgct-tccttc- 46558653


Query: 235      tcacactggct 245
                ||| ||  |||
Sbjct: 46558654 tcaaacatgct 46558664


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 192,447
Number of Sequences: 54
Number of extensions: 192447
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 2
Number of HSP's better than  0.0 without gapping: 0
Number of HSP's successfully gapped in prelim test: 2
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 2
length of query: 264
```

```
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 218
effective length of database: 1,133,627,092
effective search space: 247130706056
effective search space used: 247130706056
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|37622150|gb|AY366075.1| Garrulax canorus microsatellite
GC-GATA-23 sequence
         (264 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr8                                                                   94   2e-017

>chr8
          Length = 30024636

 Score = 93.5 bits (58), Expect = 2e-017
 Identities = 109/164 (66%), Gaps = 13/164 (7%)
 Strand = Plus / Minus


Query: 3        agtaagaaagaaaccaattacagtaagcaattaaccagaaaggtctgacaaggctcaaag 62
                ||||  ||| |||||||||||||||||||||||| ||||||   ||||||| |  | |||
Sbjct: 27577937 agtagaaaacaaaccaattacagtaagcaattaatcagaaaaccctgacaaaggcctaag 27577878


Query: 63       cttaccataccataaactcaa--gattgtgagtgattacaga-----------tcattgt 109
                 |||| || ||| | |||  |  | |  |||||||| | |||            || |||
Sbjct: 27577877 gttacaatcccacacactttagtgctcttgagtgatgaaagaaaactataaggccactgt 27577818


Query: 110      taatggatattctaaaccacagactttgaaacaagnnnnnnnnt 153
                ||| | ||| | |||| || ||||||  ||| |||        |
Sbjct: 27577817 taaagaatactttaaaacatagacttctaaaaaagtaataatgt 27577774


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 142,187
Number of Sequences: 54
Number of extensions: 142187
Number of successful extensions: 1
```

```
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 264
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 218
effective length of database: 1,133,627,092
effective search space: 247130706056
effective search space used: 247130706056
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|48256717|gb|AY622337.1| Pseudonigrita arnaudi clone GCSW10
microsatellite sequence
         (389 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr4                                                                  160   3e-037

>chr4
          Length = 90634903

 Score =  160 bits (100), Expect = 3e-037
 Identities = 238/382 (62%), Gaps = 49/382 (12%)
 Strand = Plus / Minus


Query: 17        actaacctacagtaataaagctntctcccacacaaggcaaatagttg-agcctctttact 75
                 |||||  || || || | | || |||||||  ||  |||| | |||| ||||| ||||||
Sbjct: 34023048 actaatttaaaggaagagaactgtctcccattcagagcaagt-gttgcagcct-tttact 34022991


Query: 76        agtgctaatagatgctttactgaagaacgtcagccatgacacggactcacttcttccaaa 135
                 | || ||| ||||||| |||| || ||||||| ||||||| | |||| |          |
Sbjct: 34022990 aatgttaaaagatgctctactaaataacgtcaaccatgactcagactta----------a 34022941


Query: 136       taagagatcataagttttggcattttgaagccctgcagtcattaacctatgtattttttt 195
                 || |||||| |||| |||| ||| | |||||||||||                 ||||
Sbjct: 34022940 taggagatcttaagctttgccatctgtgaagccctgc-----------------tttt-- 34022900


Query: 196       nnnnnnnnnnnnnnnnnnnnnnnnnnnnnntcctttctccccntgtgctctgaagtgga 255
                                               || |||||||||| | | ||||    |
Sbjct: 34022899 -----ctctgcagtcattaggttagaaagttctttttctcccc-tcttctct---cttac 34022849


Query: 256       aaaatta-tctctnatcagcagcagctttcagatggagctgggccttacaaaatgagatc 314
                     |||  |  | ||  |||||||||||||||   |||||||||||  | ||  |||||
Sbjct: 34022848 tcttttacacgatcattggcagcagctttcagaaaaagctgggcctttaagaaaaagatc 34022789


Query: 315       atcta----agacacaataataaaaaacaagaaaaagaagcaa---gagctggtanaaga 367
                 |  ||    | ||||| ||| |||||| || ||| | || |||   || |||||| || |
Sbjct: 34022788 aaataatataaacacagtaacaaaaaataaaaaagaaaatcaacaggatctggtagaaaa 34022729
```

```
Query: 368      caaactacaagctagatagcat 389
                ||||| || ||||||| |||||
Sbjct: 34022728 caaaccaccagctagacagcat 34022707


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 351,838
Number of Sequences: 54
Number of extensions: 351838
Number of successful extensions: 30
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 0
Number of HSP's successfully gapped in prelim test: 1
Number of HSP's that attempted gapping in prelim test: 29
Number of HSP's gapped (non-prelim): 2
length of query: 389
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 342
effective length of database: 1,133,627,038
effective search space: 387700446996
effective search space used: 387700446996
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|48256718|gb|AY622338.1| Pseudonigrita arnaudi clone GCSW13
microsatellite sequence
         (231 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr14                                                                  73   2e-011

>chr14
          Length = 20603938

 Score = 72.9 bits (45), Expect = 2e-011
 Identities = 107/223 (47%), Gaps = 20/223 (8%)
 Strand = Plus / Plus


Query: 4        ttaatttaatc-tacannnnnnnggcctgtgaaatatttaactggtaaaaaaggctgtag 62
                ||||| || |  ||||       ||||||||||||| |||||| ||||  ||  ||||||
```

```
Sbjct: 16987796 ttaatctagtaatacacatttgaggcctgtgaaatagttaacttgtaagtaactctgtag 16987855


Query: 63       aaacaccttacataaagaaacnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 122
                ||| || ||
Sbjct: 16987856 aaagacttt------------gtacgaacaggtagcttattttaattattttaaatact 16987903


Query: 123      nnnnnnnnnnnnnnnnnntctaaattgattccagtaatagtagttattcttgtacgaact 182
                                  |     || ||||||  || | |  | |||| | || ||| |
Sbjct: 16987904 tggagcagatagcactggt-----ttaattccaccaacactgataattcct-tatgaa-t 16987956


Query: 183      attttcttctcatatattaagcattatgttgactaaagttaga 225
                | |||  ||| |||| |||||  | ||| | ||||||| ||||
Sbjct: 16987957 agttttatctaatatgttaagtgtgatgctaactaaagctaga 16987999


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 129,535
Number of Sequences: 54
Number of extensions: 129535
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 1
length of query: 231
length of database: 1,133,629,576
effective HSP length: 45
effective length of query: 186
effective length of database: 1,133,627,146
effective search space: 210854649156
effective search space used: 210854649156
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|48256720|gb|AY622340.1| Pseudonigrita arnaudi clone GCSW18
microsatellite sequence
         (279 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr14                                                                 115   4e-024
```

```
>chr14
          Length = 20603938

 Score =  115 bits (72), Expect = 4e-024
 Identities = 163/273 (59%), Gaps = 39/273 (14%)
 Strand = Plus / Minus


Query: 9       tgggttcagaacagggctcctgctagtggtggaaattttccagcagcctcagtgatccta 68
               ||||  || | ||||||||||||||||||||| ||| |  |||||||||| |||||||||
Sbjct: 6240327 tgggagcaaagcagggctcctgctagtggtgggaatctctcagcagcctcggtgatccta 6240268


Query: 69      cttaagccctcaatttcaagagaaatgaaatatcttttccagacccacttttcgcagtt- 127
                ||||||||||                    || ||||||||||  | |||| ||||||
Sbjct: 6240267 tttaagccctc--------------------atgttttccagacgtagtttttgcagtta 6240228


Query: 128     -aaatacataaatttttatagatctgtgtgctcatatannnnnnnnnnnnnnnnnnnnnn 186
                ||| ||   ||     ||| || | ||      ||||
Sbjct: 6240227 gaaagaccccaa---acatacatatatg------tatatgtgctcgtgtgtgtgtgtgtg 6240177


Query: 187     nnnnnnnnnnnatgtggtatatgtgcatttgtgaagtggcttgctcaccagcactcac-- 244
                          |    || ||||| |||| ||| |||| ||  | |||||||||| ||
Sbjct: 6240176 tgtttgtgtgca----gtgtatgtacattagtgcagtgact--cgcaccagcactaactg 6240123


Query: 245     tggatgagatgctgttaaaattaattgcctctg 277
               ||| ||||| |   ||||||| |||||||| ||
Sbjct: 6240122 tgggtgagacgtatttaaaatcaattgcctttg 6240090


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 240,215
Number of Sequences: 54
Number of extensions: 240215
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 1
length of query: 279
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 233
effective length of database: 1,133,627,092
effective search space: 264135112436
effective search space used: 264135112436
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
```

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"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|48256723|gb|AY622343.1| Pseudonigrita arnaudi clone GCSW35
microsatellite sequence
         (361 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr7                                                                  250   1e-064

>chr7
          Length = 37338262

 Score =  250 bits (157), Expect = 1e-064
 Identities = 226/310 (72%), Gaps = 13/310 (4%)
 Strand = Plus / Minus


Query: 5        agacagagcacatcagttgccaacatcccactgccaagagccaaaacaaaagaaaaaggg 64
                ||| ||||  ||||| || |||   | |||||||||| ||||||| || ||||||  |||
Sbjct: 33179984 agatagagtgcatcattttccactgttccactgccaaaagccaaagcagaagaaa--ggg 33179927


Query: 65       caaagctattagtatattttttccaacaaactgaagaaaaagagtcaatcatgaga-aca 123
                |||  || ||| |||| ||||| ||||||||||||||||||||| | |||||| || | |
Sbjct: 33179926 caacactgttactataattttttcaacaaactgaagaaaaagagcccatcatgggagaga 33179867


Query: 124      aatgattgccactccatgagagataggaagattgcagctgcagaatgtaatagaatttca 183
                ||||||| ||| ||  ||||||||| ||||||  |||||||||| || || |||||||||
Sbjct: 33179866 aatgattcccattctttgagagataagaagatcacagctgcagagtgcaaaagaatttca 33179807


Query: 184      ttgacctgttattggtgtgaaaag--atgaagggttttctctagaagtgctttaaaaatn 241
                |||||||||| || || | |||||  |  ||  | ||||||||||||||||||||||||
Sbjct: 33179806 ttgacctgttgtttgtttaaaaggaaaaaaaagctttctctagaagtgctttaaaaatg 33179747


Query: 242      nnnnnnnnnnnnnnnnnnnnnnnnnnnnnngagaagggtaacagaa-agctaaaaaagtt 300
                                               |||||| ||| ||||  |||||| |||||
Sbjct: 33179746 catatacgcggcacacacatacac-------agaaggttaatagaagggctaaagaagtt 33179694


Query: 301      cagttgcaag 310
                ||| ||||||
Sbjct: 33179693 cagctgcaag 33179684


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 423,395
Number of Sequences: 54
Number of extensions: 423395
Number of successful extensions: 10
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
```

```
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 7
Number of HSP's gapped (non-prelim): 1
length of query: 361
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 315
effective length of database: 1,133,627,092
effective search space: 357092533980
effective search space used: 357092533980
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|48256725|gb|AY622345.1| Pseudonigrita arnaudi clone GCSW41
microsatellite sequence
         (360 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr4                                                                  174   1e-041

>chr4
          Length = 90634903

 Score =  174 bits (109), Expect = 1e-041
 Identities = 188/257 (73%), Gaps = 12/257 (4%)
 Strand = Plus / Minus


Query: 106      aaaatccagaatcacagaaagaagttctgtatgagtgaaagcagagattcattcacattc 165
                ||||| |||||||||| ||||||||| |||  ||||||||||| ||| | |   ||||||
Sbjct: 65582204 aaaatgcagaatcacataaagaagttatgtgcgagtgaaagcacagactaagatacattc 65582145


Query: 166      tttcaaa-tcccaacgacaaaacctaaatacatatatgcttaattattgtattcctttaa 224
                 | |||| ||  ||   ||||||  |||| | || | |||||||||||| ||||| ||||
Sbjct: 65582144 ctacaaattctgaagcccaaaacacaaatgcctacacgcttaattattgcattcccttaa 65582085


Query: 225      aaactagtataccaaagttggatactgatgatgcaattctaagagacgtattccaagaga 284
                ||  |||||||||  || || |||  ||  |||  | || ||      |||  | ||  |
Sbjct: 65582084 aatgtagtataccgcaggtgcata--ga-aatgacagtcaaa------tatcacgagtaa 65582034


Query: 285      aattcttaaagtttaaa--ctatgtttttagaagaaataaaacaaagcttatatggattt 342
                || ||||| | ||||||   | |||||| ||| |||||||||  ||| ||| ||| ||||
Sbjct: 65582033 aagtcttacactttaaatgttgtgttttcagaggaaataaaatgaaggttacatgaattt 65581974


Query: 343      aataatagcttttaaag 359
                |||| ||  ||||||||
Sbjct: 65581973 aatactacattttaaag 65581957


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54
```

```
Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 394,982
Number of Sequences: 54
Number of extensions: 394982
Number of successful extensions: 10
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 8
Number of HSP's gapped (non-prelim): 1
length of query: 360
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 314
effective length of database: 1,133,627,092
effective search space: 355958906888
effective search space used: 355958906888
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|48256726|gb|AY622346.1| Pseudonigrita arnaudi clone GCSW45
microsatellite sequence
         (284 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chrZ_random                                                           106   3e-021

>chrZ_random
          Length = 14994570

 Score =  106 bits (66), Expect = 3e-021
 Identities = 104/138 (75%), Gaps = 7/138 (5%)
 Strand = Plus / Plus


Query: 3       tcanncaatgtaaaatt-atggcttgt--ttcacacccaggtccttaataacatgctttg 59
               |||   |||| ||| || ||||||| |  ||  ||| ||  || | ||||   ||| |||
Sbjct: 8163770 tcaggtaatgcaaactttatggcttttatttttcactcaaatcttgaatagtgtgccttg 8163829


Query: 60      gtatgcagtgtccttaatgaacttctgacacttcagtggatacagtctattgcaatctga 119
                | ||||||||||||||||||||||||| |||||||||| | |||||| || ||  |||
Sbjct: 8163830 ttgtgcagtgtccttaatgaacttctgaaacttcagtggttgcagtctgttccaggctg- 8163888


Query: 120     aactgtttttattctgtt 137
                  |||||||||||| ||
Sbjct: 8163889 ---tgtttttattctttt 8163903
```

```
  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 196,099
Number of Sequences: 54
Number of extensions: 196099
Number of successful extensions: 2
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 1
Number of HSP's gapped (non-prelim): 1
length of query: 284
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 238
effective length of database: 1,133,627,092
effective search space: 269803247896
effective search space used: 269803247896
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|48256727|gb|AY622347.1| Pseudonigrita arnaudi clone GCSW47
microsatellite sequence
         (439 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr11                                                                 139   5e-031

>chr11
          Length = 19020054

 Score =  139 bits (87), Expect = 5e-031
 Identities = 104/117 (88%), Gaps = 2/117 (1%)
 Strand = Plus / Minus


Query: 154     ctgcaggttgcaccagacaggggagaagtcccgactccatggctgcatctgcagtagcaa 213
               || ||||||||||||||| | ||||||||||||||| || |||||||||||||| |||||
Sbjct: 1797238 ctacaggttgcaccagacggaggagaagtcccgactgcacggctgcatctgcagcagcaa 1797179


Query: 214     ggttcctgatggctggggattactgtgtgaaggtaagcaccacaccttggagatgct 270
                ||||||| |||||||||||||||||||||||||||| ||||  || |||||| |||
Sbjct: 1797178 -gttcctggtggctggggattactgtgtgaaggtaaggaccatgcc-tggagaagct 1797124
```

```
  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 275,247
Number of Sequences: 54
Number of extensions: 275247
Number of successful extensions: 2
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 439
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 392
effective length of database: 1,133,627,038
effective search space: 444381798896
effective search space used: 444381798896
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|48256729|gb|AY622349.1| Pseudonigrita arnaudi clone GCSW51
microsatellite sequence
         (539 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr7                                                                  180   2e-043

>chr7
          Length = 37338262

 Score =  180 bits (113), Expect = 2e-043
 Identities = 188/257 (73%), Gaps = 18/257 (7%)
 Strand = Plus / Minus


Query: 283      agtctatttatcctgatttctctttctcacagtaaccaagaggaaaagcctagggtata 342
                ||||| ||||  || |||||||||     | | |||||||||  |||||| |||
Sbjct: 19070757 agtctgtttagtctaatttctctg----agactaaccaagaacaaaagcttag------ 19070708


Query: 343      gtataaaagtagggcaaacagagatatttgcccagaacactctccagccaagcatggttt 402
                       |||||||||| |||||| |||||||||| || | |||||||| ||||||||||
```

```
Sbjct: 19070707 -------agtagggcaagcagagagatttgcccagtacgcactccagcctagcatggttt 19070655


Query: 403      gtggctcagggatgtcttgatctggaagtgatctcttcatatttaattgctcttggtagg 462
                 ||||||| ||||| ||    || ||||||||||||||  ||||| |||||| |  |||||
Sbjct: 19070654 gtggctctgggatttcccagtccggaagtgatctctttgtatttgattgctttcagtagg 19070595


Query: 463      cttttctgctgtgcagttcttcattaacatgtagtgatcatacangcattgctcagacag 522
                 ||||||| |||   | || |||| | ||   || |||| ||||| ||||  || | | ||
Sbjct: 19070594 cttttctcctgcaaattttttcaatcactcatattgattataca-gcatcactgaaagag 19070536


Query: 523      tgggagagacatcactt 539
                   | |||| ||||||||
Sbjct: 19070535 cagaagaggcatcactt 19070519


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 535,226
Number of Sequences: 54
Number of extensions: 535226
Number of successful extensions: 9
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 7
Number of HSP's gapped (non-prelim): 2
length of query: 539
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 492
effective length of database: 1,133,627,038
effective search space: 557744502696
effective search space used: 557744502696
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|48256731|gb|AY622351.1| Pseudonigrita arnaudi clone GCSW57
microsatellite sequence
         (636 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr2                                                                  125   1e-026
```

```
>chr2
          Length = 147590765

 Score =  125 bits (78), Expect = 1e-026
 Identities = 150/214 (70%), Gaps = 4/214 (1%)
 Strand = Plus / Minus


Query: 137      aaaaagccaggaaactgttacattatgagatccacgtgctccaggtctggctctgagttc 196
                |||||   ||||||   | ||| ||| |||||   || |||||| |||||||||||||||
Sbjct: 80705881 aaaaaaataggaaataatgacactatcagatctctgtactccagatctggctctgagttc 80705822


Query: 197      tcattttggtgtct-ctaaaatattcatgtgtctttcagagtatttcttgatttcaaaaa 255
                | |||||| ||||| |   || | || || || ||||||  | ||||||||||| ||| |
Sbjct: 80705821 ttattttgatgtctacatgaagaatcctgggtgtttcagtttgtttcttgattttaaaga 80705762


Query: 256      cactgttgagcacaggttaatggtgttttggtgttttgatgcatgtgtatgtattggga- 314
                |  | | ||  |||  |   |||||      ||  | ||||| |  ||||| |||||||
Sbjct: 80705761 ctgtctagaaaaca-ttggttggtgagcacatgcgtagatgcttaagtatggattgggat 80705703


Query: 315      acctggtctggtcactgaaggctgaaaatactca 348
                 ||||| ||||  ||| |  |||| |||| ||||
Sbjct: 80705702 tcctgg-ctggggactcacagctgcaaatgctca 80705670


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 454,493
Number of Sequences: 54
Number of extensions: 454493
Number of successful extensions: 2
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 1
Number of HSP's gapped (non-prelim): 1
length of query: 636
length of database: 1,133,629,576
effective HSP length: 48
effective length of query: 588
effective length of database: 1,133,626,984
effective search space: 666572666592
effective search space used: 666572666592
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|3955290|gb|AF081928.1|AF081928 Geospiza fortis clone gf2.32
microsatellite repeat region
```

```
         (423 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr1                                                                 361   7e-098
chr26                                                                152   7e-035

>chr1
          Length = 188239860

 Score =  361 bits (227), Expect = 7e-098
 Identities = 264/333 (79%), Gaps = 5/333 (1%)
 Strand = Plus / Minus


Query: 1        taaggctttgacaattgtgacagccagaagttcattctcataatcgtaccggagagtgaa 60
                |||||||||||||||||||||||||| |||||||||||||||||| ||||||||||||||
Sbjct: 55332626 taaggctttgacaattgtgacagccaaaagttcattctcataatcataccggagagtgaa 55332567


Query: 61       gttaagttttccgcatgttttcacatcttcttgttgcccgtcagaatccacagacttctg 120
                 ||||||||||||||||||||||||||||||||||| || ||||||||||||||||||||
Sbjct: 55332566 attaagttttccgcatgttttcacatcttcttgttgtccatcagaatccacagacttctg 55332507


Query: 121      tttgtagagttctggtttaattctcccaatgctggttgtggtcntctcccctttgcaaaa 180
                |||||||||||||||||| ||||||||||||||||| || ||| ||||| ||||| ||||
Sbjct: 55332506 tttgtagagttctggttttattctcccaatgctggtcgtcgtc-tctcctctttgtaaaa 55332448


Query: 181      ccgggtctgtccccatgttaaagtcaacactggacacctgcatctgccttggcaagtgcc 240
                  || ||||||||||||||||| |||||||||||||| ||||||||||||||||| ||||
Sbjct: 55332447 ttggatctgtccccatgttaaaatcaacactggacacttgcatctgccttggcaaatgcc 55332388


Query: 241      tcctgaaggaattgtgcctgnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 300
                ||||||| ||||||||||||
Sbjct: 55332387 tcctgaaagaattgtgcctgcacacatacacacacagaacgagccatggttatctccagg 55332328


Query: 301      aaacaacgatggttat--ctatg-agaaaagac 330
                |||  ||  ||| |||  ||| | |||| | ||
Sbjct: 55332327 aaaagac-ctggctattactaagtagaacatac 55332296


>chr26
          Length = 4255270

 Score =  152 bits (95), Expect = 7e-035
 Identities = 182/262 (69%), Gaps = 13/262 (4%)
 Strand = Plus / Plus


Query: 2       aaggctttgacaattgtgacagccagaagttcattctcataatcgtaccggagagtgaag 61
               || ||  ||| |||   ||||| |||    || |||||||| ||||||  ||||||||||
Sbjct: 2384036 aaagccctgagaatccggacagtcagcgtctcgttctcatagtcgtacttgagagtgaag 2384095


Query: 62      ttaagttttccgcatgttttcacatcttcttgtt---gcccgtcagaatccacagacttc 118
               |||| ||| || || |||||  |  |||||| ||   |  | ||||| || ||||||||
Sbjct: 2384096 ttaattttcccacaggtttttgctgcttcttttttggggtcctcagagtcaacagacttt 2384155


Query: 119     tgtttgtagagttctggtttaattctcccaatgctggttgtggtcntctcccctttgcaa 178
               || |||||||| || || ||||| |  || ||||      |||||  ||   ||  || |
Sbjct: 2384156 tgcttgtagagctcaggcttaatgcggccgatgc------tggtcggct--gctcggcga 2384207


Query: 179     aaccgggtctgtccccatgttaaagtcaacactggacacctgcatctgccttggcaagtg 238
                  |||||  ||  |||||  | |||| |  ||||| || ||||||||||  || | |||
```

```
Sbjct: 2384208 tggcgggtgggt--ccatgccatagtccatgctggatacgtgcatctgccggggaaggtg 2384265


Query: 239     cctcctgaaggaattgtgcctg 260
                ||  |||||||  ||||||||
Sbjct: 2384266 tcttttgaaggagatgtgcctg 2384287


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 326,277
Number of Sequences: 54
Number of extensions: 326277
Number of successful extensions: 24
Number of sequences better than 1.0e-005: 2
Number of HSP's better than  0.0 without gapping: 2
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 21
Number of HSP's gapped (non-prelim): 2
length of query: 423
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 376
effective length of database: 1,133,627,038
effective search space: 426243766288
effective search space used: 426243766288
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|3955292|gb|AF081929.1|AF081929 Geospiza fortis clone gf2.35
microsatellite repeat region
         (227 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr1                                                                  174   7e-042

>chr1
          Length = 188239860

 Score =  174 bits (109), Expect = 7e-042
 Identities = 152/211 (72%), Gaps = 18/211 (8%)
 Strand = Plus / Minus


Query: 2        ctcttcttgaagcacctacattaaaacactgggagtgaagtctgacacnnnnnnnnnnnn 61
```

```
                  || ||||||||||| |||||  |||||   | |||||||||||||||
Sbjct: 48904859 ctttcttgaagcatctacaccaaaaccaagagagtgaagtctgacattttgtgtgtgc 48904800


Query: 62       nnnnnnnnnnnnnnnnnccatgcatggttcagcattgccattcatcttcactctccaaat 121
                                        || ||||| |||||||||||||| ||  ||||||||
Sbjct: 48904799 acgtgtg-----------------tgcttcagaattgccattcatctccagcctccaaat 48904757


Query: 122      caacaattatctggagtcccccaggagggaaatgcactcctctcataagcttgcnagtaa 181
                ||||||||||| |||||||||||||||||||||||   |||| |||||||| ||  |||||
Sbjct: 48904756 caacaattatatggagtcccccaggagggaaatgtgttcctgtcataagcatg-gagtaa 48904698


Query: 182      tgactaggaagcagtggtgtgtaacaggatc 212
                ||||| |||||||||||||||||||||||||
Sbjct: 48904697 tgacttggaagcagtggtgtgtaacaggatc 48904667


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 138,858
Number of Sequences: 54
Number of extensions: 138858
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 2
length of query: 227
length of database: 1,133,629,576
effective HSP length: 45
effective length of query: 182
effective length of database: 1,133,627,146
effective search space: 206320140572
effective search space used: 206320140572
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|3955294|gb|AF081930.1|AF081930 Geospiza fortis clone gf2.40
microsatellite repeat region
         (300 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value
```

```
chr1                                                                 95   7e-018

>chr1
          Length = 188239860

 Score = 95.1 bits (59), Expect = 7e-018
 Identities = 76/91 (83%), Gaps = 2/91 (2%)
 Strand = Plus / Minus


Query: 1        tgctcataggaaaaagtcatccgaaacacccgagagctattgagctaactaaataaacaa 60
                |||||| |||||||||||||| |||| ||| ||||||||  ||||| ||||||||||||
Sbjct: 29482493 tgctcacaggaaaaagtcatctgaaatacctgagagctagcgagctgactaaataaacag 29482434


Query: 61       ctc--gagacagtgaatgtatagatgtaaaa 89
                |||  |||| |||||||||| | || | |||
Sbjct: 29482433 ctccagagatagtgaatgtacatattttaaa 29482403


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 207,058
Number of Sequences: 54
Number of extensions: 207058
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 1
Number of HSP's gapped (non-prelim): 2
length of query: 300
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 254
effective length of database: 1,133,627,092
effective search space: 287941281368
effective search space used: 287941281368
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|3955296|gb|AF081931.1|AF081931 Geospiza fortis clone gf2.41
microsatellite repeat region
         (322 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



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

```
  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 260,736
Number of Sequences: 54
Number of extensions: 260736
Number of successful extensions: 4
Number of sequences better than 1.0e-005: 0
Number of HSP's better than  0.0 without gapping: 0
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 4
Number of HSP's gapped (non-prelim): 0
length of query: 322
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 276
effective length of database: 1,133,627,092
effective search space: 312881077392
effective search space used: 312881077392
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|3955312|gb|AF081940.1|AF081940 Geospiza fortis clone gf12.16
microsatellite repeat region
         (249 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr1                                                                  191   4e-047

>chr1
          Length = 188239860

 Score =  191 bits (120), Expect = 4e-047
 Identities = 148/172 (86%), Gaps = 2/172 (1%)
 Strand = Plus / Plus


Query: 78        cacagagctatgtgcatggtggattaggcttagctggatgcaagga-gttggttgagttc 136
                 |||| || ||||  |||||||||||||||  ||| |||||| |||| |||||||||||||
Sbjct: 171499900 cacacaggtatgcacatggtggattaggccaagccggatgccaggatgttggttgagttc 171499959


Query: 137       atgacattttttcctttgaaaccatagcaaccaccaaaacccaaatactggaactagaat 196
                 ||||||||||||||||||| ||||| |||| |||   ||  |||||||||||| ||||||
Sbjct: 171499960 atgacattttttcctttgataccatggcaatcactgcaaaacaaatactggaattagaat 171500019
```

```
Query: 197       tgaaatgcatttctcgtaataaacacccttctc-tttcccagacttaagcca 247
                 ||||||||||||||  |||||||||||  |||| |||||||||||| |||||
Sbjct: 171500020 tgaaatgcatttcttctaataaacacctctctcttttcccagacttgagcca 171500071


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 189,409
Number of Sequences: 54
Number of extensions: 189409
Number of successful extensions: 2
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 249
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 203
effective length of database: 1,133,627,092
effective search space: 230126299676
effective search space used: 230126299676
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|2073031|gb|U97548.1|TGU97548 Taeniopygia guttata
microsatellite, complete sequence
         (308 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr1                                                                  188   4e-046

>chr1
          Length = 188239860

 Score =  188 bits (118), Expect = 4e-046
 Identities = 213/295 (72%), Gaps = 24/295 (8%)
 Strand = Plus / Minus


Query: 14        cagcaactcaaag-----cttcctttgttaatttaaaacaaa-----acaaagccttaaa 63
                 ||| ||||||||      ||||||| | | ||||||||||||     ||||  || |||
Sbjct: 123155972 cagtaactcaaaagtcttcttccttcgcttatttaaaacaaagcgaaacaagcccataag 123155913
```

```
Query: 64        ggcttctacaagcttgggcaaaagaagaattctggtgacttggactagtaatttgttttt 123
                 |||| ||||| |||||||||||| || ||||   |||||||| ||||  || ||| ||||
Sbjct: 123155912 ggctcctacatgcttgggcaaaacaaaaatttgagtgacttgaactaagaaattgctttt 123155853


Query: 124       gagtacaagggctgcagtattttgatttaagagaacccagtcaattyga----tgtttac 179
                 || |||| || ||| || ||||||  |||| ||||||| ||| ||| ||    |  |||
Sbjct: 123155852 gaatacacggactgtaggattttgccttaaaagaaccctgtcgatttgaaaggttgttaa 123155793


Query: 180       ttttaaaactctgaatttaaagtaattttggatatagcaccttgtcctaatgtctct-ct 238
                 |||||||||     |||| |||| ||||| | | ||||| |||||||| |||||| | ||
Sbjct: 123155792 ttttaaaac-----attttaagtcattttaggtgtagcatcttgtcctgatgtctttact 123155738


Query: 239       g---ctatggcttacaactga-attttttccctaggaaatagggtacttctctctc 289
                 |    | ||| |||  | | |  ||||||  |||||||| | ||  ||||| |||
Sbjct: 123155737 gtgtttttggtttatgatttatttttttctttaggaaatggtgtggttctccctc 123155683


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.334    0.550

Gapped
Lambda     K      H
    1.10    0.334    0.550


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 378,124
Number of Sequences: 54
Number of extensions: 378124
Number of successful extensions: 7
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 6
Number of HSP's gapped (non-prelim): 1
length of query: 308
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 262
effective length of database: 1,133,627,092
effective search space: 297010298104
effective search space used: 297010298104
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.6 bits)
S1: 14 (23.8 bits)
S2: 34 (55.6 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|21321427|gb|AF501739.1| Ramphocelus costaricensis
microsatellite sequence
         (412 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters
```

```
                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr1                                                                  120   2e-025

>chr1
          Length = 188239860

 Score =  120 bits (75), Expect = 2e-025
 Identities = 191/295 (64%), Gaps = 12/295 (4%)
 Strand = Plus / Minus


Query: 122      atcctacccatatgctcacatttttgttagcagcctgggtggggctctgcatattcagca 181
                |||||||  ||| || ||||| ||  |||  || || ||||| ||||||  | |||||||
Sbjct: 34854886 atcctacttataggcccacatattgcttactagacttggtggagctctgtgtgttcagca 34854827


Query: 182      gtgttttg---ccattaatgagcactgattttgctatactgggggactgaattatgcctc 238
                | | ||||   |||  | |  |||| || ||||||  | ||| | |    |  |||||||
Sbjct: 34854826 gggatttgaagccaaaagtaggcacagagtttgctggattggagcagaagagcatgcctc 34854767


Query: 239      ccctcctcccacctgtcg-----tacctgtcattttctagctaagctcttcaaacagtag 293
                | |||||  || || ||      | ||||   |||||| |||||||||| |||||  |
Sbjct: 34854766 ctctcctttcatctatccatttttgcctgctgttttctggctaagctctgcaaaccatca 34854707


Query: 294      tgtgcttgattctctttccccaaaagtcatctcacccctacctgttgcctctctcaccct 353
                 |  |||| ||| |  || | |  || |  ||| || || ||     |||  |    | |
Sbjct: 34854706 -gcacttggttcgccctctc-agcagccc-ctctccactgcccaccacctgcccatgcat 34854650


Query: 354      aatgccatggcc-ctgtctccatccctgaatagctgtctcctgcaagctccatct 407
                    || | ||| | | |||||||||  |  ||||| |||||||||||| || ||
Sbjct: 34854649 gggccctttgccaccgcctccatcccccagcagctgcctcctgcaagcttcagct 34854595


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 262,663
Number of Sequences: 54
Number of extensions: 262663
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 0
Number of HSP's successfully gapped in prelim test: 1
Number of HSP's that attempted gapping in prelim test: 3
Number of HSP's gapped (non-prelim): 1
length of query: 412
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 365
effective length of database: 1,133,627,038
effective search space: 413773868870
effective search space used: 413773868870
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]
```

```
Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|6468539|emb|X97562.2|HRU10MICS Hirundo rustica
microsatellite HrU10
         (1264 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr18                                                                 193   9e-047

>chr18
          Length = 8919268

 Score =  193 bits (121), Expect = 9e-047
 Identities = 228/322 (70%), Gaps = 22/322 (6%)
 Strand = Plus / Plus


Query: 469     aatgcagggatgattccgggaggacattcccagcactgcccccagcccagcggggct-gc 527
               |||| | |||||||  || |||| ||  || ||  || |  ||| |||| |  |  | ||
Sbjct: 1238809 aatgaaaggatgatctcgtgagggcaaccctagtgctcctaccaacccaactagctttgc 1238868


Query: 528     aatcagcaccaccaatccagacctt-ttccctgaggacagcacacctcagaagcgtcatc 586
               ||||||  | | | |||  | |||  ||||||||||||| || ||||||||  | | ||
Sbjct: 1238869 aatcagtgctaaccatcagggcctccttccctgaggacaacagacctcagagacataatt 1238928


Query: 587     tcatgctcctgctgtcagctgccttgcccaatttatcttctcattacccctttaa---ca 643
               |||||||| |||||||||||||||||| |||||||||||||||||||| ||||||   ||
Sbjct: 1238929 tcatgctcttgctgtcagctgccttgcacaatttatcttctcattacctctttaacagca 1238988


Query: 644     acgct--------gctgttcgaggaa-ataactcttgtngtgganacntttgctttggat 694
               | |||         ||| | |||||| |||||||||||  |||| |   | ||| ||||
Sbjct: 1238989 atgctaatcactgactgatggaggaagataactcttgtgatggagaaactggctctggaa 1239048


Query: 695     ataaagc----actgatatttttatgcagcaatataaatgttaaattcctgcagccagtg 750
               |||||||    | | || ||  |||||  ||||||||  |||   |  ||| ||||||
Sbjct: 1239049 ataaagcagtaaataatgttgctatgctacaatataa--gttgcct--ctgtagccagca 1239104


Query: 751     cctggaagaacttgggaaggtg 772
                    ||||  |||||||||||
Sbjct: 1239105 tgctaaagagtttgggaaggtg 1239126


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 1,007,497
Number of Sequences: 54
```

```
Number of extensions: 1007497
Number of successful extensions: 4
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 1
length of query: 1264
length of database: 1,133,629,576
effective HSP length: 49
effective length of query: 1215
effective length of database: 1,133,626,930
effective search space: 1377356719950
effective search space used: 1377356719950
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|53801370|gb|AY684067.1| Hemignathus virens clone Hvir62
microsatellite sequence
         (177 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr1                                                                  106   2e-021

>chr1
          Length = 188239860

 Score =  106 bits (66), Expect = 2e-021
 Identities = 103/162 (63%), Gaps = 6/162 (3%)
 Strand = Plus / Plus


Query: 1        atgcagcatttccctcagtcaatcttccttgtgacactggggcttagatagatagggcaa 60
                ||||||||||||||||||||| || ||||||||||||| ||| ||| | ||| ||||| |
Sbjct: 46832469 atgcagcatttccctcagtcagtcatccttgtgacact-gggtttacacagaaagggcga 46832527


Query: 61       attaaattaaacagccatttaattccgtagcccttccctccgacacccaggacacaggca 120
                ||| |   ||| |||||   || |||  |||||||||| |||   ||||   ||||||||
Sbjct: 46832528 attga---aaaaagccacaaaactccccagcccttccccccg--ccccaacccacaggca 46832582


Query: 121      tnnnnnnnnnnnnnnnnnnnngcaccancctnnnnnnnatga 162
                                      |||   |||        |||
Sbjct: 46832583 cacgcacccagacgcacacacacacacccctaccctacttga 46832624


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549
```

```
Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 105,294
Number of Sequences: 54
Number of extensions: 105294
Number of successful extensions: 2
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 1
Number of HSP's gapped (non-prelim): 1
length of query: 177
length of database: 1,133,629,576
effective HSP length: 45
effective length of query: 132
effective length of database: 1,133,627,146
effective search space: 149638783272
effective search space used: 149638783272
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 33 (53.9 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|13958987|gb|AF361037.1|AF361037 Vidua chalybeata clone
INDIGO 7 microsatellite sequence
         (464 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr2                                                                  175   5e-042

>chr2
          Length = 147590765

 Score =  175 bits (110), Expect = 5e-042
 Identities = 272/436 (62%), Gaps = 43/436 (9%)
 Strand = Plus / Plus


Query: 3        tccagcttgtttaatcacagatgaaggcacagatg-----ccagaaatattcctcctcat 57
                ||||||   || ||| | ||| ||   ||||| ||     ||||||||||||||||||||
Sbjct: 69427459 tccagcacattcaatgatagaaga---cacagctgttgtgccagaaatattcctcctcat 69427515


Query: 58       atatattacctatgttcttcctaaagcacatgattcatcaccttgagtgaaataagaagt 117
                ||| |  ||| |  |||||||  |||||||  ||| | | || ||| || ||| | ||||
Sbjct: 69427516 atacacaacccacattcttccataagcaca--atttagctccctgaatgcaattacaagt 69427573


Query: 118      attcaatgcatttttatgctatcaagtcaagaataaaagctatagaatgaaataaaataa 177
                 || ||   ||||| |   |||||| | || ||||||| ||||||  |||||  || ||
Sbjct: 69427574 gtttaacatattttcacagtatcaaataaaaaataaaatctatagtgtgaaactaagtag 69427633


Query: 178      caatattaaatttccttatttcctatgagtttctcattgctaagattaannnnnnnnnnn 237
                ||  ||||||||||||||||||   |||||||  ||||| ||||
Sbjct: 69427634 cagaattaaatttccttatttctattgagttttgcattgttaag-----------tagac 69427682
```

```
Query: 238      nnnnnnnnnnnnaatgcagcaaccaactaaaatttgagnnnnnnncaagcacagtctcct 297
                             || |||||| |      || || ||        ||          ||
Sbjct: 69427683 ttttgttttaaatatacagcaagc-----taagtttagctggaaataa--------aact 69427729


Query: 298      tgga-caaatctttcttggctaatg-aaaacatctggttcaaattcactgcagcttttat 355
                | || ||||| |||||  | |  ||   ||| | |   | ||| | | ||    | |||
Sbjct: 69427730 tagagcaaatttttctcaggtgctgccgaacttgtatgtaaaaat-aatg----tcttaa 69427784


Query: 356      tgtaaataaaaaatttgggaagttgtcaatattatttagtcttatagtcagttcaaggaa 415
                ||||  |  ||| |||   |||| |||||||| |||  ||||  |||||| || || |||
Sbjct: 69427785 tgtagtttcaaattttaaaaagtggtcaatatcattatgtct--tagtcattttaatgaa 69427842


Query: 416      agactgaaaactgcaa 431
                |||||||||   ||||
Sbjct: 69427843 agactgaaattagcaa 69427858


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 491,514
Number of Sequences: 54
Number of extensions: 491514
Number of successful extensions: 20
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 18
Number of HSP's gapped (non-prelim): 1
length of query: 464
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 417
effective length of database: 1,133,627,038
effective search space: 472722474846
effective search space used: 472722474846
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|13958990|gb|AF361040.1|AF361040 Vidua chalybeata clone
INDIGO 27 microsatellite sequence
         (531 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value
```

```
chr8                                                                    103   5e-020

>chr8
          Length = 30024636

 Score =  103 bits (64), Expect = 5e-020
 Identities = 277/522 (53%), Gaps = 69/522 (13%)
 Strand = Plus / Minus


Query: 6        aacca-atataagctgatctgtcaattttacaggtagtaggaactaaaaatcaattccaa 64
                 ||||| ||| || |  |||  | ||| ||| |||| |||  ||  || | ||| ||
Sbjct: 17712523 aaccacataaaaacccatccctgaatattataggtggtaaaaaaaaatactcagttttt- 17712465


Query: 65       tgagaagacaggaggctggacttaagtcttcaggaagatttctcaatagggatactccct 124
                           |||| ||||| ||||| | |||||| ||||| |||| |||  | |  | |
Sbjct: 17712464 ----------ggagactggatttaagccctcaggaggatttttcaacaggtcttccactt 17712415


Query: 125      gactgaaggaatgcatctattcatgcacagtcaatcatttggtggtacgcactacattgt 184
                   ||||  |||| |||||| |||  |||   ||||||||   || || | | | | | || |
Sbjct: 17712414 --ctgatagaatacatctagtca--cacta-caatcattccttgataagaattgcttttt 17712360


Query: 185      ctgtgttttat-atgacacttccagaaacatatcaaaatacatctggtttaccttttact 243
                  ||| || | | | ||||  |  ||||| || | |||||        | || ||||  ||
Sbjct: 17712359 -tgtcttgtcttaagacatctttagaaatatgtaaaaatt-------tctagcttt--ct 17712310


Query: 244      gagttctgatggattatcagaggtatttctgccccacnnnnnnnnnnnnnnnnnnnnnnn 303
                    ||||| || ||||||||| |||  | ||||  ||
Sbjct: 17712309 atcttctgctgaattatcagaagtacctgtgcc--actgcatatatatcacgtatggact 17712252


Query: 304      nnnnnnnnnnnnnnnnntnnnnnnnnnnnnnnnnnnnnnnnnnnnnntgagctttgaatt 363
                                                                | || | | | |
Sbjct: 17712251 ttcctttttttggcaaggaaaaaaagtatctactccaacagcagaagat-agttctcagta 17712193


Query: 364      tacctcttgtttttccaggaaaaatgtaaatctattacaacagcagaagatattttcaac 423
                   || |  ||||  |||     ||| ||  |   | |||  |||        |  ||| |
Sbjct: 17712192 acccacaagttt--cca-----aat-tacttagttgacataagc--------tcgtcagc 17712149


Query: 424      tgactttagtgataccagtttgtgtctgaaaatgctataggctgagaacccatttcataa 483
                  |       || ||| ||       | | ||||||||| | ||||||| ||||||||||
Sbjct: 17712148 agc------tgctac-ag-------caggaaatgctatggcctgagaatccatttcata- 17712104


Query: 484      cagtgatacacgaattcttagccaccatangccatacagcat 525
                        |||| |||||| |||||| | | ||||||||||||
Sbjct: 17712103 -------acactaattctaagccacaacaggccatacagcat 17712069


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 390,779
Number of Sequences: 54
Number of extensions: 390779
Number of successful extensions: 6
Number of sequences better than 1.0e-005: 1
```

```
Number of HSP's better than  0.0 without gapping: 0
Number of HSP's successfully gapped in prelim test: 1
Number of HSP's that attempted gapping in prelim test: 5
Number of HSP's gapped (non-prelim): 1
length of query: 531
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 484
effective length of database: 1,133,627,038
effective search space: 548675486392
effective search space used: 548675486392
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|13958995|gb|AF361045.1|AF361045 Vidua chalybeata clone
INDIGO 38 microsatellite sequence
         (476 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr3                                                                  291   8e-077

>chr3
          Length = 108638738

 Score =  291 bits (183), Expect = 8e-077
 Identities = 231/277 (83%), Gaps = 1/277 (0%)
 Strand = Plus / Plus


Query: 88        ttta-ggcctggcccaagtagatcctcccaacctccctggcagccaggactggccagtga 146
                 |||| ||||||||   ||  | || | ||| | ||||| |||||||| | || ||  |||
Sbjct: 105444458 tttatggcctggcttgagagggtctttccaccttccctagcagccagcagtgacccatga 105444517


Query: 147       ggctctcatgtaacccctcatgctgtccttccccagtatgaccagtacaagacgcccatg 206
                 |  |||| ||||| ||||        |||     ||||||||||||||||||||||||||
Sbjct: 105444518 gagtctcttgtaatccctttcttcaacctcttgtagtatgaccagtacaagacgcccatg 105444577


Query: 207       gagaacatcggcctgcaggactccctgctctcccgttttgacctgctcttcatcgtgctg 266
                 |||||||| ||||||||||||||| |||||||||| || ||||||||||||||| |||||
Sbjct: 105444578 gagaacattggcctgcaggactccttgctctcccgcttcgacctgctcttcatcatgctg 105444637


Query: 267       gaccagatggaccccgagcaggacaaggagatctcggaccacgtcctgcggatgcaccgc 326
                 |||||||||||| | ||||||||||| ||||||||| || ||||||||||| |||||||||
Sbjct: 105444638 gaccagatggactctgagcaggacagggagatctcagatcacgtcctgcgaatgcaccgc 105444697


Query: 327       taccgcaaccccaacgagcaggatggggatggtgagt 363
                 ||||||||||||| |||||||||||||||||||||||
Sbjct: 105444698 taccgcaaccccaatgagcaggatggggatggtgagt 105444734


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54
```

```
Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 250,062
Number of Sequences: 54
Number of extensions: 250062
Number of successful extensions: 6
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 5
Number of HSP's gapped (non-prelim): 1
length of query: 476
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 429
effective length of database: 1,133,627,038
effective search space: 486325999302
effective search space used: 486325999302
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|13958996|gb|AF361046.1|AF361046 Vidua chalybeata clone
INDIGO 40 microsatellite sequence
         (449 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr3                                                                  182   6e-044

>chr3
          Length = 108638738

 Score =  182 bits (114), Expect = 6e-044
 Identities = 283/455 (62%), Gaps = 74/455 (16%)
 Strand = Plus / Plus


Query: 1        ctcttcttggtaaaaaggtatagaaatctattatatttt--taaaaatatgcctggcaga 58
                || ||||||||||||| || ||| || || | |||  ||  ||||||||| ||||||| |
Sbjct: 50088138 cttttcttggtaaaaacgtgtagcaaactgtaatacattcataaaaatattcctggcaaa 50088197


Query: 59       ctgaatgaatacagaaaacaaaaaccgaaacaacagaaacagttggtatatttaagtttt 118
                | ||||||||| |   |             || ||||| || ||| ||||||||||  |
Sbjct: 50088198 cagaatgaatataatta-------------cagcagaagcacttgctatatttaagcctg 50088244


Query: 119      attaattatgttcattctaagcctgtttttaaagctgatcataactttctgagagtgnnn 178
                ||  ||||| |||||||||||||| |||||||||| ||||||||||||    |||||
Sbjct: 50088245 atgtattattttcattctaagcctatttttaaagccgatcataacttt----gagtgtat 50088300
```

```
Query: 179      nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnngtatgtat 238
                                                                       |||||
Sbjct: 50088301 atttatc------------------------------------------------tgtat 50088312


Query: 239      gcgtgtaatgtagctaaattaccataaagcagc-ttgtttataaattacaaaacatataa 297
                | |||||| || |   |||||   || | | || ||||||||||||| ||   |||  ||
Sbjct: 50088313 gtgtgtaaggtggtacaattatggtacaccggcgttgtttataaattgcatg-catgcaa 50088371


Query: 298      gagtcaggacattcacttagcgttctcagtgaaccagtaattcacctgtc---tcaatac 354
                 |||||||||||||||| || ||| |   || |||  ||||| | || ||   | ||| |
Sbjct: 50088372 aagtcaggacattcactgagtgtttttgatgtacctataattaatctatcttgttaatgc 50088431


Query: 355      tcaatatagagaagtgctctgcttcatgttgactgtgattgcaagataccgagtgcannn 414
                 |  |||||  || ||||    |||||||| |||||||| | ||||||| |||||||
Sbjct: 50088432 gcggtataggaaattgctgaagttcatgttaactgtgatggtaagatactgagtgcattt 50088491


Query: 415      nnnnnnnccactggcttagcttgaaatgcttcaca 449
                        |||||||||| || |||   |||||||
Sbjct: 50088492 tttttt--cactggcttaactggaagcacttcaca 50088524


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 421,469
Number of Sequences: 54
Number of extensions: 421469
Number of successful extensions: 16
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 12
Number of HSP's gapped (non-prelim): 3
length of query: 449
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 402
effective length of database: 1,133,627,038
effective search space: 455718069276
effective search space used: 455718069276
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|51537957|gb|AY696183.1| Chasiempis sandwichensis sclateri
clone K49 microsatellite sequence
         (334 letters)
```

```
Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr2                                                                  156   2e-036

>chr2
          Length = 147590765

 Score =  156 bits (98), Expect = 2e-036
 Identities = 180/255 (70%), Gaps = 29/255 (11%)
 Strand = Plus / Minus


Query: 100      ttgctgaacttcattcatatgaatgtangtggcactttaataaaaagcattaaaaatatg 159
                |||||  | ||||||||||  |||| | || ||||||||||||||||| ||||  |||||
Sbjct: 63566047 ttgctacatttcattcataaaaatgaaagtagcactttaataaaaagtattatcaatatc 63565988


Query: 160      ttcaccttc--------cctg-----catccctt------atacttattccccatcatta 200
                ||   ||||        |||      ||| ||||      ||| |||||| ||| |||||
Sbjct: 63565987 ttagtcttcagcacatacctttttcacatacctttttcacatagttattctccaccatta 63565928


Query: 201      aantgtgtgagatgggatagtaaaatggatttgcaaatctgttatntctcctcaatactg 260
                ||  |||||||||||     | ||||||||||||||||||||||| |||||||| |||||
Sbjct: 63565927 aaaggtgtgagatgg-----ttaaatggatttgcaaatctgttatttctcctcagtactg 63565873


Query: 261      tagcctcaaaccctattatcagtttcagaatcggagctaggctgaag-----acagacat 315
                || | |||   | || || ||||| | ||| |  ||  |||||||||     | || |||
Sbjct: 63565872 taacttcagtgcttactaacagttactgaagcacaggcaggctgaagaaaaaaaaggcat 63565813


Query: 316      tttctaacagtcgag 330
                |||||| |  || ||
Sbjct: 63565812 tttctagcgatcaag 63565798


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 235,253
Number of Sequences: 54
Number of extensions: 235253
Number of successful extensions: 5
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 1
length of query: 334
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 288
effective length of database: 1,133,627,092
effective search space: 326484602496
effective search space used: 326484602496
T: 0
A: 0
```

```
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|51537961|gb|AY696187.1| Chasiempis sandwichensis sclateri
clone K91 microsatellite sequence
         (329 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr9                                                                  126   2e-027

>chr9
          Length = 23409228

 Score =  126 bits (79), Expect = 2e-027
 Identities = 198/337 (58%), Gaps = 48/337 (14%)
 Strand = Plus / Plus


Query: 1       ccttccaattctctataaagtattctctcccaaataaccagagaatatangtttagcaac 60
               |||||||||| |||||||| |||||||| ||| ||||||| | |||| |  |||||  ||
Sbjct: 2298868 ccttccaatttctataaactattctcttccacataaccaaacaataga--tttaggtac 2298925


Query: 61      tggaagtgtgggaatatatataaatgcacttcaaggtgctacagcttctctgccaccatc 120
               ||||| | |         | |        | ||  |||| |||||||| |||| |||| |
Sbjct: 2298926 tggaaattt---------ttt--------tgcagagtgcaacagcttccctgctaccagc 2298968


Query: 121     agtgcctctaaacagcctgcagggaacattaattt----gctcttaannnnnnnnnnnnn 176
               ||||||| |  ||||||| || || | |||  | |    |||  |||
Sbjct: 2298969 agtgcctttccacagcctccacggcaaattttgtcatagcttctaaacttcacagcaat 2299028


Query: 177     nnnnnnnnnnnnnnnnnnnnnnnnn--------------------cctgcatattaaatt 216
                                                            |||||||||||| ||
Sbjct: 2299029 tttatctttaaaacctaaaacattcttattgatatgtatatccatcctgcatattaagtt 2299088


Query: 217     tataaatctcatttaatg-gcattttacatgcagctttaccctacacagaaggtaaaac 275
               |||| | || ||||   | ||| |||||||||||   ||    ||||||||||||||||
Sbjct: 2299089 tatagaccttatttgagtgcacttttacatgcactcttttgttacacagaaggtaaaat 2299148


Query: 276     atcttaggaggtcgaggaagact-agtaaagggtcag 311
                ||||| |||  ||  ||||||| |  |||||| |||
Sbjct: 2299149 ctctta-gag--cgctgaagactgaaaaaagggccag 2299182


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549
```

```
Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 264,759
Number of Sequences: 54
Number of extensions: 264759
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 0
Number of HSP's successfully gapped in prelim test: 1
Number of HSP's that attempted gapping in prelim test: 3
Number of HSP's gapped (non-prelim): 1
length of query: 329
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 283
effective length of database: 1,133,627,092
effective search space: 320816467036
effective search space used: 320816467036
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|54292788|gb|AY752875.1| Chiroxiphia lanceolata clone 103-275
microsatellite sequence
         (180 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                  Score    E
Sequences producing significant alignments:                       (bits) Value

chr2                                                                    76   2e-012

>chr2
          Length = 147590765

 Score = 76.1 bits (47), Expect = 2e-012
 Identities = 104/188 (55%), Gaps = 15/188 (7%)
 Strand = Plus / Minus


Query: 1        cctctggcttctgggtgctctgtcctgtaactgaggagggaggaaggaggaggtcagtgc 60
                || |||||||| |||||||| ||||||||||||  |||||    |||||||||||||||
Sbjct: 90078389 cccctggcttcggggtgctcagtcctgtaactgcagaggg----aggaggaggtcagtg- 90078335


Query: 61       agggtcgactgctgccacagcagnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 120
                 ||| |    ||||||   ||||
Sbjct: 90078334 tggggctgtggctgcccgggcagacagacacacgctcactcagagatgggcaacgagcac 90078275


Query: 121      gggtgatgagcaaagagca-cggcagaagagctgaaagc--------aggcagaagcctg 171
                 || |  ||||  | |||| || |    || |  | |||        || ||||| | ||
Sbjct: 90078274 -ggagcagagctgaaagcagcgccctgggaccacatagccctcagaaagccagaaacatg 90078216


Query: 172      gtgatgaa 179
                ||||||||
Sbjct: 90078215 gtgatgaa 90078208


  Database: WholeChickenGenome.txt
```

```
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 135,427
Number of Sequences: 54
Number of extensions: 135427
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 1
length of query: 180
length of database: 1,133,629,576
effective HSP length: 45
effective length of query: 135
effective length of database: 1,133,627,146
effective search space: 153039664710
effective search space used: 153039664710
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 33 (53.9 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|21885931|emb|Y16820.2|LSC16820 Loxia scotica genomic
microsatellite sequence, LOX1
         (510 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr2                                                                  171   2e-040

>chr2
          Length = 147590765

 Score =  171 bits (107), Expect = 2e-040
 Identities = 129/161 (80%), Gaps = 4/161 (2%)
 Strand = Plus / Plus


Query: 324       tatatacatcatgccggccctttgannnnnnnnnnnnnnacaaaatcagatgtagagatt 383
                 ||||||| || |||  | |||||||                ||||||||||||||||  ||
Sbjct: 125040273 tatatacgtcgtgctagtcctttgatgtttacaaaaa----aaaatcagatgtagaggtt 125040328


Query: 384       ttgctgtaacaatagagtgaatgtgtgtggataacattactcacagtgctggtgagagtt 443
                 || |||  |||||||| ||||||||||||||||| ||||||||||| |||||| ||||||
Sbjct: 125040329 tttctgcgacaatagaatgaatgtgtgtggataatattactcacagcgctggtaagagtt 125040388
```

```
Query: 444       caaaggctggaatgtccagactaaatacacagcagaaagat 484
                 |||||||||||||||||||||||||||||||||  | ||||
Sbjct: 125040389 caaaggctggaatgtccagactaaatacacagccaagagat 125040429



 Score =  147 bits (92), Expect = 2e-033
 Identities = 107/119 (89%), Gaps = 6/119 (5%)
 Strand = Plus / Plus


Query: 1         gatcaaaatttctttttaatttgaaaagaagagangtgattaaaac-gaaaatgatggt 59
                 |||||||||||||||||||||||||||||| ||| ||||||||||| ||||||||||||
Sbjct: 125040061 gatcaaaatttctttttaatttgaaaagaacagaggtgattaaaactgaaaatgatggt 125040120


Query: 60        aagtctaatgaaagcttcctccctcc-----ttcccaagagctggtgtaatgggctgag 113
                  || ||||||||||||||||||||||     | |||||||||| |||||||||||||||
Sbjct: 125040121 gaggctaatgaaagcttcctccctccctccttccccaagagctagtgtaatgggctgag 125040179


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 310,710
Number of Sequences: 54
Number of extensions: 310710
Number of successful extensions: 7
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 4
Number of HSP's gapped (non-prelim): 2
length of query: 510
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 463
effective length of database: 1,133,627,038
effective search space: 524869318594
effective search space used: 524869318594
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|4138152|emb|Y16821.1|LSC16821 Loxia scotica genomic
microsatellite sequence, LOX2
         (519 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
```

```
Sequences producing significant alignments:                      (bits) Value

chr2                                                                  188   9e-046

>chr2
          Length = 147590765

 Score =  188 bits (118), Expect = 9e-046
 Identities = 225/319 (70%), Gaps = 18/319 (5%)
 Strand = Plus / Plus


Query: 199      catacggnnnnnnncttgtcttgccttgattgcgct--aaaaatccacatgaaactg--a 254
                |||| |          |||||||||    || |     |||||||| ||||||  |   |
Sbjct: 85981758 catatgagtttgcttgtgtcttgccccagttacatagaaaaaatcctcatgaagttccaa 85981817


Query: 255      ctgagaaac-agg-----acaatga--ttttttaaaattttgaattccactttttcttct 306
                ||||||||  |||     | || ||  ||||| |  ||||  ||| |  ||||  ||| |
Sbjct: 85981818 ctgagaaatgaggtactgagaaagaggtttttcagtatttctaatacatcttta-ctttt 85981876


Query: 307      tgttgttttgttatttgtatggaagtccacatgccaaggaaaatttgtggaatagtacaa 366
                |   ||||| | |||   |||||||| ||||| |||||| || ||| |  || ||| |||
Sbjct: 85981877 taa-gttttctcattcccatggaagtgcacataccaaggtaatttttttcaacagtgcaa 85981935


Query: 367      tttacaattgaatattttatagatagagc-aggaaaaagaaagtcagttttaacaatacg 425
                | |||| | ||| |  |||||| |||| | |||| ||| |  || |||| |||||| ||
Sbjct: 85981936 tatacagtggaaaaaattataggtagaactaggagaaata--gttagttgtaacaagaca 85981993


Query: 426      aataaagaatgt-ttcttgtgttatatatgaatcatgcaattagtgaattccactaagga 484
                ||| | |||||  || | |||||||  ||||||||||||||||||||||| |||||| |
Sbjct: 85981994 aatgaggaatgagttgtcgtgttatgaatgaatcatgcaattagtgaatttcactaaagg 85982053


Query: 485      tagtaattgttcattactt 503
                |||||||||||||||||||
Sbjct: 85982054 tagtaattgttcattactt 85982072


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 490,611
Number of Sequences: 54
Number of extensions: 490611
Number of successful extensions: 20
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 19
Number of HSP's gapped (non-prelim): 1
length of query: 519
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 472
effective length of database: 1,133,627,038
effective search space: 535071961936
effective search space used: 535071961936
T: 0
A: 0
X1: 7 (11.1 bits)
```

```
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|4138156|emb|Y16825.1|LSC16825 Loxia scotica genomic
microsatellite sequence, LOX8
         (642 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                  Score    E
Sequences producing significant alignments:                      (bits) Value

chr1                                                                  172   7e-041
chrUn                                                                  67   6e-009
chr13                                                                  59   1e-006

>chr1
          Length = 188239860

 Score =  172 bits (108), Expect = 7e-041
 Identities = 196/296 (66%), Gaps = 19/296 (6%)
 Strand = Plus / Plus


Query: 324      ctttcagtcatgtgacaaaaagagagcggaagaatctttttaatggcctcaactttagat 383
                ||||||   |||   |||||| ||| |   ||||| ||||| ||    ||||||  ||||
Sbjct: 38362941 ctttcaagtatgaatcaaaaacagaacaagagaatattttttataagttcaactaaagat 38363000


Query: 384      aaatttatctggaaac--tacaacattaga----------aaaagactgacttgactgac 431
                |||||||||   |||   || ||||| ||           |||||| | |||||||||||
Sbjct: 38363001 aaatttatccataaaacttataacatcagttaaaagttggaaaagaataacttgactgac 38363060


Query: 432      atttgaaattaggatagttaaatccatcccaacaagtag-------tggnnnnnnnnnnn 484
                 |||||| | ||  | |||||||  |||  |  || ||        |
Sbjct: 38363061 ttttgaagtaagagttgttaaattaatcatagtaattatcaataaatatttaactatttt 38363120


Query: 485      nnnnnnnctttgacccccttgtgaaaatatctgacatgcttctcttgagcaaaattgcat 544
                        |||   ||||||||| ||| |||||| |||| |  ||| |||||||||||||
Sbjct: 38363121 ttcatctttttattccccttgtggaaacatctgatatgccttacttcagcaaaattgcat 38363180


Query: 545      gaacttggatgtctgccttgcccagtatgtccaatgcaaatgaggtgagaagaaga 600
                ||| ||||||||||||||| |  ||||   ||| ||||||||||||||||||||||
Sbjct: 38363181 gaaattggatgtctgcctttcatagtacacccactgcaaatgaggtgagaagaaga 38363236


>chrUn
          Length = 165033910

 Score = 66.6 bits (41), Expect = 6e-009
 Identities = 41/41 (100%)
 Strand = Plus / Minus


Query: 1        ccaagcttgcatgcctgcaggtcgactctagaggatctaga 41
                |||||||||||||||||||||||||||||||||||||||||
Sbjct: 85415995 ccaagcttgcatgcctgcaggtcgactctagaggatctaga 85415955


>chr13
          Length = 17279963
```

```
 Score = 58.6 bits (36), Expect = 1e-006
 Identities = 36/36 (100%)
 Strand = Plus / Plus


Query: 2       caagcttgcatgcctgcaggtcgactctagaggatc 37
               ||||||||||||||||||||||||||||||||||||
Sbjct: 1053516 caagcttgcatgcctgcaggtcgactctagaggatc 1053551



 Score = 58.6 bits (36), Expect = 1e-006
 Identities = 36/36 (100%)
 Strand = Plus / Plus


Query: 2       caagcttgcatgcctgcaggtcgactctagaggatc 37
               ||||||||||||||||||||||||||||||||||||
Sbjct: 1051760 caagcttgcatgcctgcaggtcgactctagaggatc 1051795


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 444,521
Number of Sequences: 54
Number of extensions: 444521
Number of successful extensions: 16
Number of sequences better than 1.0e-005: 3
Number of HSP's better than  0.0 without gapping: 3
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 8
Number of HSP's gapped (non-prelim): 6
length of query: 642
length of database: 1,133,629,576
effective HSP length: 48
effective length of query: 594
effective length of database: 1,133,626,984
effective search space: 673374428496
effective search space used: 673374428496
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|37499684|gb|AY360359.1| Liocichla steerii microsatellite
lsgata7 sequence
         (284 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
```

```
Sequences producing significant alignments:                      (bits) Value

chr1                                                                 144   1e-032

>chr1
          Length = 188239860

 Score =  144 bits (90), Expect = 1e-032
 Identities = 160/272 (58%), Gaps = 12/272 (4%)
 Strand = Plus / Minus


Query: 1       ctgttcctgaacagcccagttggctgttttccctttcattaaattcattgga-------- 52
               ||| | |||||||||||| |||||||||||||||||||||||||| | || |
Sbjct: 1760306 ctgattctgaacagcccatttggctgttttccctttcattaaattaactgaaatacaata 1760247


Query: 53      ---tnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnaaacatttcc 109
                  |                                              ||||| ||||
Sbjct: 1760246 atgtagatagataattaaatagattgatagatggatgacagacagatgtaaaacacttcc 1760187


Query: 110     ttttttgcaatgatgtgtggtaaattaataaatactgatagatttaatttcagaaaaaag 169
                ||||||||| | |   |  ||| ||||| |||| | ||  ||||||||||| |||| ||
Sbjct: 1760186 ctttttgcaaagcttcctaataacttaatgaatattaattcatttaatttcaaaaaatag 1760127


Query: 170     caaagtaatgtagggtgtttgataattgactgaaagacagttattgagagggtgacttgt 229
               || || | | | ||   ||||||| || | | ||  | || |||||||| | || | |
Sbjct: 1760126 cagagaagtatgggacttttgatattttattcaaccagagctattgaga-gttgtcataa 1760068


Query: 230     tcaaattcagcctagggagtcaggttttcaaa 261
               |  | ||  | ||||| || ||| ||||| ||
Sbjct: 1760067 ttcagtttggtctaggtagacagattttccaa 1760036


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 288,226
Number of Sequences: 54
Number of extensions: 288226
Number of successful extensions: 4
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 1
length of query: 284
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 238
effective length of database: 1,133,627,092
effective search space: 269803247896
effective search space used: 269803247896
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]
```

```
Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|37499685|gb|AY360360.1| Liocichla steerii microsatellite
lsgata12 sequence
         (371 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chrZ                                                                   82   6e-014

>chrZ
          Length = 33651169

 Score = 82.4 bits (51), Expect = 6e-014
 Identities = 139/217 (64%), Gaps = 24/217 (11%)
 Strand = Plus / Plus


Query: 6        aagcaactcagatcataaaattaactaagtgagcacattacactg----------tctat 55
                ||| || |||||  ||||  ||  |||||  ||||||  ||||||          |||
Sbjct: 17549196 aagtaattcagagtataa--ttgcctaagcaagcacaggacactgctcgcaggagtctgc 17549253


Query: 56       tgcctgttgctgtattcctctgccacggtgaaagtaacaagactgtgtt----ccttcta 111
                ||| |||||||| ||||||||||  |  || |||||||||||| |  ||    || | |
Sbjct: 17549254 tgcatgttgctggattcctctgctccactggaagtaacaagacaggattcagaccctttc 17549313


Query: 112      ctttttactaaatgtc-------tacagcaattgtcatttcttacccattattttagtgc 164
                ||||||| | ||  ||        | |  ||     | | |||| |||||| ||||||||
Sbjct: 17549314 ctttttattgaaactccaacaaaaaaaaaaaaaaaaaatccttatccattactttagtgc 17549373


Query: 165      taggagtgattgtatacttttttggtttggtttactt 201
                | |   | |||  || | ||| |  ||| ||||||||
Sbjct: 17549374 tggatattattacattc-tttctatttttgtttactt 17549409


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 246,019
Number of Sequences: 54
Number of extensions: 246019
Number of successful extensions: 4
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 0
Number of HSP's successfully gapped in prelim test: 1
Number of HSP's that attempted gapping in prelim test: 4
Number of HSP's gapped (non-prelim): 1
length of query: 371
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 325
```

```
effective length of database: 1,133,627,092
effective search space: 368428804900
effective search space used: 368428804900
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|5852470|gb|AF129092.1|AF129092 Limnothlypis swainsonii clone
Lswmu9 microsatellite sequence
         (141 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr5                                                                  103   1e-020

>chr5
          Length = 56310377

 Score =  103 bits (64), Expect = 1e-020
 Identities = 84/100 (84%), Gaps = 2/100 (2%)
 Strand = Plus / Minus


Query: 3        tcatccac-agtgctcc-ttcatgagctggagcacatccaagaggcaatatgggaatttc 60
                ||||| || |||| ||| ||||    |||||    |||||||||| ||||||||||||||
Sbjct: 55257924 tcatctaccagtgttcccttcacacactggatagaatccaagaggtaatatgggaatttc 55257865


Query: 61       tgtatgcagttaaagtttatgagactgcctgcctgaatgc 100
                || ||| | ||||||||||||||||||||||||||||||
Sbjct: 55257864 tgaatgtacttaaagtttatgagactgcctgcctgaatgc 55257825


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 86,745
Number of Sequences: 54
Number of extensions: 86745
Number of successful extensions: 2
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 1
Number of HSP's gapped (non-prelim): 1
length of query: 141
length of database: 1,133,629,576
effective HSP length: 44
```

```
effective length of query: 97
effective length of database: 1,133,627,200
effective search space: 109961838400
effective search space used: 109961838400
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 33 (53.9 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|5852479|gb|AF129101.1|AF129101 Limnothlypis swainsonii clone
Lswmu11 microsatellite sequence
         (750 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                  Score    E
Sequences producing significant alignments:                       (bits) Value

chr2                                                                   144   2e-032

>chr2
          Length = 147590765

 Score =  144 bits (85), Expect = 2e-032
 Identities = 214/328 (65%), Gaps = 34/328 (10%)
 Strand = Plus / Minus


Query: 11       tacaatattcttt-gaactcaagtgtatgtgctaaacgttgcattcattacaaactgcat 69
                || ||  |||||| ||||| ||||| |  ||||||| ||| |||               |
Sbjct: 74667484 tagaaagttctttagaacttaagtgcacctgctaaatgttacatc--------------t 74667439


Query: 70       attactaatttaatttgaaggaggactgattccagttatgataccaacagctgcgaatgt 129
                ||||||||| ||||||||||||  |||||||||||||  ||||   |||    ||| |||
Sbjct: 74667438 attactaatgtaatttgaaggataactgattccagtttggatatgtaca---acgagtgt 74667382


Query: 130      aaaagtacagagatgaccaccttccattagcattaaaattc---atagga--ggtgggtt 184
                 ||||| |||| ||| | ||||| ||||  ||||| |||||   ||| ||  |||||| |
Sbjct: 74667381 gaaagtgcagacatggctacctt-cattgccattataattcacaataagatgggtgggat 74667323


Query: 185      aagcacttcacatwgtcattaca-ttgttttcctggggcaatcagaatgctgttg--aga 241
                || || ||||||   || ||||| || |||||||     |||| || || |  ||  ||
Sbjct: 74667322 aa-cagttcacactttccttacatttttttttcctataaaaatctgattgattatgttagg 74667264


Query: 242      cttgatgaaaatgt-gatatwgcaaagagccttaawctggcctagta--twtcacatkya 298
                  |||||||||| |    || || ||  || | || ||    | |||  | || |||
Sbjct: 74667263 gctgatgaaaatatctgcatagctaatggcttgaaact--atttgtaattttcccattt- 74667207


Query: 299      taaggygsccagtawamtattacaamat 326
                | ||     || |    ||||| || ||
Sbjct: 74667206 tgagctactcattgatctattataaaat 74667179


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
```

```
    1.17    0.344    0.583

Gapped
Lambda     K      H
    1.17    0.344    0.583


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 324,096
Number of Sequences: 54
Number of extensions: 324096
Number of successful extensions: 7
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 6
Number of HSP's gapped (non-prelim): 1
length of query: 750
length of database: 1,133,629,576
effective HSP length: 45
effective length of query: 705
effective length of database: 1,133,627,146
effective search space: 799207137930
effective search space used: 799207137930
T: 0
A: 0
X1: 6 (10.1 bits)
X2: 17 (28.6 bits)
S1: 13 (23.4 bits)
S2: 33 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|5852473|gb|AF129095.1|AF129095 Limnothlypis swainsonii clone
Lswmu14 microsatellite sequence
         (732 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr2                                                                  290   3e-076

>chr2
          Length = 147590765

 Score =  290 bits (182), Expect = 3e-076
 Identities = 228/283 (80%), Gaps = 7/283 (2%)
 Strand = Plus / Minus


Query: 1        gatcanngccacaacataaaggagaggaatctaaacagttggcttatctttgtccttcat 60
                |||||  |||||||||||||||| || |||||||||||||||||||||||||||||||||
Sbjct: 34040172 gatcaaagccacaacataaaggaaagaaatctaaacagttggcttatctttgtccttcat 34040113


Query: 61       tgtgacacaataccataaaattact-----atataaanggcaggcaaagcttcgtgcagc 115
                |||||||||||||||||||||||||     ||||||| |||| |||||||||| || |||
Sbjct: 34040112 tgtgacacaataccataaaattactttactatataaaaggcaagcaaagcttcatgtagc 34040053


Query: 116      acactctgaaanggtgaacttcttgttatgctcaacaaaatagataaactcttctgggag 175
                ||||||||||| ||||||||||||| || |||||||||||||||||||||||| |  |
Sbjct: 34040052 acactctgaaaaggtgaacttcttgctaggctcaacaaaatagataaactcttatcagta 34039993
```

```
Query: 176      atattttgngcagggnaacgtaaagttagcgmtgatgtctttagantttggaagaagttt 235
                ||||||||   | || || |||||||||||  | |  |||||  | |||| |  |||| |
Sbjct: 34039992 atattttgtataaggaaa-gtaaagttagctgttacatcttttcactttgaaccaagtct 34039934


Query: 236      ccacctntncctgccttgttaangcacaattanatntntntnt 278
                 || || |  ||||||| | ||  |||||| |  | | | | |
Sbjct: 34039933 tcatctttttctgcctttttcaaatcacaatgat-tttttatat 34039892



 Score = 77.7 bits (48), Expect = 3e-012
 Identities = 57/64 (89%), Gaps = 2/64 (3%)
 Strand = Plus / Minus


Query: 671      taggaaaaactctacaaggtctggagatattcta--ggaataaaaatcttgaatgatttt 728
                ||| ||||  |||||||| |||||||||||||||  ||||| ||||||||||||||||||
Sbjct: 34039729 tagtaaaagatctacaagctctggagatattctataggaattaaaatcttgaatgatttt 34039670


Query: 729      gatc 732
                ||||
Sbjct: 34039669 gatc 34039666


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.334    0.550

Gapped
Lambda     K      H
    1.10    0.334    0.550


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 385,178
Number of Sequences: 54
Number of extensions: 385178
Number of successful extensions: 5
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 2
length of query: 732
length of database: 1,133,629,576
effective HSP length: 48
effective length of query: 684
effective length of database: 1,133,626,984
effective search space: 775400857056
effective search space used: 775400857056
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.6 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|5852480|gb|AF129102.1|AF129102 Limnothlypis swainsonii clone
Lswmu17 microsatellite sequence
         (697 letters)

Database: WholeChickenGenome.txt
```

```
          54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr2                                                                  313   2e-083

>chr2
          Length = 147590765

 Score =  313 bits (197), Expect = 2e-083
 Identities = 296/444 (66%), Gaps = 15/444 (3%)
 Strand = Plus / Minus


Query: 1        gatcaaagccacaacataaaggagaggaatctaaacagttggcttatctttgtccttcat 60
                 ||||||||||||||||||||||| || |||||||||||||||||||||||||||||||||
Sbjct: 34040172 gatcaaagccacaacataaaggaaagaaatctaaacagttggcttatctttgtccttcat 34040113


Query: 61       tgtgacacaataccataanattact-----atataaanggcaggcaaagcttcgtgcagc 115
                 |||||||||||||||||| ||||||     ||||||| |||| |||||||||| || |||
Sbjct: 34040112 tgtgacacaataccataaaattactttactatataaaaggcaagcaaagcttcatgtagc 34040053


Query: 116      acactctgaaanggtgaacttcttgttatgctcaacaaaatagataaactcttctgggag 175
                 ||||||||||| ||||||||||||| || |||||||||||||||||||||||| |  |
Sbjct: 34040052 acactctgaaaaggtgaacttcttgctaggctcaacaaaatagataaactcttatcagta 34039993


Query: 176      atattttgtgcagggaaagtaaagttagcgcatgatgtctttagaatttggaagaagttt 235
                 |||||||||  | ||||||||||||||||   | |  |||||  | |||| |  |||| |
Sbjct: 34039992 atattttgtataaggaaagtaaagttagc-tgttacatcttttcactttgaaccaagtct 34039934


Query: 236      tcatcttttcctgccttnttaaagcacaattacatatatatannnnnnnnnnnnnnnnnn 295
                 ||||||||| ||||||| | ||| |||||| |  | | ||||
Sbjct: 34039933 tcatctttttctgccttttcaaatcacaatga-ttttttatattaaaatgcttttataaa 34039875


Query: 296      nnnnnnnctt-gca-atcttcattatatanctatccnacacc---accnnnnnnnnnnnn 350
                         ||  || || || ||  |  |   ||   |  ||
Sbjct: 34039874 tctatacattaacatattttaatattgaacaaatgtaatgcccttcagagtgaactatat 34039815


Query: 351      nnnnnnnnnnnnnnnnnctctgtggggt---gttgtgtgcgtctctgggagacaattaat 407
                                   |||||  | |    ||| |  | ||||||  | ||||||| |
Sbjct: 34039814 gatatgttttagaagtaatctgtatgatatgtttgggaacttctctgaaatacaattagt 34039755


Query: 408      caagacgntatatnacttgtagng 431
                 |||| |    | | ||||| || |
Sbjct: 34039754 caaggcacactgtcacttgaagag 34039731



 Score = 74.5 bits (46), Expect = 3e-011
 Identities = 56/64 (87%), Gaps = 1/64 (1%)
 Strand = Plus / Minus


Query: 635      taggaaaaactctacaaggtctggagatattac-taggaataaaaatcttgaatgatttt 693
                 ||| ||||  |||||||| ||||||||||||   ||||||| ||||||||||||||||||
Sbjct: 34039729 tagtaaaagatctacaagctctggagatattctataggaattaaaatcttgaatgatttt 34039670


Query: 694      gatc 697
                 ||||
Sbjct: 34039669 gatc 34039666


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
```

```
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 426,853
Number of Sequences: 54
Number of extensions: 426853
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 2
length of query: 697
length of database: 1,133,629,576
effective HSP length: 48
effective length of query: 649
effective length of database: 1,133,626,984
effective search space: 735723912616
effective search space used: 735723912616
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|26541614|gb|AF515776.1| Manacus manacus clone Man1
microsatellite sequence
         (564 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr5                                                                  473   e-131

>chr5
          Length = 56310377

 Score =  473 bits (298), Expect = e-131
 Identities = 424/586 (72%), Gaps = 66/586 (11%)
 Strand = Plus / Plus


Query: 1        gatcagagccacgcggaccacataccggcatttcaacacgagaacacagctcccagcgcc 60
                 |||||||| |||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct: 55073851 gatcagagacacgcggaccacataccggcatttcaacacgagaacacggctcccagcgcc 55073910


Query: 61       tgccgaacctcggaatttgcaccttgtaacactaggaacggacatctgtagacgaaagaa 120
                 ||||||||||||||||||||||||||||||||||| || |||||||||||||||||||||
Sbjct: 55073911 tgccgaacctcggaatttgcaccttgtaacactagaaatggacatctgtagacgaaagaa 55073970


Query: 121      aaccccgtgtgtgcacagcgggttttgtggagcaagannnnnnnnnntctttcatccctc 180
                 || |||  |||| ||||| || |||| ||||||              |||||||||||||
```

```
Sbjct: 55073971 aaaccctcgtgtacacag-ggattttatggagc----cgaggggggctctttcatccctc 55074025


Query: 181      cagcgctgcgagggcagtccctgctgccaactcttccctttgggatgagaagtgcaagtt 240
                || | |||| |||||||| ||||||||||||  |||||| | ||||  ||| ||| ||||
Sbjct: 55074026 caacactgcaagggcagt-cctgctgccaacagttccctgttggatatgaattgcgagtt 55074084


Query: 241      tagcagcgctcnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 300
                 |||  ||||
Sbjct: 55074085 cagccacgct--------------------------------------ggtgtgtgtgtg 55074106


Query: 301      nnnncctacgtgcatgggtgcacgcctgcgttattctgggattagaaatcttttccaggc 360
                    ||||||||| ||||||||| |  ||||| ||| |||||||||  ||| ||||||||
Sbjct: 55074107 catgcctacgtgcgtgggtgcacacgcgcgttgttcggggattagaggtctcttccaggc 55074166


Query: 361      tcaacaacaaagggtggcacatggcagctattgtcctcgctcagccagggtgaagtcggg 420
                |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct: 55074167 tcaacaacaaagggtggcacatggcagctattgtccccgctcagccagggtgaagtcggg 55074226


Query: 421      ggaggtcacagatgtcctggccatatttagctgtcagaacaggattcatttagtttag-- 478
                ||||||||||| ||||||| |||||||||||| ||||||||||||| |||||||||||
Sbjct: 55074227 ggaggtcacagctgtcctgaccatatttagctctcagaacaggattaatttagtttagct 55074286


Query: 479      --------------------attaannnnnnnnnnnnnnnnnnnnctctctaagggagaa 518
                                     ||                      |||||  ||| | ||
Sbjct: 55074287 ttttcttttctttcctttctttctttttgttctttatttttttcctctccgaggaataa 55074346


Query: 519      atttctggctggctggcaggaatgcaagtcacaagtttcaggacca 564
                ||| |||||||| | ||| |||||||||||||||||||| ||||||
Sbjct: 55074347 attgctggctggttagcaagaatgcaagtcacaagtttcgggacca 55074392


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 280,300
Number of Sequences: 54
Number of extensions: 280300
Number of successful extensions: 5
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 3
length of query: 564
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 517
effective length of database: 1,133,627,038
effective search space: 586085178646
effective search space used: 586085178646
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]
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Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|2108135|gb|U82387.1|U82387 Malurus cyaneus microsatellite
McyU3
         (189 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr3                                                                  103   2e-020

>chr3
          Length = 108638738

 Score =  103 bits (64), Expect = 2e-020
 Identities = 93/159 (58%), Gaps = 3/159 (1%)
 Strand = Plus / Minus


Query: 1        gtgaaggcatccctcttctgactacactaaagtaacaaccacagactacaagcaagctgg 60
                ||| |||||| || ||||||| ||| || ||||||||  ||| |||| |||||| || |
Sbjct: 39145155 gtggaggcattccccttctgattacgctgaagtaacagtcaccgacttcaagcaggcag- 39145097


Query: 61       cattgctcacaaaattagtctaaatctgtccagtagagggcaatgacatnnnnnnnnnn 120
                | |||| || ||| ||| ||| |||||| |||||||||||||||||||
Sbjct: 39145096 cgttgc-ca-aaagttattctgaatctgcccagtagagggcaatgacatacacgtataga 39145039


Query: 121      nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnngtgaaaa 159
                                                   ||||
Sbjct: 39145038 gaaaagttggatttgaagtgcacgtttgtaaaaacaaaa 39145000


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 91,845
Number of Sequences: 54
Number of extensions: 91845
Number of successful extensions: 1
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 0
Number of HSP's successfully gapped in prelim test: 1
Number of HSP's that attempted gapping in prelim test: 1
Number of HSP's gapped (non-prelim): 1
length of query: 189
length of database: 1,133,629,576
effective HSP length: 45
effective length of query: 144
effective length of database: 1,133,627,146
effective search space: 163242309024
effective search space used: 163242309024
T: 0
```

```
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 33 (53.9 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|2108136|gb|U82388.1|U82388 Malurus cyaneus microsatellite
McyU4
         (170 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr5                                                                   90   9e-017

>chr5
          Length = 56310377

 Score = 90.3 bits (56), Expect = 9e-017
 Identities = 73/89 (82%), Gaps = 1/89 (1%)
 Strand = Plus / Minus


Query: 83       gacaggcaaacaaaatatggcaaatttatattcagcatttatt-tttagcgtgactgatt 141
                || || ||||||| | |||||||| |||||||||||||||||| |||||| | |||   |
Sbjct: 29168226 gatagacaaacaataaatggcaaaattatattcagcatttattgtttagcataactagat 29168167


Query: 142      gatncacaaaccatgatagacaattgcta 170
                ||| ||||||| ||| |||| ||| ||||
Sbjct: 29168166 gatgcacaaactatgttagaaaatagcta 29168138


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 92,466
Number of Sequences: 54
Number of extensions: 92466
Number of successful extensions: 1
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 170
length of database: 1,133,629,576
effective HSP length: 45
effective length of query: 125
effective length of database: 1,133,627,146
effective search space: 141703393250
effective search space used: 141703393250
```

```
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 33 (53.9 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|2245456|gb|U96322.1|U96322 Mimus polyglottos clone 18
microsatellite sequence
         (285 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr1                                                                  90   2e-016

>chr1
          Length = 188239860

 Score = 90.3 bits (56), Expect = 2e-016
 Identities = 97/130 (74%), Gaps = 5/130 (3%)
 Strand = Plus / Plus


Query: 156       attaataattcagggt-aattaaatttttagcttgaattcttgttttgggtggtaatatt 214
                 |||  ||| |||  |  ||||| |||| |||||| ||  ||||||||||    || || |
Sbjct: 156301994 attgctaaatcattgacaattagatttctagctttaa--cttgttttggagaatagtaat 156302051


Query: 215       tgaacttgtaaccatggtaattgttcaatacctctctcct-attttgaagaatgtgataa 273
                 ||||||||||||||||| ||||| |||||   ||| ||||  | || || ||| | ||||
Sbjct: 156302052 tgaacttgtaaccatggcaattgctcaattaatctttcctgctattaaacaat-ttataa 156302110


Query: 274       atatgaaaga 283
                 |||  |||||
Sbjct: 156302111 atacaaaaga 156302120


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 185,674
Number of Sequences: 54
Number of extensions: 185674
Number of successful extensions: 4
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 3
Number of HSP's gapped (non-prelim): 1
length of query: 285
```

```
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 239
effective length of database: 1,133,627,092
effective search space: 270936874988
effective search space used: 270936874988
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|2245460|gb|U96326.1|U96326 Mimus polyglottos clone 45
microsatellite sequence
         (492 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr17                                                                 107   2e-021

>chr17
          Length = 10632206

 Score =  107 bits (67), Expect = 2e-021
 Identities = 142/202 (70%), Gaps = 15/202 (7%)
 Strand = Plus / Plus


Query: 254     gatcaaacccctgct-tcatcctgcttgatttccactgtgatttgccagacagctctcag 312
               || | || ||| ||| |  |||  || | |||  | ||  ||||||  ||||||||||||
Sbjct: 8451564 gacccaaacccagctctgctcca-ctcgcttta-attgccatttgctggacagctctcag 8451621


Query: 313     ctgcaggg--aaaagtaaaatcaatctctttttccactctctcacacagcagcttcatgc 370
               ||||| ||  |||| |||| || |||| ||||  | | | ||||  || ||| |||
Sbjct: 8451622 ctgcaaggcaaaaattaaagtccatctatttctcccac-ctcatccatcagtttc---- 8451676


Query: 371     tccgnnnggcatcgagcct-ctgctggcaggatgagctccccagcaactggccaccacca 429
               |||    | ||   ||||| |||||| ||||| | ||||  ||||| |||||||||
Sbjct: 8451677 tcccagtgaca---agcctgctgctgccaggagg-gctcttcagcagctggccaccgtgg 8451732


Query: 430     aagcagcccagggccatttggt 451
               |   ||||||||||||||||||
Sbjct: 8451733 agcgagcccagggccatttggt 8451754


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
```

```
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 448,977
Number of Sequences: 54
Number of extensions: 448977
Number of successful extensions: 7
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 0
Number of HSP's successfully gapped in prelim test: 1
Number of HSP's that attempted gapping in prelim test: 6
Number of HSP's gapped (non-prelim): 1
length of query: 492
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 445
effective length of database: 1,133,627,038
effective search space: 504464031910
effective search space used: 504464031910
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|2245461|gb|U96327.1|U96327 Mimus polyglottos clone 83
microsatellite sequence
         (195 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr2                                                                  120   9e-026

>chr2
          Length = 147590765

 Score =  120 bits (75), Expect = 9e-026
 Identities = 89/103 (86%)
 Strand = Plus / Plus


Query: 6        ctcagtgattcctcttcccttctatctctaaaagtttccagaatgtaaagatatttgcca 65
                ||||||||||||||||||||||| ||  ||||||||||||| |||||||| |||||| ||
Sbjct: 80369628 ctcagtgattcctcttcccttctgtcattaaaagtttccaggatgtaaagttatttggca 80369687


Query: 66       aattcttgcatgattgacatttacacttttccttgaaattgca 108
                ||||| ||  ||||||||| |||  ||| ||||| ||||||||
Sbjct: 80369688 aattcctgtgtgattgacacttatgcttgtccttaaaattgca 80369730


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549
```

```
Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 135,988
Number of Sequences: 54
Number of extensions: 135988
Number of successful extensions: 1
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 195
length of database: 1,133,629,576
effective HSP length: 45
effective length of query: 150
effective length of database: 1,133,627,146
effective search space: 170044071900
effective search space used: 170044071900
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|2245463|gb|U96329.1|U96329 Mimus polyglottos clone 86
microsatellite sequence
         (392 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr1                                                                  128   9e-028

>chr1
          Length = 188239860

 Score =  128 bits (80), Expect = 9e-028
 Identities = 240/402 (59%), Gaps = 64/402 (15%)
 Strand = Plus / Plus


Query: 3        tccacggagttgaggcaatatgggggaagaactccatgggctgcaaatgttgtttagcta 62
                |||| ||| | || |  |||| ||| || || |   ||| ||||||| |  |||||||||
Sbjct: 14339559 tccatggactggaagtgatatagggaaaaaagtgt-tggactgcaaaagcggtttagcta 14339617


Query: 63       ggaagggaaaggggcagagatagaagattctctaagctcttgtcacttgtctacgtaagt 122
                |||||||||  ||  ||| ||| |||||| ||     || || |     ||||  ||| |
Sbjct: 14339618 ggaagggaagaggatagaaatacaagattttcatttttcatgcc-----tcta--taaat 14339670


Query: 123      tagacaagtggcnnnnnnnnnnnnnnnnnnnntatttgagatgtggcaccagcatgggta 182
                ||                              | ||| || |||| |||  | | |||||
Sbjct: 14339671 ta---------------------atactcatcttttt-agttgtgtcacttgtacgggta 14339708


Query: 183      gtttaaactgactgacttttcacag------gcacaaccatgctgt--tgcttgacctct 234
                  ||| |||||||||| ||||| ||      |||| | |||  ||   | ||| || |||
Sbjct: 14339709 acttacactgactgacatttcaaagttgcatgcacgagcatattgccattctt-acgtct 14339767


Query: 235      gccttgaagagggcacnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnngtgcagcaga 294
                | |||||| |||||||                                   ||||| |
```

```
Sbjct: 14339768 gtcttgaaaagggcactatcaaaaatatagaaa------------------tgcagaatg 14339809


Query: 295      cacatgttggatttccaaatgaggtaaactgggcagatggcttatttaatgagaacaa-- 352
                |||||| ||| ||||||||||||  ||||   ||| |||||| |||  | | ||||||
Sbjct: 14339810 cacatgctggttttccaaatgagagaaac-atgcaaatggctgatt--aagtgaacaatg 14339866


Query: 353      --tttaatgagtgttgtacatcttctaaagtgctctgagatc 392
                  |||||| |||||||| |||  | |||| | ||||||||||
Sbjct: 14339867 cttttaataagtgttgtgcattgtataaaatactctgagatc 14339908


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 248,778
Number of Sequences: 54
Number of extensions: 248778
Number of successful extensions: 2
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 2
length of query: 392
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 345
effective length of database: 1,133,627,038
effective search space: 391101328110
effective search space used: 391101328110
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|2245464|gb|U96330.1|U96330 Mimus polyglottos clone 95
microsatellite sequence
         (356 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr2                                                                  234   9e-060

>chr2
          Length = 147590765

 Score =  234 bits (147), Expect = 9e-060
```

```
 Identities = 241/351 (68%), Gaps = 28/351 (7%)
 Strand = Plus / Plus


Query: 6        ctcagtgattcctcttcccttctatctctaaaagtttccagaatgtaaagatatttgcca 65
                ||||||||||||||||||||||| ||  ||||||||||||| |||||||| |||||| ||
Sbjct: 80369628 ctcagtgattcctcttcccttctgtcattaaaagtttccaggatgtaaagttatttggca 80369687


Query: 66       aattattgcatgattgacatttacacttttccttgaanttgcagagatgnnnnnnnnnnn 125
                ||||  ||  ||||||||| |||  ||| ||||| || |||||
Sbjct: 80369688 aattcctgtgtgattgacacttatgcttgtccttaaaattgca----------------- 80369730


Query: 126      nnnnnnnnnnnnnnnnnnnnnnnnnnnnntcttagggaaaacttaagcatcagattataa 185
                                             ||| || |||||||| |   ||| |||| |
Sbjct: 80369731 ----------tgggttattgttttttctttctgagagaaaacttgaatgtcacattacag 80369780


Query: 186      ggaggtacttatagagcatacaacaaagtatgtttcagataatggcatattttagtaaac 245
                |||| |  | |||   ||| ||  ||||  || | |||||| || ||| |||||||||||
Sbjct: 80369781 ggagatgttcataacacatgcaggaaagagtgctgcagatattgacattttttagtaaac 80369840


Query: 246      agagaaaggactattctgctggggaaaagatagaagagaaaatattgtataacaaattca 305
                |  |||||| ||  |||||  || ||||||||||| ||||||||||| ||  |||| |||
Sbjct: 80369841 aaggaaagggctcatctgccagg-aaaagatagaatagaaaatattgcatgtcaaactca 80369899


Query: 306      gttcagtgtgctgtgattttaactctgacacattctagagaccttgggatc 356
                ||||| ||  ||||||||||||| ||||||| | |  | ||||||||||||
Sbjct: 80369900 gttcactgctctgtgattttaacactgacacttcccggggaccttgggatc 80369950


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 301,878
Number of Sequences: 54
Number of extensions: 301878
Number of successful extensions: 10
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 6
Number of HSP's gapped (non-prelim): 3
length of query: 356
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 310
effective length of database: 1,133,627,092
effective search space: 351424398520
effective search space used: 351424398520
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
```

```
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|5816702|dbj|AB031375.1| Locustella pryeri DNA,
microsatellite sequence
         (200 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr8                                                                  109   2e-022

>chr8
          Length = 30024636

 Score =  109 bits (68), Expect = 2e-022
 Identities = 136/203 (66%), Gaps = 22/203 (10%)
 Strand = Plus / Plus


Query: 1       gatcaatcaaaaac-gcttcctgaatcagaaatgaaatctc---ccgcttcatttaatca 56
               |||||||||||||  | |||||||| ||  || ||||||||   ||  ||||| | || |
Sbjct: 5272193 gatcaatcaaaaagtgtttcctgaaccaacaaagaaatctctttccatttcatgtcatga 5272252


Query: 57      atttnnnnnnnnnnnnngtctttcttgtttaaataaaaatttgggtccatttcaaaccaa 116
                |||                ||||||| ||  ||| ||||||||||||   ||||||  ||
Sbjct: 5272253 ttttccccctccctcct---tttcttttt--aatcaaaatttgggtcagcttcaaaagaa 5272307


Query: 117     ttaaactgctttaaaaacgtaactttgaaaaatag-aacttcccatctttctggggtgga 175
               | |||         || ||   |||   ||||||  |||||  ||||||||||||| |||
Sbjct: 5272308 tcaaa---------aagcg---cttcagaaaataataactttgcatctttctggggcgga 5272355


Query: 176     agtatccaaattatttgctgaat 198
               ||   ||||||||||| ||||||
Sbjct: 5272356 agaggccaaattatttcctgaat 5272378


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 210,742
Number of Sequences: 54
Number of extensions: 210742
Number of successful extensions: 5
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 3
Number of HSP's gapped (non-prelim): 1
length of query: 200
length of database: 1,133,629,576
effective HSP length: 45
effective length of query: 155
effective length of database: 1,133,627,146
effective search space: 175712207630
effective search space used: 175712207630
```

```
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|5816705|dbj|AB031378.1| Locustella pryeri DNA,
microsatellite sequence
          (240 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr4                                                                  107   8e-022

>chr4
          Length = 90634903

 Score =  107 bits (67), Expect = 8e-022
 Identities = 153/254 (60%), Gaps = 28/254 (11%)
 Strand = Plus / Minus


Query: 1        tcttttgtcccacactccttcatcaccatggcaacaaatgggcaaatattatagtgt-tt 59
                |||||||| |||||||||||||||||||  | |||||||||||||||||||| || | |
Sbjct: 84254724 tcttttgttccacactccttcatcaccacaggaacaaatgggcaaatattat-gtatcta 84254666


Query: 60       tc-------------gggtttgggnnnnnnnnnnnnnnnnnnnaatttgcaagttagact 106
                ||                | |                      | |||||||| |||||
Sbjct: 84254665 tctatctatctatctatctatctatctatctatctatctatttattttgcaag-tagac- 84254608


Query: 107      tggtgagttttcaagacnnnnnnnnnnnnnnnngagccacacagtacgtgtagttcaaac 166
                |||| ||||||||||||                    |||| | | |  ||||||||| |
Sbjct: 84254607 tggtaagttttcaagaccacacacaca----------cacagaatgcaagtagttcaagc 84254558


Query: 167      tcagggattagcacattaaaaccatgggtttaaccagtaactcgggctgtggcctggctc 226
                |   || | ||||| |||||||  |||| |||| | |||||   | |   ||||   |||
Sbjct: 84254557 tgcaggttgagcacgttaaaactctgggattaagccgtaacctcgaccacggcccaactc 84254498


Query: 227      caggccaatgccca 240
                ||  ||| ||||||
Sbjct: 84254497 ca-tccagtgccca 84254485


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


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

```
Number of Hits to DB: 108,144
Number of Sequences: 54
Number of extensions: 108144
Number of successful extensions: 1
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 240
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 194
effective length of database: 1,133,627,092
effective search space: 219923655848
effective search space used: 219923655848
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|32478845|gb|AY320051.1| Malurus splendens melanotus
microsatellite Msp6 sequence
         (400 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr12                                                                 94   3e-017

>chr12
          Length = 19821895

 Score = 93.5 bits (58), Expect = 3e-017
 Identities = 92/124 (74%), Gaps = 4/124 (3%)
 Strand = Plus / Minus


Query: 9        ggaaatgtgaccacagcttggcaccatatcaagctgtttttacctccagtaagctgacta 68
                |||||||||||||||| ||    |||||  ||| |||||| | || ||||||||||||||
Sbjct: 19756302 ggaaatgtgaccacagtttaaggccatacaaagatgttttaatctgcagtaagctgacta 19756243


Query: 69       agggtgcaggtttt----taatggcatcaagctggtttaagaagaaatttacctttgttt 124
                |  || ||| | ||     ||| |||||| |  | |||| | |  |||||| ||||| ||
Sbjct: 19756242 acagttcagttattaaagaaatagcatcaggtagttttaggcacgaatttatctttggtt 19756183


Query: 125      ttca 128
                ||||
Sbjct: 19756182 ttca 19756179


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
```

```
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 301,666
Number of Sequences: 54
Number of extensions: 301666
Number of successful extensions: 8
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 7
Number of HSP's gapped (non-prelim): 1
length of query: 400
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 353
effective length of database: 1,133,627,038
effective search space: 400170344414
effective search space used: 400170344414
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|32478846|gb|AY320052.1| Malurus splendens melanotus
microsatellite Msp10 sequence
         (483 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr1                                                                  74   2e-011

>chr1
          Length = 188239860

 Score = 74.5 bits (46), Expect = 2e-011
 Identities = 91/129 (70%), Gaps = 11/129 (8%)
 Strand = Plus / Minus


Query: 104       cctctcgttccc-tccagtctagacagaacttgaagccaggtctgcagctgaacaacgtt 162
                 || | | ||| | |||||||||||||||||| |||||||| | |  ||| | |||||  |
Sbjct: 100526519 ccaccctttctcatccagtctagacagaactggaagccagctttatagccggacaacact 100526460


Query: 163       tctgttggcgctggctgctgctagtccgggcctancacacgt-ctggtggcgtcccacac 221
                 || | |  | ||||||||       ||||||||| ||| ||| |||| |  ||| |
Sbjct: 100526459 tcggatccctctggctgc------cccgggcctagcacgcgtgctggggatgtctc---g 100526409


Query: 222       acgtccccc 230
                 || ||||||
Sbjct: 100526408 acctccccc 100526400


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
```

```
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 200,668
Number of Sequences: 54
Number of extensions: 200668
Number of successful extensions: 2
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 1
Number of HSP's gapped (non-prelim): 1
length of query: 483
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 436
effective length of database: 1,133,627,038
effective search space: 494261388568
effective search space used: 494261388568
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|51537967|gb|AY696193.1| Chasiempis sandwichensis ibidis
clone O142 microsatellite sequence
         (327 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr1                                                                  301   7e-080

>chr1
          Length = 188239860

 Score =  301 bits (189), Expect = 7e-080
 Identities = 256/321 (79%), Gaps = 11/321 (3%)
 Strand = Plus / Plus


Query: 1         accaaagcattctcattgtctttgtgactaatcagggcagcatatcagttcatcttactt 60
                 |||||||  |||  ||  |||||| ||||||| | |||| || |||||||||| |  |||
Sbjct: 162016380 accaaagtgttccaatcatctttgagactaattaaggcaacacatcagttcatttctctt 162016439


Query: 61        aactgggatgtcaaatttaggagctctcttgcctgaaggctctctagggggaagtggttt 120
                 ||||| ||||||||| |||||||  || |||| || ||||||| |  ||||||||| |||
Sbjct: 162016440 aactgcgatgtcaaacttaggagtactgttgc-tggaggctctgtgaggggaagtgcttt 162016498


Query: 121       tcaaa-tctaaatcatccccaggtgcatatctttcctgtgatagatagagagtgtcagga 179
                 ||||| |||| ||||||||||||||||||||||| |||||  | |||||| ||| || ||
```

```
Sbjct: 162016499 tcaaaatctacatcatccccaggtgcatatcttttctgtggcaaatagagtgtgcca-ga 162016557


Query: 180       aatctggaatcataatttaagtgccttgatcaggtaggatgaatttgggctgaggcatat 239
                 | || |||||||||||||| || |||||||||||| ||||| ||||||||||||||||||
Sbjct: 162016558 agtcgggaatcataatttaggtaccttgatcaggtcggatggatttgggctgaggcatat 162016617


Query: 240       aa-tttttaggcagatannnnnnnnnnnnnnntttcgaaaagtgtcaatcccaattaatt 298
                 || || |||||||||                 |||| || ||||||||| ||||| ||||
Sbjct: 162016618 aacttcttaggcaga-----aaatatgtgagctttcaaacagtgtcaat-ccaatcaatt 162016671


Query: 299       attgaatgtcttggagaagca 319
                  || |||||||||||||||||
Sbjct: 162016672 ctt-aatgtcttggagaagca 162016691


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 230,836
Number of Sequences: 54
Number of extensions: 230836
Number of successful extensions: 4
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 1
length of query: 327
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 281
effective length of database: 1,133,627,092
effective search space: 318549212852
effective search space used: 318549212852
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|51537968|gb|AY696194.1| Chasiempis sandwichensis ibidis
clone O156 microsatellite sequence
         (278 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr10                                                                 147   1e-033
```

```
>chr10
          Length = 20909726

 Score =  147 bits (92), Expect = 1e-033
 Identities = 123/187 (65%), Gaps = 5/187 (2%)
 Strand = Plus / Plus


Query: 93       aggaagaggagcaaacgcannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnt 152
                ||||||||  |  |  | |
Sbjct: 20184109 aggaagagctg--atgggattttagaaatagaactaaatggtttgtgtatgtgtgtgca 20184166


Query: 153      gggaagcgcagtgtccntcaggagataggaaaa-taatggataa-tgaataagagcgcag 210
                ||||||| ||| | |  |||||||||||||||| ||||| |||| ||||||| |||||||
Sbjct: 20184167 gggaagcacagggcctctcaggagataggaaaaataatgtataaatgaataacagcgcag 20184226


Query: 211      caaacattcatcttcatagctgaaattggagag-aaagctgagggtattataaatcctat 269
                |||||||||||||||| |||  ||||||  ||| ||||||||||||||||||||||| ||
Sbjct: 20184227 caaacattcatcttcaaagccaaaattgaggagtaaagctgagggtattataaatcccat 20184286


Query: 270      tttgctg 276
                |||||||
Sbjct: 20184287 tttgctg 20184293


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 177,480
Number of Sequences: 54
Number of extensions: 177480
Number of successful extensions: 4
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 1
Number of HSP's gapped (non-prelim): 1
length of query: 278
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 232
effective length of database: 1,133,627,092
effective search space: 263001485344
effective search space used: 263001485344
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|51537964|gb|AY696190.1| Chasiempis sandwichensis ibidis
clone O26 microsatellite sequence
```

```
         (610 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr1                                                                 241   2e-061

>chr1
          Length = 188239860

 Score =  241 bits (151), Expect = 2e-061
 Identities = 188/219 (85%), Gaps = 3/219 (1%)
 Strand = Plus / Minus


Query: 1         ccaccccaaaaagcccaactttatgatagatcttttccttttaaatgacttttggcttaa 60
                 |||| ||| ||||||||| |||||||| ||||||||||||||||||||||| ||||| ||
Sbjct: 171500122 ccacgccagaaagcccaa-tttatgatggatcttttccttttaaatgacttctggctcaa 171500064


Query: 61        gtctgggaaaagagaaaggcgtttattacgagaaa-gcatttcaattctagttccagtat 119
                 ||||||||||||||| ||| ||||||||  ||||| |||||||||||||| |||||||||
Sbjct: 171500063 gtctgggaaaagagagaggtgtttattagaagaaatgcatttcaattctaattccagtat 171500004


Query: 120       ttgagttttggtggttgctatggtttcaaaggaaaaactgccatgaactcaaccaac-tc 178
                 |||  ||   ||| |||| ||||| |||||||||||| || |||||||||||||||| ||
Sbjct: 171500003 ttgttttgcagtgattgccatggtatcaaaggaaaaaatgtcatgaactcaaccaacatc 171499944


Query: 179       cttccatccagttaagcctaattcaccatgtacatacct 217
                 ||  ||||| | |  ||||||| |||||||| |||||||
Sbjct: 171499943 ctggcatccggcttggcctaatccaccatgtgcatacct 171499905


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.334    0.550

Gapped
Lambda     K      H
    1.10    0.334    0.550


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 493,667
Number of Sequences: 54
Number of extensions: 493667
Number of successful extensions: 4
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 1
length of query: 610
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 563
effective length of database: 1,133,627,038
effective search space: 638232022394
effective search space used: 638232022394
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.6 bits)
S1: 14 (23.8 bits)
```

```
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|11137531|emb|AJ279806.1|PCA279806 Parus caeruleus
microsatellite DNA, clone Pca4
         (410 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr8                                                                  157   2e-036

>chr8
          Length = 30024636

 Score =  157 bits (98), Expect = 2e-036
 Identities = 161/216 (74%), Gaps = 10/216 (4%)
 Strand = Plus / Minus


Query: 199      ccagaagcttcaagtttcttatttccccatccttagtgaaagaacaggaacatacagttg 258
                ||| || || ||  | || |||||| ||  |||| || |||  | |||| ||  | |||
Sbjct: 24798145 ccaaaatct-cacatctcctatttctccccccttggtaaaagagaggagcacgctgttc 24798087


Query: 259      ataacaga--atgctccaagtgcagcaatactcccaagaaagcaacacagctttttgtcc 316
                |||||| |  |  ||||||||||| | ||||| |||||||| |||| ||||| ||||||
Sbjct: 24798086 ataacacagcacactccaagtgcaccgatacttccaagaaaacaacgcagctgtttgtca 24798027


Query: 317      ctgacagc--agttactatattaaatataaagccacctgtttcatgagtgccccacagtg 374
                ||| ||||  |||||||   ||||||| ||||||||||||||   || |||||     ||
Sbjct: 24798026 ctggcagcagagttacttctttaaatacaaagccacctgttttgggaatgccc-----tg 24797972


Query: 375      ctccatatagtacctccacaaaacctgcagaagatc 410
                |  ||||  |||||| ||||||| ||||||| ||||
Sbjct: 24797971 cagcatactgtaccttcacaaaatctgcagaggatc 24797936


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.334    0.550

Gapped
Lambda     K      H
    1.10    0.334    0.550


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 304,700
Number of Sequences: 54
Number of extensions: 304700
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 1
Number of HSP's gapped (non-prelim): 1
length of query: 410
```

```
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 363
effective length of database: 1,133,627,038
effective search space: 411506614794
effective search space used: 411506614794
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.6 bits)
S1: 14 (23.8 bits)
S2: 34 (55.6 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|18653124|gb|AF373222.1| Prunella collaris microsatellite
Pco2 sequence
         (538 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr5                                                                  171   2e-040

>chr5
          Length = 56310377

 Score =  171 bits (107), Expect = 2e-040
 Identities = 268/524 (51%), Gaps = 49/524 (9%)
 Strand = Plus / Minus


Query: 1        gatctgtctcccactgtctctaaaacacagcatcccagtctgcacttggtagttgtttcc 60
                ||| |  || || |||| | ||||||||  ||||| | |||||| ||| ||  |||||||
Sbjct: 43008062 gatttaccttcccctgtatttaaaacacgacatccaattctgcatttgatacctgtttcc 43008003


Query: 61       catggaaacaaaatagaataaatcttttgtacctgccagta--ttggagacattcaaaac 118
                ||  ||    |||||   |  | ||   | | ||  || ||  | | ||||| |  ||||
Sbjct: 43008002 cacagagggtaaatattttgtacctgcag-atcttacattaggtagcagacactgtaaac 43007944


Query: 119      ctttctgcagcttt-----catttattaaa-at--attactcattct-tgcattgataca 169
                | ||||  ||||||     ||   | || | ||  |||||| ||||| ||  ||  ||||
Sbjct: 43007943 ccttctatagctttttatccaaacaatatagattcattactgattctatg--tttctaca 43007886


Query: 170      ggatttcttttacctcccatttttgccttctagtggtcagtgcatgactgaggtgcaggg 229
                |||    |||| ||    |||||| ||||||||||| |||| ||| ||||||||||||||
Sbjct: 43007885 ggaccaattttccca---atttttcccttctagtggccagtacataactgaggtgcaggg 43007829


Query: 230      aaggcatagaaccgtgaccccagagaaacagacagagaaagagnnnnnnnnnnnnnnnnn 289
                || |  ||| ||| | |||||||||    ||||||||| ||||
Sbjct: 43007828 aaagtgtagcaccataaccccagag----agacagagacagag---------------ag 43007788


Query: 290      nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnaaatgtcaaagcgaattc 349
                                                          |||| ||| ||| |||||
Sbjct: 43007787 gaaggggaggcaggagaaggggaacggagggagggaaaagagaaatatcagagcaaattc 43007728


Query: 350      ctaaacatcctctttagcatggaattacgtacagtgcagctgcagatgttccagtccaag 409
                  |||||||| ||||||  ||||| ||  |||    |||       || |||| | ||||
Sbjct: 43007727 taaaacatcccctttagactggaaata--tac----cag-------tgctccaatgcaag 43007681
```

```
Query: 410      tgcaaatgacagcacaggtgtgnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 469
                ||||  ||| | ||||||| ||
Sbjct: 43007680 tgcagctgataacacaggtatgcacaaacatacacgcaaacacacagagccaaaaagcaa 43007621


Query: 470      nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnntgtca 513
                                                         |||
Sbjct: 43007620 ggaaaaatgacagaaatgatcttacaaagctactgcagtaatca 43007577


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 418,060
Number of Sequences: 54
Number of extensions: 418060
Number of successful extensions: 2
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 1
Number of HSP's gapped (non-prelim): 1
length of query: 538
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 491
effective length of database: 1,133,627,038
effective search space: 556610875658
effective search space used: 556610875658
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|18653127|gb|AF373225.1| Prunella collaris microsatellite
Pco6 sequence
         (373 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr17                                                                 190   2e-046
chr12                                                                  55   7e-006

>chr17
          Length = 10632206

 Score =  190 bits (119), Expect = 2e-046
 Identities = 252/396 (63%), Gaps = 42/396 (10%)
```

```
 Strand = Plus / Minus


Query: 1       gatcctctgcccctcccc-ggagcccc----cagga---cgccctgg---ctggcagcag 49
               || | ||| ||||||| | || |||||    | |||   | ||| ||   |   ||||
Sbjct: 9835070 gaacgtcttcccctccacaggtgccccacacctggagagcacccaggggccccccagcca 9835011


Query: 50      tgggcagggcaggagccagcccgtgc-ctctgcacggctggagagcagcgagccc----- 103
               ||||   ||||||||  ||  |  || ||  ||  ||||||||||||||||||||
Sbjct: 9835010 tggg---ggcaggagtgagtgcaagcacttggcttggctggagagcagcgagcccaacag 9834954


Query: 104     ---ggcacagcagcactgcagaaatcatccagcactatgtaggtcagcactggcagctgc 160
                  ||||  | |   ||||||||||||||| ||||||||||||||| ||||| |||||||
Sbjct: 9834953 cctggcagggaaatgctgcagaaatcatcctgcactatgtaggtcaacactgtcagctgc 9834894


Query: 161     nnnnnnnttatctaccctggaatgcagggnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 220
                            |   ||   | | |||
Sbjct: 9834893 gaaaaaa------aggatg---ttccggggatgtgagagagggagggagctgctgtttga 9834843


Query: 221     nnnnctgcaggctgggctggagagggtggacagacacacagagag-tgcagccatcatga 279
                   ||| ||    || |||| ||   | ||||||||| ||| || |     |||||| |
Sbjct: 9834842 a---ctggaga---gggtggacagacag-acagacacatagatagcttttaacatcatca 9834790


Query: 280     accctcctgaggggca--ctcggtttatagcacaggtatgaggtagcagagcagaagcat 337
               |||||||||| |||||  |||| |||| | |||| ||||||||||  |||  |||| |||
Sbjct: 9834789 accctcctgatgggcattctcgatttacaccacacgtatgaggtactagactagaaacat 9834730


Query: 338     gcatcagttaccttatcagaatagatagacatgcgt 373
               ||||||||||||||||||||||| ||||||||||||
Sbjct: 9834729 gcatcagttaccttatcagaatatatagacatgcgt 9834694


>chr12
          Length = 19821895

 Score = 55.5 bits (34), Expect = 7e-006
 Identities = 58/74 (78%), Gaps = 4/74 (5%)
 Strand = Plus / Plus


Query: 44      cagcagtgggcaggg-caggagccagcccgtgcctctgcacggctggagagcagcgagc- 101
               || |||   |||||| | |||||||||||| | ||||||  | | |||||||||| |||
Sbjct: 2546540 caccagccagcagggactggagccagcccgagtctctgcgggacaggagagcagc-agct 2546598


Query: 102     ccggca-cagcagc 114
               |||||| || ||||
Sbjct: 2546599 ccggcaccaccagc 2546612


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 265,376
Number of Sequences: 54
Number of extensions: 265376
Number of successful extensions: 15
Number of sequences better than 1.0e-005: 2
```

```
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 1
Number of HSP's that attempted gapping in prelim test: 7
Number of HSP's gapped (non-prelim): 7
length of query: 373
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 327
effective length of database: 1,133,627,092
effective search space: 370696059084
effective search space used: 370696059084
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, 
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), 
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|18653129|gb|AF373227.1| Prunella collaris microsatellite
Pco9 sequence
         (570 letters)

Database: WholeChickenGenome.txt 
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr5                                                                   89   1e-015

>chr5 
          Length = 56310377

 Score = 88.8 bits (55), Expect = 1e-015
 Identities = 68/81 (83%)
 Strand = Plus / Minus

                                                                            
Query: 1        gatcaaggaatttcagaaaattgcaggcattttcatttcacatgagctgtgccaggaaca 60
                ||| |||||||||||||||||| ||||| || ||||| | | |||||| |||||| ||||
Sbjct: 51149694 gattaaggaatttcagaaaattacaggcgttctcattccgcgtgagctttgccagaaaca 51149635

                                
Query: 61       ccaagccctggagaaggatgg 81
                |  |||||||| |||||| ||
Sbjct: 51149634 ctgagccctggggaaggaagg 51149614


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54
  
Lambda     K      H
    1.10    0.333    0.549 

Gapped
Lambda     K      H
    1.10    0.333    0.549 


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 531,296
Number of Sequences: 54
Number of extensions: 531296
Number of successful extensions: 3
```

```
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 1
length of query: 570
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 523
effective length of database: 1,133,627,038
effective search space: 592886940874
effective search space used: 592886940874
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|18653131|gb|AF373229.1| Prunella collaris microsatellite
Pco12 sequence
         (248 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr2                                                                  164   5e-039

>chr2
          Length = 147590765

 Score =  164 bits (103), Expect = 5e-039
 Identities = 127/145 (87%), Gaps = 5/145 (3%)
 Strand = Plus / Minus


Query: 5         tgtcctgagaatgtgaagtgaggagagattgatgcatggactacctgtccaggaatttgg 64
                 |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||  |
Sbjct: 107431021 tgtcctgagaatgtgaagtgaggagagattgatgcatggactacctgttcaggaattctg 107430962


Query: 65        tagtactggattggattttccatggtttctctctctcttaattttactgaaattac-aca 123
                 |||||||||||  |||||||||||||||| |||||||||  ||||||||||||||| |||
Sbjct: 107430961 tagtactggatcagattttccatggtttccctctctctttgttttactgaaattactaca 107430902


Query: 124       t-ca---gttgcatgtacacatcca 144
                 | ||    |  |||| |||||| ||
Sbjct: 107430901 tgcatgcatcccatgcacacataca 107430877


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549
```

```
Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 184,380
Number of Sequences: 54
Number of extensions: 184380
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 1
length of query: 248
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 202
effective length of database: 1,133,627,092
effective search space: 228992672584
effective search space used: 228992672584
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|18653132|gb|AF373230.1| Prunella collaris microsatellite
Pco15 sequence
         (252 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr2                                                                  109   3e-022
chrUn                                                                 106   3e-021

>chr2
          Length = 147590765

 Score =  109 bits (68), Expect = 3e-022
 Identities = 138/232 (59%), Gaps = 15/232 (6%)
 Strand = Plus / Plus


Query: 19        tgcacagaaggatgaggccaagccaaacacagagcaccactggtttgctacaggattgcc 78
                 |||||||||||| ||||||||| |   ||  || |||      ||| || ||| | | ||
Sbjct: 113788300 tgcacagaaggacgaggccaagtcgggcatggatcacagtacttttacttcagaagttcc 113788359


Query: 79        tagggaaaaatccagctttcttttaaaacacatgtnnnnnnnnnnnnnnnnnnnnnnnnn 138
                  | |||||||||||||         ||  |    |
Sbjct: 113788360 catggaaaaatccagc---------aatgagcctttgctttaaaacacgcacatgctcac 113788410


Query: 139       nnnnnnnnntacgtacactacgt-cagagtttgtgtcttctgcattgacatgagaaattc 197
                           ||  |||| || | |||| ||||  | |||| |  ||||| | |||||||
Sbjct: 113788411 acacacacacacacacac-acatacaga-tttgaattttctactctgacacgtgaaattc 113788468


Query: 198       t---acctaagcttcctttgtgggaagaaatggtaaatgaagataacacatt 246
                 |   |||| |||| |||||||||||||||||||||||||   | ||||||||
Sbjct: 113788469 tctgacctgagctccctttgtgggaagaaatggtaaatgtgcacaacacatt 113788520


>chrUn
```

```
          Length = 165033910

 Score =  106 bits (66), Expect = 3e-021
 Identities = 137/232 (59%), Gaps = 17/232 (7%)
 Strand = Plus / Plus


Query: 19        tgcacagaaggatgaggccaagccaaacacagagcaccactggtttgctacaggattgcc 78
                 |||||||||||| ||||||||| |   ||  || |||      ||| || ||| | | ||
Sbjct: 110678530 tgcacagaaggacgaggccaagtcgggcatggatcacagtacttttacttcagaagttcc 110678589


Query: 79        tagggaaaaatccagctttcttttaaaacacatgtnnnnnnnnnnnnnnnnnnnnnnnnn 138
                  | |||||||||||||         ||  |    |
Sbjct: 110678590 catggaaaaatccagc---------aatgagcctttgctttaaaacacgcacatgctcac 110678640


Query: 139       nnnnnnnnntacgtacac-tacgtcagagtttgtgtcttctgcattgacatgagaaattc 197
                           ||  |||| |||   ||| ||||  | |||| |  ||||| | |||||||
Sbjct: 110678641 acacacacacacacacacatac---aga-tttgaattttctactctgacacgtgaaattc 110678696


Query: 198       t---acctaagcttcctttgtgggaagaaatggtaaatgaagataacacatt 246
                 |   |||| |||| |||||||||||||||||||||||||   | ||||||||
Sbjct: 110678697 tctgacctgagctccctttgtgggaagaaatggtaaatgtgcacaacacatt 110678748


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 222,912
Number of Sequences: 54
Number of extensions: 222912
Number of successful extensions: 6
Number of sequences better than 1.0e-005: 2
Number of HSP's better than  0.0 without gapping: 2
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 2
length of query: 252
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 206
effective length of database: 1,133,627,092
effective search space: 233527180952
effective search space used: 233527180952
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|2570062|emb|Y15125.1|PDSATDOU5 Passer domesticus
microsatellite DNA, Pdo mu 6
         (327 letters)
```

```
Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr1                                                                   74   1e-011

>chr1
          Length = 188239860

 Score = 74.5 bits (46), Expect = 1e-011
 Identities = 53/235 (22%)
 Strand = Plus / Plus


Query: 93       aatgctntgggnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 152
                 |||| | |
Sbjct: 75545409 aatggtgtcccctcatcacactgcatcgtggtgctgcgtagatgggactctctgtacctg 75545468


Query: 153      nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 212

Sbjct: 75545469 ctcacaggaacagagttccaggtgctcccgttccattcttggagatagtcggtaggctct 75545528


Query: 213      nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 272

Sbjct: 75545529 gtggaacagcatatgcagtaaaaaaaaaaatggaaaagaacaagagaaagaaaaagaaac 75545588


Query: 273      nnnnnntttcatagctctctaagcacagacatgcctaacttcctgcttaaggatc 327
                       ||||||||||||| ||||||||||||||||| |||||||||||||||||
Sbjct: 75545589 acatcatttcatagctctccaagcacagacatgcctagcttcctgcttaaggatc 75545643


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 106,162
Number of Sequences: 54
Number of extensions: 106162
Number of successful extensions: 1
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 327
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 281
effective length of database: 1,133,627,092
effective search space: 318549212852
effective search space used: 318549212852
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]
```

```
Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|33621307|gb|AY289550.1| Petroica goodenovii microsatellite
Pgm1 sequence
         (785 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr3                                                                  240   3e-061

>chr3
          Length = 108638738

 Score =  240 bits (151), Expect = 3e-061
 Identities = 432/765 (56%), Gaps = 75/765 (9%)
 Strand = Plus / Plus


Query: 45       ttgagactaagtatctcacaatatactta----aaatgttatcattctgttttcccatgc 100
                ||||||||||| | || |||| || ||  |    |||| || |||| | | |||| ||||
Sbjct: 76079639 ttgagactaaatctcccacagtaaacacacctgaaatattttcatcccgatttcgcatga 76079698


Query: 101      c--------acttt-------ct-gtaagaacgaacagatttagaggag-ta--ttccag 141
                |        |||||       || |||| |  || | |||   |||||  ||  ||||||
Sbjct: 76079699 cgttgttttacttttctcttgctagtaaaatggacctgatcaggaggaaataagttccag 76079758


Query: 142      tacttgaggggtggttgtttacacaaattcctttctccaccatatcatatacaaagaaga 201
                ||||| || |||  ||||||||||||||||||||| ||||  ||| |  |||| |||| |
Sbjct: 76079759 tacttaagaggtaattgtttacacaaattcctttccccactgtataagttacagagaaaa 76079818


Query: 202      gacaacagtgttctgctctgtcatactccttatcaagccatgcattcaaattaattgcaa 261
                |  ||  || || ||  |||||| | | | |||||||||||| || |||||  || ||||
Sbjct: 76079819 gtgaaatgtcttatgtgctgtcacatttcctatcaagccatgtatccaaatctatcgcaa 76079878


Query: 262      gaacattgacttttgagctgttacatttacttgcttagcagaaatggcannnnnnnnnnn 321
                ||||| ||| |||||| || | | || |    ||| |  | |||  | |
Sbjct: 76079879 gaacactgaattttgaactttcatatatgagggctca--aaaaaatgtatttgaaagctc 76079936


Query: 322      nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 381

Sbjct: 76079937 caacagatttacagaaaggaaggatttctttctttccatttttttaaccagtatttct 76079996


Query: 382      nnnnnnnnnnnnnnnnnnnnnnnnctctacttatgcagtatttctcatgatagttttgta 441
                                        || | ||| ||     |||| ||   |  | | | |
Sbjct: 76079997 cctgatatttttgtatttcttttact-tccttctg-----tttcacactgttctctggaa 76080050


Query: 442      tttcttt---tgcttct-ttgttttccactg--ttctggaattaca--gtacaagata-- 491
                || |  |    | |  |  ||| | |||  |    | ||| | | |  | ||| ||||
Sbjct: 76080051 ttccagtacaagataatcatgtgtaccaaagaaaacaggagtaaaattgcacatgatact 76080110


Query: 492      --------atcctatg---cac-aaaaattgtgaaaggtctatataaacttcagaattgt 539
                         ||  |||   |||    || | ||||||| ||||||| |  |||||| |||
Sbjct: 76080111 gtaactttttcagatgttacactgtgaactttgaaaggcctatatagatgtcagaaatgt 76080170


Query: 540      aataacctccnactgctaac--agaaagacaattaagcatcaa--taaggtttataggcc 595
                  |||  |||  ||||||||  | ||||| ||||||  | |||  |    |||||||| |
```

```
Sbjct: 76080171 cctaaaatccagctgctaacaaaaaaagaaaattaaatagcaatctttattttataggtc 76080230


Query: 596      tatcgtgtcccttcatgacttcggagaatgtaaaaaatccacataagtgcataaatgtca 655
                  ||  | |   |  ||| |  |||||||||||||||||||        |||||||||||
Sbjct: 76080231 agtccagccatcttgtgattatggagaatgtaaaaaatcca--------cataaatgtca 76080282


Query: 656      ttcatgtttgacctgttcttacataaatgaatg--------gcataata-aagaatctgc 706
                |||||||||||| |||||||| ||||| || ||         |  |||| | ||| ||||
Sbjct: 76080283 ttcatgtttgacttgttcttatataaaagagtgatagaggaactaaatacaggaacctgc 76080342


Query: 707      aagata-tcctacttcagattgtacccatgcaaaagggttcttct 750
                |||||| |  ||| | || || |||| |  ||||| |  || |||
Sbjct: 76080343 aagatatttgtaccttaggttttacctagtcaaaatgtctcatct 76080387


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 633,810
Number of Sequences: 54
Number of extensions: 633810
Number of successful extensions: 14
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 9
Number of HSP's gapped (non-prelim): 3
length of query: 785
length of database: 1,133,629,576
effective HSP length: 48
effective length of query: 737
effective length of database: 1,133,626,984
effective search space: 835483087208
effective search space used: 835483087208
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|33621308|gb|AY289551.1| Petroica goodenovii microsatellite
Pgm2 sequence
         (915 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr3                                                                  228   2e-057
```

```
>chr3
          Length = 108638738

 Score =  228 bits (143), Expect = 2e-057
 Identities = 527/923 (57%), Gaps = 108/923 (11%)
 Strand = Plus / Minus


Query: 21       ttgctgggcaccactgtaccaaagtatttatcatcccacatctcaggttttgct-tncaa 79
                 |||||||||| |||    ||  | | |  |||| |||  |||||||   |  |  | |
Sbjct: 63302946 ttgctgggcagcacct--cctgactttccatcagccct-atctcagccctcccacttccc 63302890


Query: 80       aaaagtngaggatgaaaatac-ctcaggaaaaacgtgctgataggagtcacntttggaag 138
                || ||  |||  |||||  |  ||  || ||||| |||||  ||||||||| | ||||||
Sbjct: 63302889 aacaggagagtgtgaaaccaatcttgggcaaaacatgctgcgaggagtcacatgtggaag 63302830


Query: 139      tactgcaaaaagacaacttcatc-caggggtgcaacacactattagaaatcaagaattgc 197
                 |||||     |||||  | ||  | ||||| || |   | | | || |||| | | ||
Sbjct: 63302829 cactgct----gacaagctgatttcgggggtacagcgtgcaactggagatcaggcactgg 63302774


Query: 198      agtgacaggccctcaaaccttggagaag-caaggggaggcaaatcctgctgcctccttga 256
                  | |   |        |||| |  | | | | ||||||  || || |
Sbjct: 63302773 gctaaggtgaggcatggcctttggtatggcgatgggaggggaacccag------------ 63302726


Query: 257      gaacagctccccagctctgtctcttatttttgggctccacagagctgtctctcagtt-at 315
                    |||| | |   |||   ||  | | ||||||  | ||||| |||| ||| ||  ||
Sbjct: 63302725 ----agctgcactt-tcttattc--actattgggcatctcagaggtgtccctcggtggat 63302673


Query: 316      gg-cttagaaatatcactacacatgacacannnnnnnaacatgnnnnnnngccgacacag 374
                |  ||||||||| | ||    |||| ||||        | ||        || |||||||
Sbjct: 63302672 gttcttagaaatgttac----catggcacacagggg--atataactacgtgctgacacag 63302619


Query: 375      ctattgtggtaaaagccttaacacaaatacacttgacaatggcattccttttctcagccg 434
                || |||||||| |||||  || |||  |||| | ||  ||  ||||| |||||  |  |
Sbjct: 63302618 ctcttgtggtagaagccgaaatacatttacagtgga--at--cattctttttcaaacgct 63302563


Query: 435      ttacatctccga-caccttatacacaag---------caactttacactggtatatccct 484
                  || |||   | |||||  ||||  |          ||     || |||  | ||
Sbjct: 63302562 aaacctctgtaagcacctggtacatcattggtcctgccagagaaacgctgtgagatggtc 63302503


Query: 485      gct-------cctgtcaca----gaaactctatgac------aactttttatgtggaagg 527
                |||       |||  |||     || | |||||||       | |||| | ||||||||
Sbjct: 63302502 gctgtgggtcccttccacctcaggatattctatgattctatgacctttgtgtgtggaagc 63302443


Query: 528      cacagtagaaaagtagt-attttcatcttcgtaactgattagtcctgttacaaaacacta 586
                ||| | || | | | || | || ||   || || || ||||||||| || ||| |||| |
Sbjct: 63302442 cactgcagcacaatggtgagttccacactcatacctcattagtccttttgcaatacacca 63302383


Query: 587      atgaggnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 646
                 | | |
Sbjct: 63302382 gtcaaggtgggggttgttggcgggttttttttttcttttttttttttttttcccttgcttt 63302323


Query: 647      nnnnnnnnnnnnnnnncctctccctgcctcttggaaggagattaaaagaccaggaacttg 706
                                    |||||     |||||||||||| |||||| || ||||||
Sbjct: 63302322 tt------------------tccct-----ttggaaggagatgaaaagatcaagaactta 63302286


Query: 707      agtaaagaacaagtttaagaaagaggaatctcccctccagcatatctct--ttgcttggt 764
                ||| |||  |||| ||||||| |||||||||||||| |||| ||| | |  ||||| |
Sbjct: 63302285 agtgaagtgcaagattaagaatgaggaatctcccctgcagcgtatttgttcttgctggag 63302226


Query: 765      gcataaaggtgtggtgagacaaggagcagcccggtagctgatgagctcaagatgtcattc 824
                 | ||||||||||||| ||||  ||||||||| |  |||| || ||         ||  |
```

```
Sbjct: 63302225 tcctaaaggtgtggtgtgacagtgagcagcccagcggctgctgggc---------cagcc 63302175


Query: 825      gaggggttaaatcttgtttttgcacctcacagtcaa-gggtttgggttag-cgatagctg 882
                    ||||| |||| ||  | |||||||||| |||| |||| |  |||||   | |||||
Sbjct: 63302174 acatggttacatctggtggtggcacctcaca-tcaaggggtctctgttagaacagagctg 63302116


Query: 883      tccaggttttaactgcactggga 905
                ||||||||   | ||||||||||
Sbjct: 63302115 tccaggttgcga-tgcactggga 63302094


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 652,743
Number of Sequences: 54
Number of extensions: 652743
Number of successful extensions: 2
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 915
length of database: 1,133,629,576
effective HSP length: 48
effective length of query: 867
effective length of database: 1,133,626,984
effective search space: 982854595128
effective search space used: 982854595128
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|33621309|gb|AY289552.1| Petroica goodenovii microsatellite
Pgm3 sequence
         (677 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr8                                                                  782   0.0

>chr8
          Length = 30024636

 Score =  782 bits (493), Expect = 0.0
```

```
 Identities = 567/707 (80%), Gaps = 30/707 (4%)
 Strand = Plus / Plus


Query: 1        tttacaatagatgtgttaatcgcaaataattttcatacaaagtttcaattattgatggag 60
                ||||||||||||| |||||| |||||||||||||||||||||||||||||||||||||||
Sbjct: 27179897 tttacaatagatgcgttaattgcaaataattttcatacaaagtttcaattattgatggag 27179956


Query: 61       taataagcagtttttcatgcattat--gaatctaaaacacacaacaaaaa-tagattt-- 115
                ||||||||||||||||||||| | |  |||||||||||  |||||||||| ||||| |
Sbjct: 27179957 taataagcagtttttcatgcagtctctgaatctaaaacgtacaacaaaaagtagatatat 27180016


Query: 116      -tttcttannnnnnnnnnaaacctcatcccgtttgccacattcttttcatcaaaagtaag 174
                 ||  ||           ||||||| || | |||||||| ||||||| ||||||||||||
Sbjct: 27180017 cttattttccttatccccaaacctcttcacatttgccacgttcttttaatcaaaagtaag 27180076


Query: 175      ctagagagcagattttaatgttttaaagacaaataaagctttgaaaattacctcatgcat 234
                ||||||||| |||||||||||||||||||||||||||||||| |||||||||||||||||
Sbjct: 27180077 ctagagagccgattttaatgttttaaagacaaataaagcttttaaaattacctcatgcat 27180136


Query: 235      cgtctggctgcacaaaatctcagctgcacagtgctaaacttcggtttggtactgccagca 294
                |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Sbjct: 27180137 cgtctggctgcacaaaatctcagctgcatagtgctaaacttcggtttggtactgccagca 27180196


Query: 295      tacaaagagatgagtgaataccccttgcacccatatggactcagctgccagcactgggat 354
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct: 27180197 tacaaagagatgagtgaataccccttgcacccatatggactcagctgccagcactgtgat 27180256


Query: 355      atgcaattttgctttttaatgaatcgtaaacaatttgtgtgtcaagcgagggagtttgtt 414
                ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct: 27180257 atgcaattttgctttttaatgaatcgtaaacaatttgtgtgtcaaacgagggagtttgtt 27180316


Query: 415      ttctttctggagcaggtcctaaatccatttgaagctatagctgtgtactgtactggagca 474
                ||||||||||||||||| |||||||   || ||||||||||||||||||||||||||  |
Sbjct: 27180317 ttctttctggagcaggttctaaatcaggtttaagctatagctgtgtactgtactggacta 27180376


Query: 475      ttatgcccaaatttaaaggttctgtgtcactgggatgaaaagacctgttataatgaaaga 534
                ||||||||||||||||||||||||||||| |  |||||||||||||||||||||||||||
Sbjct: 27180377 ttatgcccaaatttaaaggttctgtgtcattttgatgaaaagacctgttataatgaaaga 27180436


Query: 535      aacggctttataaaaggctgggtgtagtaa-nnnnnnnnnnnnnnnnnnnnnnnnnnnnn 593
                ||||||||||||||||||||||||||||||
Sbjct: 27180437 aacggctttataaaaggctgggtgtagtaatctctctttctttctttctctctctctctc 27180496


Query: 594      nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnacccca--------------- 638
                                                       ||| ||
Sbjct: 27180497 tctctctctctctctccctctccctctccccgtctctcaacctcacactctccctctttc 27180556


Query: 639      ------gtctatagcatgtttatagccagct--ctggagataatgga 677
                      |||||||||||||||||||| ||||  ||||||||||||||
Sbjct: 27180557 actctggtctatagcatgtttatagctagctagctggagataatgga 27180603


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549
```

```
Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 616,145
Number of Sequences: 54
Number of extensions: 616145
Number of successful extensions: 2
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 677
length of database: 1,133,629,576
effective HSP length: 48
effective length of query: 629
effective length of database: 1,133,626,984
effective search space: 713051372936
effective search space used: 713051372936
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|33621310|gb|AY289553.1| Petroica goodenovii microsatellite
Pgm4 sequence
         (567 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr3                                                                  139   6e-031

>chr3
          Length = 108638738

 Score =  139 bits (87), Expect = 6e-031
 Identities = 126/163 (77%), Gaps = 4/163 (2%)
 Strand = Plus / Minus


Query: 397      ttttagaaaatagctagacaagaagttaaggtattaaacgtgaaacaataacccaagttg 456
                ||||| | | | | || ||| | | ||||| | ||||| ||||||    |||  || |
Sbjct: 93181625 ttttatacagtggatacacagggatttaagatgttaaatgtgaaagtgcaacaaaattc- 93181567


Query: 457      aagaattgtatattgaaacctgataaatgaaaaatgagcacagtatcaaaattaatcaca 516
                   || || || |||||| ||||||||||||||||| |||  |||||||| |||||||||
Sbjct: 93181566 ---aactgcattttgaaatctgataaatgaaaaatgggcatggtatcaaatttaatcaca 93181510


Query: 517      tttgtattcacaagatgttgagagctgacactgatttatgatc 559
                ||||||||||   | |||||||||| |||||||||||||||||
Sbjct: 93181509 tttgtattcatgtgttgttgagagcagacactgatttatgatc 93181467



 Score =  112 bits (70), Expect = 8e-023
 Identities = 127/180 (70%), Gaps = 5/180 (2%)
 Strand = Plus / Minus
```

```
Query: 88       agtttcccagtaccactttcagtctataagagaagttatctatacagtctcaggtgaatt 147
                || || |  |||| ||| |||||||||||  ||   |||  || || ||||||||||||
Sbjct: 93182069 agctttcttgtactactctcagtctataaatgacactattgatgcactctcaggtgaatc 93182010


Query: 148      aagtttgagggtgaatacccacatccacaatctaactt---gtggtgctatcgaaggtaa 204
                ||| ||||| ||||||| ||||||||||  ||| ||||         || ||  ||| |
Sbjct: 93182009 aagattgagagtgaatatccacatccactgtctcacttccctaacctctgtcacaggcag 93181950


Query: 205      ttccttactagcgggacagaaatatatatggattattttgtctgttttatctacagatac 264
                 ||| | |||  | ||||  | | ||| ||| | ||| |||||||||  ||| |||||||
Sbjct: 93181949 ctccctgctactgagacaacagtgtatgtggttcattgtgtctgttt--tcttcagatac 93181892


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 406,771
Number of Sequences: 54
Number of extensions: 406771
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 1
Number of HSP's gapped (non-prelim): 2
length of query: 567
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 520
effective length of database: 1,133,627,038
effective search space: 589486059760
effective search space used: 589486059760
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|33621312|gb|AY289555.1| Petroica goodenovii microsatellite
Pgm6 sequence
         (929 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr9                                                                  104   3e-020

>chr9
          Length = 23409228
```

```
 Score =  104 bits (65), Expect = 3e-020
 Identities = 380/684 (55%), Gaps = 99/684 (14%)
 Strand = Plus / Plus


Query: 291      gcaggccctgggtaaggaaaagctgacc--ttcttcc--ctgg-tctgttttaactcagc 345
                |||||| |  | ||   ||||  || |   || ||||  || | ||| |||||   | ||
Sbjct: 18764345 gcaggctccagatagccaaaaattgcctcttttttccagctcgatctattttactgctgc 18764404


Query: 346      agaggagccaggctgtctgtgctccatcacctcactggagatgcagatg-tgtcaccacc 404
                ||||  | ||| ||  ||||    || |||  || ||   | ||| |   |||||||||
Sbjct: 18764405 agagatgtcagccttcctgttagtcaccaca-caatg---aggcatagcatgtcaccact 18764460


Query: 405      cagttgggcttgtccagannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 464
                 || ||||  |||| |||
Sbjct: 18764461 gagctgggtctgtctagatgccctttgttcttctctcttccacatgta------------ 18764508


Query: 465      nnnncctgcccttgttccttcacaaatttgctttctttggtaatgctttcttggtggcag 524
                    ||| | | ||  |||| | | || || ||||| |||   | ||  ||||    |||
Sbjct: 18764509 ----cctcctcatg--cctt-agacatctgttttctgtggatctcctc-cttgca--cag 18764558


Query: 525      cccaaggtagagaggaggctcaaactgagaaccacagggatttctgtgaggtctttgcaa 584
                |      || |||| ||| | ||||  |   | |   ||| |||||| ||| ||||||||
Sbjct: 18764559 c------taaagagaaggtttaaacctaaggcgagcaggacttctgtcaggcctttgcaa 18764612


Query: 585      taaag--------tct---tctggcaatgctgtgtttctactaggggttaagaggtatat 633
                ||| |        |||   ||  ||||  | |||||||||  || | | |||||   | |
Sbjct: 18764613 taaggaagcagcatctctctcctgcaa--cagtgtttctatcagagatcaagagaggtct 18764670


Query: 634      ttttaaagtgttttgtgagcta-tttatatgactaataatatag-tcatataataaggaa 691
                ||  || | ||||||   || | | |  |||||   |  | ||| ||  |  ||||||||
Sbjct: 18764671 ttcaaaggcgttttgcatgcaactatccatgac---tggtgtagttctcaccataaggaa 18764727


Query: 692      ggccataaagctcagtggattgagaggcacaagcataaggcattcttggattctcagctt 751
                ||||||  |||| |||||  ||||||         |  ||| | |||||||      | |
Sbjct: 18764728 ggccatgcagcttagtggtatgagag---------tcgggcgtgcttggat------cct 18764772


Query: 752      cactggtaaggccaataacctgggtttgcactcttaata----ccatttcagattatcct 807
                | |||| || | ||||||||||   |||||  |||   |       || ||  | | |||
Sbjct: 18764773 cgctggcaaagtcaataacctgaccttgcagactttgcagggttagttccatctcagcct 18764832


Query: 808      ttcttatcaggagcnnnnnnncccccaaaaatattttcacagggaaagaactacagcaat 867
                 |  |||| | |          |  |  | |     | ||||||||| ||| |||| |||
Sbjct: 18764833 attgtatctgta--ttgtttttctgctcagactgcatgacagggaaataaccacaggaat 18764890


Query: 868      t---------------tcagtgctg-------tgctttccagcttgctgtagctactttc 905
                |                || |||||        ||||| || ||| ||||| || |   |
Sbjct: 18764891 tctgcagctgtgtccaacactgctgcattcctggcttttcaacttactgtaactgcacgc 18764950


Query: 906      tgtgtaagaattttgcttttcttt 929
                || || | |||||||||||| |||
Sbjct: 18764951 tgagtcacaattttgctttttttt 18764974


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
```

```
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 916,488
Number of Sequences: 54
Number of extensions: 916488
Number of successful extensions: 4
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 0
Number of HSP's successfully gapped in prelim test: 1
Number of HSP's that attempted gapping in prelim test: 4
Number of HSP's gapped (non-prelim): 2
length of query: 929
length of database: 1,133,629,576
effective HSP length: 48
effective length of query: 881
effective length of database: 1,133,626,984
effective search space: 998725372904
effective search space used: 998725372904
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|30024593|dbj|AB094107.1| Parus major DNA, microsatellite
Pma69u
         (214 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr14                                                                 126   1e-027

>chr14
          Length = 20603938

 Score =  126 bits (79), Expect = 1e-027
 Identities = 134/192 (69%), Gaps = 14/192 (7%)
 Strand = Plus / Minus


Query: 1        cccagacaaagcatcactgg---taaaagtaatatagagct--ggagttcattaatcttc 55
                ||||||  |||||||||||    ||  | ||||| ||||||  ||||||||||| ||||
Sbjct: 18845980 cccagatgaagcatcactgaagatattactaataaagagctaaggagttcattattctt- 18845922


Query: 56       ctaaannnnnnnnnnnnnnatgtacagctagagaaaaatactgaaaatccaagagctaata 115
                                  || || || || | || || |||||||||||||||  |||||
Sbjct: 18845921 -------tgcgtgaatgtatatatagttacaaaataacactgaaaatccaagaattaata 18845869


Query: 116      ataga-ccaggtgacagcatctgcaaataaatggctcctccatgggagcttctgaactga 174
                ||| | |||| ||||| || ||| ||||||||   | | ||||| ||  |||||||||||
Sbjct: 18845868 ataaaaccagatgacaacacctgtaaataaattatttccccatgagaatttctgaactga 18845809


Query: 175      tgttttccagtc 186
                  ||||||| ||
Sbjct: 18845808 cattttccattc 18845797
```

```
  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 189,597
Number of Sequences: 54
Number of extensions: 189597
Number of successful extensions: 2
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 214
length of database: 1,133,629,576
effective HSP length: 45
effective length of query: 169
effective length of database: 1,133,627,146
effective search space: 191582987674
effective search space used: 191582987674
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|32482542|gb|AY260526.1| Parus major clone PmaC25
microsatellite sequence
         (597 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr12                                                                 244   2e-062

>chr12
          Length = 19821895

 Score =  244 bits (153), Expect = 2e-062
 Identities = 315/498 (63%), Gaps = 34/498 (6%)
 Strand = Plus / Plus


Query: 106     aataatcngtgaatgcncctttatgttttgatca-gcatnaacgtaacnacaaaatcaca 164
               ||||||   | |||||  ||||| | | | |  | |||   |  || | |||||| ||||
Sbjct: 5488895 aataataaat-aatgcatctttaggatataaaaaagcacata--tagcaacaaaaccaca 5488951


Query: 165     g-agacgttttgcctccttgatatgacactactcaaagctgcactgcacgtcctgctgtt 223
                 |||  | |||| |  |||||| || | | |||||  ||| | | ||   | |  ||||
Sbjct: 5488952 ccagaa-tgttgctttattgataggatattgctcaagactgtagtacattcctttttgtt 5489010
```

```
Query: 224     tgtatttctgtactgaaaagacagatagcactttaatatgacaaagcatttgagcaaaat 283
                 ||||| | || | |||||||||||   ||||| |||||||||| ||||  |||||||
Sbjct: 5489011 actatttatatattcaaaagacagattatactttatatgacaaatcattcaagcaaaac 5489070


Query: 284     agaagagacatccttgactcatcactgacagaattcctngcatcctgcattgctgcttgg 343
                |||||  |  | |||||||||||             || ||||||| ||||| |  |
Sbjct: 5489071 ggaagaaa--ttcttgactcatc-------------ctagcatcctacattgttttt--- 5489112


Query: 344     atgcaaagtgaacagtttcctcatttttccccctgctatacacagacta-ctcactttat 402
               |||||||||    | | |  || | |||||||||  |   ||| |  |  | ||||
Sbjct: 5489113 atgcaaagt----attgtgttc-tgttttccccttttcatcactgtttttcccactgcta 5489167


Query: 403     taccctgnnnnnnaaatacccatatgcacannnnnnnnnnnnnnnnnnnnnnnnnnnnnn 462
                |   ||        |||  |  || |   |
Sbjct: 5489168 aatattgctttattcaatttcattaggttaaatttttcagtatctatatacacaaacaca 5489227


Query: 463     nnnnnnntaaatacattt--aatatacagaat-ttcatctgcccnaaaaggtaacaccct 519
                      |   | |||||  || |||||||   |||||||||   |||||||||||||||
Sbjct: 5489228 accagcatctgtgcatttctaagatacagatcattcatctgctaaaaaggtaacaccct 5489287


Query: 520     aaaaatggttcatggaaagaaacctatccaacaataaaccgatgactactcccacttctg 579
               |||||||||||||||||||||||||| | |||||||||| ||| |||||||||||||||
Sbjct: 5489288 aaaaatggttcatggaaagaaacctaccaaacaataaactgatcactactcccacttct- 5489346


Query: 580     ggaatcctcaacacagat 597
               ||||||||||||||||||
Sbjct: 5489347 ggaatcctcaacacagat 5489364


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 428,351
Number of Sequences: 54
Number of extensions: 428351
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 1
Number of HSP's gapped (non-prelim): 1
length of query: 597
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 550
effective length of database: 1,133,627,038
effective search space: 623494870900
effective search space used: 623494870900
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]
```

```
Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|32482546|gb|AY260530.1| Parus major clone PmaCAn1
microsatellite sequence
         (415 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr3                                                                  103   4e-020

>chr3
          Length = 108638738

 Score =  103 bits (64), Expect = 4e-020
 Identities = 154/242 (63%), Gaps = 26/242 (10%)
 Strand = Plus / Minus


Query: 181     tngcnattgttcacaaagcgccaacttgctctgcatctccctgtcaccacctatgcctga 240
               | || | || | ||| |   | | || ||||  ||| ||||  | | ||||| ||| ||
Sbjct: 1645405 ttgctactgcttacagaagactacctggctccacatttcccaatgatcacctctgcatgc 1645346


Query: 241     ctggagctcattctggagagtatttcacaagtgtctccnagaaatcggtgtcattctctg 300
                || | |   ||||| |  ||| |||| |  | ||||             |  || |
Sbjct: 1645345 ttgaaacaggttctgaattgtacttcatacatatctc-------------tacttattga 1645299


Query: 301     agagtgtctgattggcataaaattacaanaactgctgggaagaggatgagcanaatcctg 360
               || |  | || || ||||||||||| || ||||| |||||||| |||||||| |||  ||
Sbjct: 1645298 agggcatgtgtttagcataaaattagaagaactgatgggaagaagatgagcagaattgtg 1645239


Query: 361     ccttcctggccatcagtctctggag------tc-------tgcacgaggtctctgacctc 407
               ||||||||| ||||| ||||  |||      ||       ||||| ||||| ||| ||||
Sbjct: 1645238 ccttcctggtcatcaatctccagagcagcaatctgcatgttgcacaaggtccctggcctc 1645179


Query: 408     tg 409
               ||
Sbjct: 1645178 tg 1645177



 Score = 55.5 bits (34), Expect = 8e-006
 Identities = 52/66 (78%), Gaps = 2/66 (3%)
 Strand = Plus / Minus


Query: 32      gaggcacatagatgtgcttattcccccaacctcttttcccagcctcca-gaat-tgcttc 89
               || ||| | | ||||| ||||| |||||||   || |||||||||||| |||| |||| |
Sbjct: 1645636 gacgcagagatatgtggttatttccccaactaattctcccagcctccaggaatgtgctgc 1645577


Query: 90      tcggga 95
               || |||
Sbjct: 1645576 tcagga 1645571


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549
```

```
Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 258,063
Number of Sequences: 54
Number of extensions: 258063
Number of successful extensions: 4
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 2
length of query: 415
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 368
effective length of database: 1,133,627,038
effective search space: 417174749984
effective search space used: 417174749984
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|32482545|gb|AY260529.1| Parus major clone PmaD130
microsatellite sequence
         (619 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr5                                                                  160   4e-037

>chr5
          Length = 56310377

 Score =  160 bits (100), Expect = 4e-037
 Identities = 157/207 (75%), Gaps = 10/207 (4%)
 Strand = Plus / Plus


Query: 55      ggctgttgaact-tatgtttcctttccatgttgagtggaaagatgctggctaattattca 113
               |||| |||| |  | ||||||||||||| | ||| |||| | || ||||||||||||||
Sbjct: 9849734 ggct-ttgatccatctgtttcctttccacgctgaatggacatatactggctaattattcc 9849792


Query: 114     tgantggctacntctgattccattaccttgctccttttacagccatgcaaagttgatgtg 173
               |||  |||||  ||||||||  ||| ||||| ||||||||||| |||||||| || ||||
Sbjct: 9849793 tgagaggctagatctgattctgttatcttgcaccttttacagcaatgcaaagctggtgtg 9849852


Query: 174     aaacactactgt-taggaattaattggtgcttcatagtcccaatgcactggcaaaaatgg 232
               |||||||||| | |  |||| ||      |||| || || ||  ||| || |||||||
Sbjct: 9849853 aaacactactatatgtgaatgaa------cttcctattcacacggcagtgacaaaaatac 9849906


Query: 233     ctgggttagacataaggcng-ggagaa 258
```

```
               || ||||||| | |  || | ||||||
Sbjct: 9849907 ctaggttagatacacagcagtggagaa 9849933


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 254,724
Number of Sequences: 54
Number of extensions: 254724
Number of successful extensions: 2
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 1
Number of HSP's gapped (non-prelim): 1
length of query: 619
length of database: 1,133,629,576
effective HSP length: 48
effective length of query: 571
effective length of database: 1,133,626,984
effective search space: 647301007864
effective search space used: 647301007864
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|32482547|gb|AY260531.1| Parus major clone PmaGAn11
microsatellite sequence
         (567 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr2                                                                  221   9e-056

>chr2
          Length = 147590765

 Score =  221 bits (139), Expect = 9e-056
 Identities = 332/506 (65%), Gaps = 35/506 (6%)
 Strand = Plus / Minus


Query: 7         ctgcctccattaagagtcacaa------atcaggaaaacaccttcacatcttatttattt 60
                  |||| |||||||  || ||| |      | |  ||||||||   ||||  |||||  | |
Sbjct: 101244271 ctgcttccattagcagccactagctgcaacccagaaaacacacacacactttattagtgt 101244212
```

```
Query: 61        aaggcatcannnnnnnnnnnnnnnnnnggctgagtgggtgatttttccagatgcattcct 120
                  |||||||                   | |||   |||||  |||||||||| |||||||
Sbjct: 101244211 gaggcatc----------catccctcagcctggcagggtgcattttccagatacattcct 101244162


Query: 121       gactgagctgaaaggtgtctgcaggacacaaagctccccacacacccactgcacaactct 180
                 |||||||||| |  | |||||||||||||||| ||  |||  | |||| |||| ||  |
Sbjct: 101244161 gactgagctgcagagagtctgcaggacacaaacct--ccaagctcccattgcataatgca 101244104


Query: 181       tgtccatgccggctccgggcactgagcatgacttcttcccactcacgcctctctcccaac 240
                    ||  | | ||||| |||||  | ||   |   |||||  ||| | |||   ||| ||
Sbjct: 101244103 cagccccgtcagctccaggcaccca-cagagccctttcccgttcatg-ctc---ccccac 101244049


Query: 241       ctctctccactttccagagtctcagcccactcacctaacccaggctggaacagga-caaa 299
                 | | | ||  || || ||  |  |  ||||   | | |||| ||||| | ||| | || |
Sbjct: 101244048 cacccacctgttaccggacccctaagccaccagcttgaccctggctgaagcagaatcaga 101243989


Query: 300       tggaaatttcttggctct-tggctgcatcacctaaggtttacccatatacagaaggctaa 358
                 | ||||| ||| ||||||  | |||| ||  || ||||||| |||||| ||||||  |||
Sbjct: 101243988 t-gaaatgtctgggctctccgcctgc-tctgcttaggtttagccatatgcagaagattaa 101243931


Query: 359       ttgagggtgggtaaaattttaatccaaactttattttggctaatcttttgtagtacagca 418
                 |||||  ||| |||||  | ||| | | ||||  ||||||||| || ||||  | |  ||
Sbjct: 101243930 ttgagattggataaaa-ctgaattccagctttcctttggctaaactgttgtgttgcttca 101243872


Query: 419       cagtggagtttg----aattggatttgact-tagcaa--agcagcatactgttagtgttt 471
                 | || |||||||    ||||  | || | |  |||||   || ||    ||| ||||| |
Sbjct: 101243871 cggtagagtttggtttaattttagtttagtgaagcaatgtgctgccccttgtcagtgtct 101243812


Query: 472       gcaacaggacaaataatcctaaaata 497
                 |||| |||  |||  | |||||||||
Sbjct: 101243811 gcaataggcaaaaacagcctaaaata 101243786


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 494,478
Number of Sequences: 54
Number of extensions: 494478
Number of successful extensions: 1
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 567
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 520
effective length of database: 1,133,627,038
effective search space: 589486059760
effective search space used: 589486059760
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
```

```
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|32482548|gb|AY260532.1| Parus major clone PmaGAn27
microsatellite sequence
         (543 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr6                                                                   84   3e-014

>chr6
          Length = 33893787

 Score = 84.0 bits (52), Expect = 3e-014
 Identities = 136/261 (52%), Gaps = 6/261 (2%)
 Strand = Plus / Minus


Query: 17       ctcctggcacgccacatgaagcactccggcacttttccaaagcaggctgccacttctgga 76
                |||||| |||   || |||  || | | ||| |  |  |||  ||| |||||||||||||
Sbjct: 33720428 ctcctgccactg-ac-tgacccagttctgcaatggttaaaactagggtgccacttctgga 33720371


Query: 77       actcatgtcagacaaaagagtaagtgggttttggctgaccgtggtttgcagcattataaa 136
                | ||| |  || | ||||  |      ||| || | || |  |||   |||||   |||
Sbjct: 33720370 attcacg--agcccaaagcatctccatgttctg-cggatcacggtgcacagcaccgtaat 33720314


Query: 137      ccacagccacacgcacaaggatagtaccctgcatccttactggaagatgtgtttcattag 196
                |||||||||||   ||||  | ||||||   | | ||| |   |  |||| || |||||
Sbjct: 33720313 ccacagccacagttacaaacacagtaccgcactttctttcccaacaatgtattccattaa 33720254


Query: 197      gttaattaacatgcagtatttgtctttgtnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 256
                |||||| ||  | || ||||  |  ||||
Sbjct: 33720253 gttaatgaagct-cactattccttgttgtccatccatcattatcatccttattttaacct 33720195


Query: 257      nnnnnnnnnnnnnnnnnnnnt 277
                                    |
Sbjct: 33720194 ttgcaggcctggtagcatctt 33720174


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 378,520
Number of Sequences: 54
Number of extensions: 378520
Number of successful extensions: 4
Number of sequences better than 1.0e-005: 1
```

```
Number of HSP's better than  0.0 without gapping: 0
Number of HSP's successfully gapped in prelim test: 1
Number of HSP's that attempted gapping in prelim test: 4
Number of HSP's gapped (non-prelim): 1
length of query: 543
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 496
effective length of database: 1,133,627,038
effective search space: 562279010848
effective search space used: 562279010848
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|32482550|gb|AY260534.1| Parus major clone PmaGAn30
microsatellite sequence
         (639 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr20                                                                 269   5e-070
chrUn                                                                  71   2e-010
chr11                                                                  71   2e-010

>chr20
          Length = 13506680

 Score =  269 bits (169), Expect = 5e-070
 Identities = 294/426 (69%), Gaps = 9/426 (2%)
 Strand = Plus / Plus


Query: 157      ctgttctgtaggagatgggtgaaacacaaa-cacagatttgatgaagaatgtttctgccc 215
                || |||| ||| || ||| | | ||||||| | |||  || ||   |||     ||| ||
Sbjct: 13338697 ctcttctctagaaggtgg-tcagacacaaatctcagtgttcatagtgaaaaa--ctgtcc 13338753


Query: 216      aaatggtgtcttgctaacctctttttcctaattgcc--tgagcgtatgttcattcagact 273
                |  || || ||   |||||  || |||||  || ||  ||  | ||  |  ||||||  |
Sbjct: 13338754 acgtgatgcctcattaacca-ttgttcctcgttaccattggccttagatgtattcaggtt 13338812


Query: 274      gggtagatcacatgtgcttgtaaatagctaagttagaggcagattaacaaataaacttgt 333
                ||||||||| ||||||  |||||| |  | | ||||| | |||| | ||||||||| |||
Sbjct: 13338813 gggtagatctcatgtggctgtaaacacatgatttagaagtagataagcaaataaacctgt 13338872


Query: 334      aaaacaagaataagatgtgactgtgtcagtaaaaatgctgtgtttgtctgannnnnnnnn 393
                 ||||||| | |   ||||  | | ||||||||||   ||  |||  |
Sbjct: 13338873 gaaacaagtagacagtgtggatttatcagtaaaaaaaatgatttttacatctctaactgt 13338932


Query: 394      nnnnnnnnnnnnattcaagttgcaggagttattacagccgacttcctctcaggattgttc 453
                            ||||||||||||||||| |||||||| ||||| || |||||||| ||
Sbjct: 13338933 atgtctctctcaattcaagttgcaggagtaattacagcagactttctgtcaggattattt 13338992


Query: 454      cactggggagcagatacctggggatctgtggagctgcccatcattggaaaggtctgacat 513
                |||||||||||||| |||||||| ||||||||||| |||||| |||| ||||| ||| ||
```

```
Sbjct: 13338993 cactggggagcagacacctgggggtctgtggagctacccatcgttggcaaggtttgagat 13339052


Query: 514      tgttattcttgagct-tgaaaaagtcctgaagtcc-cttctgcagcactggcagtgctcc 571
                | |||| ||| | ||  |||||| |  |||| |||  ||||| | ||||  ||| | ||
Sbjct: 13339053 tcttatccttaaactgggaaaaattaatgaaatcctattctgaaacacttccagcgttct 13339112


Query: 572      aagctg 577
                 |||||
Sbjct: 13339113 cagctg 13339118


>chrUn
          Length = 165033910

 Score = 71.3 bits (44), Expect = 2e-010
 Identities = 84/139 (60%), Gaps = 3/139 (2%)
 Strand = Plus / Plus


Query: 369      tgctgtgtttgtctgannnnnnnnnnnnnnnnnnnnnnattcaagttgcaggagttattac 428
                ||||| ||||  ||                        ||| |||||| ||| |||||||
Sbjct: 72072748 tgctg-gtttagcttctacagttaacactccttttcatttccagttgctggaattattac 72072806


Query: 429      agccgacttcctctcagg-attgttccactggggagcagatacctggggatctgtggagc 487
                ||| || ||   | |||| |  |||| |||||||||| | ||||||||| ||    ||
Sbjct: 72072807 agctgattttgccccaggcacagttc-actggggagctggtacctggggttccactgata 72072865


Query: 488      tgcccatcattggaaaggt 506
                | ||  ||| |||  ||||
Sbjct: 72072866 tccctgtcactggcgaggt 72072884


>chr11
          Length = 19020054

 Score = 71.3 bits (44), Expect = 2e-010
 Identities = 84/139 (60%), Gaps = 3/139 (2%)
 Strand = Plus / Plus


Query: 369     tgctgtgtttgtctgannnnnnnnnnnnnnnnnnnnnnattcaagttgcaggagttattac 428
               ||||| ||||  ||                        ||| |||||| ||| |||||||
Sbjct: 7121462 tgctg-gtttagcttctacagttaacactccttttcatttccagttgctggaattattac 7121520


Query: 429     agccgacttcctctcagg-attgttccactggggagcagatacctggggatctgtggagc 487
               ||| || ||   | |||| |  |||| |||||||||| | ||||||||| ||    ||
Sbjct: 7121521 agctgattttgccccaggcacagttc-actggggagctggtacctggggttccactgata 7121579


Query: 488     tgcccatcattggaaaggt 506
               | ||  ||| |||  ||||
Sbjct: 7121580 tccctgtcactggcgaggt 7121598


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 624,683
Number of Sequences: 54
```

```
Number of extensions: 624683
Number of successful extensions: 5
Number of sequences better than 1.0e-005: 3
Number of HSP's better than  0.0 without gapping: 3
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 3
length of query: 639
length of database: 1,133,629,576
effective HSP length: 48
effective length of query: 591
effective length of database: 1,133,626,984
effective search space: 669973547544
effective search space used: 669973547544
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|32482552|gb|AY260536.1| Parus major clone PmaGAn40
microsatellite sequence
         (481 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr21                                                                 164   1e-038

>chr21
          Length = 6202554

 Score =  164 bits (103), Expect = 1e-038
 Identities = 187/442 (42%), Gaps = 12/442 (2%)
 Strand = Plus / Plus


Query: 1       ttgaaagctgcttcttttgaatgccatgcattcggctcacgttcctcct-ttgctttctg 59
               |||||||||||||||||||||||||||||||| ||||| |   ||||||    || |||
Sbjct: 1529317 ttgaaagctgcttcttttgaatgccatgcatttggctcgcacccctcctccctctctctt 1529376


Query: 60      tctgtct-gnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 118
               ||| |||
Sbjct: 1529377 tctctctctctctctccccccttccctcacttttctcccctctctctcccactctct 1529436


Query: 119     nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 178

Sbjct: 1529437 cctttcctttcctcctctcttccccccttcccacatctcctcccttctctctccttcccct 1529496


Query: 179     nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 238

Sbjct: 1529497 tttactcttcttccatctttgccctttttaccctccttcccctctctccctttttcttttttc 1529556


Query: 239     nnnnnnnnncacccagtgatcccgccagtaatgatgggaaactgcac--agtgaacaact 296
                        |||| |  | ||||  |||||||||||||||| |||||   |||   ||||
Sbjct: 1529557 cctttttctcacctaacggtcccctcagtaatgatgggaaattgcactgcgtggtgaact 1529616


Query: 297     tggctgggaggagaaaganggagcttttcactccctaaaagatgagctagaaatctctcc 356
```

```
               ||||| ||| |||  ||| || ||||||| |||   |||||||||||| |||  || ||
Sbjct: 1529617 tggct-ggaagag-cagagggtgcttttcgctctgcaaaagatgagctggaagcctttct 1529674


Query: 357     acagggtggtcnatactattcactgccgcctgtctgtggactgatgtctgcaggatgnca 416
                ||    | ||   | |||||||||    | |||||   ||  ||||||| | |||  |
Sbjct: 1529675 gcataacgatcaggagtattcactg----cagtctgcacaccaatgtctgtacgattacc 1529730


Query: 417     ngggctct--naattcccactg 436
                | |||||   |||  || |||
Sbjct: 1529731 cgcgctctagaaatctcccctg 1529752


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 213,426
Number of Sequences: 54
Number of extensions: 213426
Number of successful extensions: 4
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 1
Number of HSP's gapped (non-prelim): 2
length of query: 481
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 434
effective length of database: 1,133,627,038
effective search space: 491994134492
effective search space used: 491994134492
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|32482553|gb|AY260537.1| Parus major clone PmaTAGAn71
microsatellite sequence
         (628 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr7                                                                  290   3e-076

>chr7
          Length = 37338262
```

```
 Score =  290 bits (182), Expect = 3e-076
 Identities = 379/625 (60%), Gaps = 41/625 (6%)
 Strand = Plus / Plus


Query: 6        tatcacacaagtcacgtcacacatgagcctcataaggaaggccctaaagtcaataagtca 65
                ||| |||||| |||  ||||| |||||| |||||| || | ||||  ||||||  | | |
Sbjct: 14215170 tattacacaactcatatcacatatgagcatcataaagaggcccctggagtcaaacactaa 14215229


Query: 66       gcctctacactgcttttctctagcatgtgcatgtc-caagataccaccaggactgagccc 124
                || || ||||| |||| ||||| ||| | | | || || |||||   |
Sbjct: 14215230 gcatccacactacttt-ctctaccatttac-tatctcaggatactctc------------ 14215275


Query: 125      tggaattgctgccaactcagcctccaaggaaaacagtctttatctgtagaagagctcaca 184
                        ||||| |||||  |||||  ||||  ||  ||||| || | |    |  |||
Sbjct: 14215276 --------ctgcctactcaaactccagtgaaactaggttttatgtgcacata--caaaca 14215325


Query: 185      ccttaccctgttacttttgcacttctatatctaactgccannnnnnnnnnnnnnnnnnnn 244
                | |    | |||| ||||  |     | | |  ||| | |
Sbjct: 14215326 cttggttcagtta-ttttctatcaggacaac--acttc-actgtttgctgtttctgcact 14215381


Query: 245      nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnna 304
                                                                           |
Sbjct: 14215382 gacattcctaacttccaggacacaacatgtatgctatatggtattgcgtatgctgtcaaa 14215441


Query: 305      cactgcatggtgttgcttatgctatcattccatggctatgactgtgcttgctttaggtgt 364
                || | |||    ||||| |   || |||  |||| |||||| |   | ||| |||||| |
Sbjct: 14215442 ca-tccataaa-ttgctaaa--ta-catggcatgtctatgaatacacctgcgttaggtat 14215496


Query: 365      gtgcagggagac-ctgaaaaaataagagctaatcaagattttcagagctgaaaccagtat 423
                 |  || ||||  ||||   |||||||||     | |||| ||| |||   || |||| |
Sbjct: 14215497 ctatagtgagatactgatggaataagagc-----atgattctcaaagcctgaatcagtgt 14215551


Query: 424      tcaccctcacttcttacaaacagaactctgaagacctttgagacgtaatagcaactccct 483
                |||  |||||||| ||||||||| |||||||||| ||||||||| ||  || |||
Sbjct: 14215552 tcaaactcacttcctacaaacagcactctgaagatctttgagacatac-aggaacatttg 14215610


Query: 484      taacttggaaatgtcacagtactgtaaacctgcttgccttaccaatgacatagagatgtg 543
                |||  ||| ||| || |||||||| ||| ||||||| |||||||||||| ||||| || |
Sbjct: 14215611 taagctgggaatatcccagtactggaaagctgcttggcttaccaatgacgtagagttgcg 14215670


Query: 544      tcccattgcccttgttcataaaatagggtggggggtacatccgctccatcttgcaaatgt 603
                ||||||| ||||||||||| || || ||||| ||||||||||||||||||||||| |  |
Sbjct: 14215671 tcccatttcccttgttcatgaagtatggtggagggtacatccgctccatcttgcagacat 14215730


Query: 604      aaagcccggtgtcatttgcttgcag 628
                |||| || || ||||| ||||||||
Sbjct: 14215731 aaagaccagtatcattagcttgcag 14215755


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 421,422
```

```
Number of Sequences: 54
Number of extensions: 421422
Number of successful extensions: 1
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 628
length of database: 1,133,629,576
effective HSP length: 48
effective length of query: 580
effective length of database: 1,133,626,984
effective search space: 657503650720
effective search space used: 657503650720
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|32482556|gb|AY260540.1| Parus major clone PmaTGAn42
microsatellite sequence
         (723 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr2                                                                  164   2e-038

>chr2
          Length = 147590765

 Score =  164 bits (103), Expect = 2e-038
 Identities = 386/658 (58%), Gaps = 98/658 (14%)
 Strand = Plus / Minus


Query: 19       ttctgtaggtctgatgttttgtgactacttaacattacactgtcccatttattgc----- 73
                || | || | |||||||||| ||||| |||| || |  |  |||||||| | | |
Sbjct: 61201058 ttttttaagcctgatgttttatgactgcttagcactggatagtcccattgaattctgatc 61200999


Query: 74       ---aattttaatgctgtaccacttccacatgccagtttccttaaaacaaggcactcagaa 130
                   | | | ||||||  |   ||| ||||   ||||  |||||||  |||     |||||
Sbjct: 61200998 actactgtgaatgctc-agtgctttcacacatcagtgcccttaaag-aagctgtgcagaa 61200941


Query: 131      aaatcaagagtacacatatgcaactgtctatggaaaatttgactcaaatttcttacctca 190
                || |||| | |||   | | || |     ||| |||| |   || |||||  ||| ||||
Sbjct: 61200940 aa-tcaaaaatactagttttcagcg----atgaaaaactcctcttaaattaattatctca 61200886


Query: 191      -----caggaatctgttgga-atagcaaaactgagttatttgggataatatttatctttt 244
                     ||||||||| ||| | |||  | |||   ||||||| | || ||||||||||||
Sbjct: 61200885 aatcacaggaatctattgtatatataagaacat-gttattttgtatcatatttatctttc 61200827


Query: 245      acagataactgaaaagattaataaaactgaggtcagtcagagctttnnnnnnnnnnnnnn 304
                |  ||||| | ||||||   | | | ||||||||||| | |||| |
Sbjct: 61200826 atggataatt-aaaaga---acagacctgaggtcagtta-agctctcctttcattcacct 61200772
```

```
Query: 305      nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnncccacctct 364
                                                       ||| |
Sbjct: 61200771 gctcatctatctg------------------------------------------cctgt 61200754


Query: 365      ctgccttaacaacatatnaacctgctgggcantttcaacccagtttcacagaaggtcagt 424
                | ||| |   ||  | | | ||||||||||| ||||| ||   ||||||||||||||| |
Sbjct: 61200753 cagccctgcaaatgtgtgagcctgctgggcagtttcagcctcatttcacagaaggtcact 61200694


Query: 425      gatgtcaaaaacaattaatactccccagatttggcacacttgggtatnagctggggacct 484
                ||||||||| | ||  |   ||||     ||    |||| ||||||  || || | |||
Sbjct: 61200693 gatgtcaaagataacca--cctcc-----tt---aacacctgggtagaag-tgagcaccc 61200645


Query: 485      agaatgggctcagatacaacatgcatacntttgcttaggcaaagcagggaagttacagag 544
                |||| || | | | | ||| |||||  | |||||||||| ||| ||| |||| ||||  |
Sbjct: 61200644 agaaaggccccgggtgcaatatgcagccatttgcttagg-aaaacagagaagctacatgg 61200586


Query: 545      g----taagggaangagttt--aatgaataaatggctggaaaccataggaaagcagtatt 598
                |    |  ||| |  ||| |  || |||| || ||| ||||||  |  |||| | |  ||
Sbjct: 61200585 gtggatgtgggtaaaagtatcaaaggaatgaaaggcaggaaactgtgtgaaaactggttt 61200526


Query: 599      ---tgatnc----gtgcatgaaa----gtatttacctatggacttccatatcttccaa 645
                   | || |    || ||| |||     |||||   | |  |||| ||||  ||||||
Sbjct: 61200525 cactaattctgtagttcattaaaagatttatttttttgttaacttacataggttccaa 61200468


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 566,336
Number of Sequences: 54
Number of extensions: 566336
Number of successful extensions: 5
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 3
Number of HSP's gapped (non-prelim): 2
length of query: 723
length of database: 1,133,629,576
effective HSP length: 48
effective length of query: 675
effective length of database: 1,133,626,984
effective search space: 765198214200
effective search space used: 765198214200
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|32482557|gb|AY260541.1| Parus major clone PmaTGAn45
```

```
microsatellite sequence
         (704 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



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

  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 682,287
Number of Sequences: 54
Number of extensions: 682287
Number of successful extensions: 7
Number of sequences better than 1.0e-005: 0
Number of HSP's better than  0.0 without gapping: 0
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 7
Number of HSP's gapped (non-prelim): 0
length of query: 704
length of database: 1,133,629,576
effective HSP length: 48
effective length of query: 656
effective length of database: 1,133,626,984
effective search space: 743659301504
effective search space used: 743659301504
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|1432068|gb|U59113.1|PCU59113 Phylloscopus occipitalis
microsatellite Pocc1 sequence
         (456 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr7                                                                142   5e-032
chr2                                                                 63   4e-008
chr3                                                                 62   1e-007
chrZ_random                                                          60   3e-007
chrUn                                                                60   3e-007
chr6                                                                 60   3e-007
chr1_random                                                          60   3e-007
chr11                                                                60   3e-007
chr1                                                                 60   3e-007
```

```
chr9                                                                   59   1e-006
chr14                                                                  59   1e-006
chrZ                                                                   57   3e-006
chr8                                                                   57   3e-006
chr5                                                                   57   3e-006
chr4                                                                   57   3e-006
chr28                                                                  57   3e-006
chr20                                                                  57   3e-006
chr15                                                                  57   3e-006
chr12                                                                  57   3e-006
chr22                                                                  55   9e-006

>chr7
          Length = 37338262

 Score =  142 bits (89), Expect = 5e-032
 Identities = 128/215 (59%), Gaps = 4/215 (1%)
 Strand = Plus / Plus


Query: 236     ctgnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnaaggga 295
               |||                                                   |||| |
Sbjct: 6128827 ctgtttcaggttgcttactgtggctgtggacactcagatgaagacatatacacaaaggaa 6128886


Query: 296     agctcggcaatttaagctcaaaatacaaaactacactggctcttacaagttaattgaagt 355
               | || |  |||||||||| ||||||   || || | ||||  | |  ||||||   ||||
Sbjct: 6128887 aacttgataatttaagcttaaaatatttaattatattggccatcatgagttaaagtaagt 6128946


Query: 356     ggtgctggaagcaagactcttntcagacataagnacaatcattttaaaggtcagcacta 415
               | || ||||||||| || ||| ||||||||    ||||||||||||||||||||||||||
Sbjct: 6128947 gatgttggaagcaataccctt-tcagacat---gacaatcattttaaaggtcagcacta 6129002


Query: 416     aagcaaaaccaactggcttttcttggcagatcaaa 450
                || | |||||||| || |||| ||||||| ||||
Sbjct: 6129003 cagtacaaccaacttgcctttcctggcagaacaaa 6129037



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 10657221 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 10657175


>chr2
          Length = 147590765

 Score = 63.4 bits (39), Expect = 4e-008
 Identities = 43/47 (91%)
 Strand = Plus / Plus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||||||||||||||||||||||||||| || |||| |||||
Sbjct: 72764833 gatgatcttcaaggtcccttccaacccaaaccattccaggattctat 72764879



 Score = 60.2 bits (37), Expect = 3e-007
 Identities = 42/47 (89%)
 Strand = Plus / Minus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||| ||||| ||||||||||||||||||||||| || |||| |||||
Sbjct: 137212900 gatgatcttaaaggtcccttccaacccaaaccattccaggattctat 137212854
```

```
 Score = 60.2 bits (37), Expect = 3e-007
 Identities = 42/47 (89%)
 Strand = Plus / Minus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||| ||||| |||||||||||||||||||||||||| | || |||||
Sbjct: 133145082 gatgatcttaaaggtcccttccaacccaaaccactctacgattctat 133145036



 Score = 60.2 bits (37), Expect = 3e-007
 Identities = 42/47 (89%)
 Strand = Plus / Minus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||||||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 115003540 gatcatctttaaggtcccttccaacccaaaccattctatgattctat 115003494



 Score = 60.2 bits (37), Expect = 3e-007
 Identities = 42/47 (89%)
 Strand = Plus / Minus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||||||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 113627946 gatcatcttaaaggtcccttccaacccaaaccattctatgactctat 113627900



 Score = 60.2 bits (37), Expect = 3e-007
 Identities = 42/47 (89%)
 Strand = Plus / Plus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||| ||||| |||||||||||||||||||||||||| | || |||||
Sbjct: 110573893 gatgatcttaaaggtcccttccaacccaaaccactctatgattctat 110573939



 Score = 58.6 bits (36), Expect = 1e-006
 Identities = 42/48 (87%)
 Strand = Plus / Minus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctatc 48
                ||| ||||| ||||||||||||||||||||||| || | || ||||||
Sbjct: 94392414 gatgatcttaaaggtcccttccaacccaaaccattctatgattctatc 94392367



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 143255385 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 143255339



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 128406805 gatgatcttaaaggtcccttccaacccaaaccattctacgattctat 128406759
```

```
 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 39/43 (90%)
 Strand = Plus / Plus


Query: 5         atcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||||| |||||||||||||||||||||||||| | || |||||
Sbjct: 124974206 atcttaaaggtcccttccaacccaaaccactctatgattctat 124974248



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||||||||| ||||||||||||||||||||||| || | || | |||
Sbjct: 122430061 gatcatctttaaggtcccttccaacccaaaccattctatgattttat 122430015



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 112755797 gatgatcttaaaggtcccttccaacccaaaccattctatgactctat 112755751



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 108220879 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 108220833



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 94209724 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 94209678



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Plus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| |||||||||||||||||||||||||| | || || ||
Sbjct: 76597107 gatgatcttaaaggtcccttccaacccaaaccactctatgattccat 76597153



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 50088586 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 50088540
```

```
 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 42213602 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 42213556



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 36717952 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 36717906



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 29692893 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 29692847



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Plus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 24819981 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 24820027



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Plus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 24353122 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 24353168



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 19783002 gataatcttaaaggtcccttccaacccaaaccattctatgattctat 19782956



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 40/45 (88%)
 Strand = Plus / Plus


Query: 2        atcatcttcaaggtcccttccaacccaaaccactcgaggaatcta 46
                || ||||| |||||||||||||||||||||||||| | || ||||
Sbjct: 19714659 atgatcttaaaggtcccttccaacccaaaccactctatgattcta 19714703
```

```
 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Plus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 13116699 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 13116745



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1       gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
               ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 8430893 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 8430847



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1       gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
               ||| || || |||||||||||||||||||||||||| | || |||||
Sbjct: 5341717 gatgattttaaaggtcccttccaacccaaaccactctacgattctat 5341671



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1       gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
               ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 3019419 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 3019373



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 43/52 (82%)
 Strand = Plus / Minus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctatctcac 52
                 |||  |||| ||||||||||||||||||||||| || | || |||||  |||
Sbjct: 145576125 gattgtctttaaggtcccttccaacccaaaccattctatgattctatgacac 145576074



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 38/42 (90%)
 Strand = Plus / Minus


Query: 5         atcttcaaggtcccttccaacccaaaccactcgaggaatcta 46
                 ||||| ||||||||||||||||||||||| || | |||||||
Sbjct: 136770854 atcttaaaggtcccttccaacccaaaccattctatgaatcta 136770813



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 41/48 (85%)
 Strand = Plus / Plus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctatc 48
                 ||| ||||| ||||||||||||||||||||||| || | || ||| ||
```

```
Sbjct: 132674624 gatgatctttaaggtcccttccaacccaaaccattctatgattctttc 132674671



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 42/50 (84%)
 Strand = Plus / Minus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctatctc 50
                  |||||||||  |||||||||||| ||||||||| || | || ||||| ||
Sbjct: 125576830 gatcatctttgaggtcccttccagcccaaaccattctatgattctatatc 125576781



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 42/50 (84%)
 Strand = Plus / Minus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctatctc 50
                  ||| ||||| |||||| |||||||||||||||| || | || ||||| ||
Sbjct: 116286586 gatgatcttaaaggtctcttccaacccaaaccattccatgattctatatc 116286537



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 41/48 (85%)
 Strand = Plus / Plus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctatc 48
                  ||| ||||| ||||||||||||||||||||||  || | || ||||||
Sbjct: 116086602 gatgatcttaaaggtcccttccaacccaaaccgttctatgactctatc 116086649



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Minus


Query: 2         atcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                  || ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 112135230 atgatcttaaaggtcccttccaacccaaaccattctatgattctat 112135185



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Minus


Query: 2         atcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                  || ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 112114150 atgatcttaaaggtcccttccaacccaaaccattctatgattctat 112114105



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Minus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatcta 46
                  ||| ||||| |||||||||||||||||||||||  | | |||||||
Sbjct: 104985233 gatgatcttaaaggtcccttccaacccaaaccatcctatgaatcta 104985188



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 46/58 (79%)
 Strand = Plus / Plus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctatctcaccccgaa 58
```

```
                 ||| ||||| ||||||| ||||||||||||||| || | || ||||  | ||| | ||
Sbjct: 100976537 gattatcttaaaggtcctttccaacccaaaccattctatgattctaagttaccacaaa 100976594



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Plus


Query: 2        atcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                || ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 95693525 atgatcttaaaggtcccttccaacccaaaccattctatgattctat 95693570



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Plus


Query: 2        atcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                || ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 36065813 atgatcttaaaggtcccttccaacccaaaccattctatgattctat 36065858



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 38/42 (90%)
 Strand = Plus / Minus


Query: 6        tcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                |||| |||||||||||||||||||||||||| | || |||||
Sbjct: 14291703 tctttaaggtcccttccaacccaaaccactctatgattctat 14291662


>chr3
          Length = 108638738

 Score = 61.8 bits (38), Expect = 1e-007
 Identities = 66/92 (71%), Gaps = 1/92 (1%)
 Strand = Plus / Plus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctatctcaccccgaacc 60
                 ||| ||||| ||||||||||| ||||||||||| || | || |||||    | | |  ||
Sbjct: 106588590 gatgatcttaaaggtcccttcaaacccaaaccattctatgattctatgattcactgtgcc 106588649


Query: 61        tggtg-tttacagaacttgggtcatcaatggt 91
                  |||| |||||  || | ||   | | |||||
Sbjct: 106588650 aggtgttttaccaaagtgggacaacctatggt 106588681



 Score = 60.2 bits (37), Expect = 3e-007
 Identities = 42/47 (89%)
 Strand = Plus / Minus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||||||||||||||||||||||||||| || | || |||||
Sbjct: 81611820 gatgatcttcaaggtcccttccaacccaaaccattccatgattctat 81611774



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 107498861 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 107498815
```

```
 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Plus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 106792223 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 106792269



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 106654303 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 106654257



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Plus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||||||||| ||||||||||||||| ||||||| || | || |||||
Sbjct: 99382795 gatcatcttaaaggtcccttccaactcaaaccattctatgattctat 99382841



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Plus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 98447594 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 98447640



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 42/49 (85%)
 Strand = Plus / Minus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctatct 49
                ||| ||||| ||||||||||||||||||||| | || | || |||||||
Sbjct: 86313913 gatgatcttaaaggtcccttccaacccaaactattctatgattctatct 86313865



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 83677415 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 83677369



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Plus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 79332640 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 79332686
```

```
 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 43/51 (84%)
 Strand = Plus / Plus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctatctca 51
                ||| ||||| ||||||||||||||||||||||| ||   || ||||| |||
Sbjct: 78978978 gatgatcttgaaggtcccttccaacccaaaccattctgtgattctatgtca 78979028



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Plus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 74198890 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 74198936



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Plus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 69385816 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 69385862



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Plus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 58736321 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 58736367



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Plus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 58199304 gatgatcttaaaggtcccttccaacccaaaccattctatgactctat 58199350



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| |||||||||||||||||||||| ||| | || |||||
Sbjct: 57013156 gatgatcttaaaggtcccttccaacccaaaccgctctacgattctat 57013110



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 45/53 (84%), Gaps = 1/53 (1%)
 Strand = Plus / Plus


Query: 1        gatcatcttcaa-ggtcccttccaacccaaaccactcgaggaatctatctcac 52
                ||||||||| || ||||||||||||||||||||| || | || |||||  |||
```

```
Sbjct: 49153517 gatcatcttaaaggtcccttccaacccaaaccattccatgattctatgacac 49153569



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Plus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||||||||| |||||||||||||| |||||||| || | || |||||
Sbjct: 46764609 gatcatcttaaaggtcccttccaaaccaaaccattctatgattctat 46764655



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 46602118 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 46602072



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 42/49 (85%)
 Strand = Plus / Plus


Query: 2       atcatcttcaaggtcccttccaacccaaaccactcgaggaatctatctc 50
                |||||||| ||||| ||||||||||||||||| || | || ||||| ||
Sbjct: 8290322 atcatcttaaaggttccttccaacccaaaccattctatgattctatttc 8290370



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 43/51 (84%)
 Strand = Plus / Minus


Query: 1       gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctatctca 51
                ||| ||||| ||||||||||||||||||||||| ||   || ||||| |||
Sbjct: 2187065 gatgatcttaaaggtcccttccaacccaaaccattctgtgattctatatca 2187015



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Plus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatcta 46
                  ||| ||||| ||||||||||||||||||||||| || | || ||||
Sbjct: 106033145 gatgatcttgaaggtcccttccaacccaaaccattctatgattcta 106033190



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Minus


Query: 2        atcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 || ||||| |||||||||||||||||||| ||||| | || |||||
Sbjct: 98649559 atgatcttaaaggtcccttccaacccaaatcactctatgattctat 98649514



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 41/48 (85%)
 Strand = Plus / Plus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctatc 48
```

```
                ||| |||||||||||  ||||||||||||||||||| |  | ||||||
Sbjct: 52000293 gatgatcttcaaggtttcttccaacccaaaccactctaaaattctatc 52000340



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Minus


Query: 2       atcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
               |||| ||| ||||||||||||||||||||||| || | || |||||
Sbjct: 8449630 atcaccttaaaggtcccttccaacccaaaccattctatgattctat 8449585



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 41/48 (85%)
 Strand = Plus / Plus


Query: 5       atcttcaaggtcccttccaacccaaaccactcgaggaatctatctcac 52
               ||||| ||||||||||||||||||| ||| || |||| |||||  |||
Sbjct: 2673335 atctttaaggtcccttccaacccaagccattccaggattctatgacac 2673382


>chrZ_random
          Length = 14994570

 Score = 60.2 bits (37), Expect = 3e-007
 Identities = 42/47 (89%)
 Strand = Plus / Minus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| |||||||||||||||||||||||||| | || |||||
Sbjct: 14787991 gatgatcttaaaggtcccttccaacccaaaccactctatgactctat 14787945


>chrUn
          Length = 165033910

 Score = 60.2 bits (37), Expect = 3e-007
 Identities = 42/47 (89%)
 Strand = Plus / Plus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||| ||||| |||||||||||||||||||||||||| | || |||||
Sbjct: 126913683 gatgatcttaaaggtcccttccaacccaaaccactccatgattctat 126913729



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 148188796 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 148188750



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Plus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 144808166 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 144808212



 Score = 57.1 bits (35), Expect = 3e-006
```

```
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||||| ||| ||||||||||||||||||| ||| || | ||||||||
Sbjct: 135690605 gatcaccttaaaggtcccttccaacccaagccattctatgaatctat 135690559



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||||| ||| ||||||||||||||||||| ||| || | ||||||||
Sbjct: 135689731 gatcaccttaaaggtcccttccaacccaagccattctatgaatctat 135689685



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Plus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 93416629 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 93416675



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 39/43 (90%)
 Strand = Plus / Minus


Query: 5        atcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||||| |||||||||||||||||||||||||| | || |||||
Sbjct: 92365536 atcttaaaggtcccttccaacccaaaccactctatgattctat 92365494



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 86986838 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 86986792



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 75184214 gatgatcttaaaggtcccttccaacccaaaccattctatgactctat 75184168



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 68/95 (71%), Gaps = 3/95 (3%)
 Strand = Plus / Minus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctatctcac-cccgaac 59
                ||| ||||| ||||||||||||||||||||||  || | || |||||  | |   |  ||
Sbjct: 48824147 gatgatcttaaaggtcccttccaacccaaacctttctatgattctatgactctaacttac 48824088


Query: 60       ctggtgttt-aca-gaacttgggtcatcaatggtt 92
```

```
                ||| | ||| | | ||  ||  | || |||| |||
Sbjct: 48824087 ctgtttttcatacgacttttgacaccaattgtt 48824053



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Plus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 47257960 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 47258006



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Plus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| |||||||||||||||| ||||||||| | || |||||
Sbjct: 46135414 gatgatctttaaggtcccttccaacctaaaccactctatgattctat 46135460



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Plus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 29216021 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 29216067



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Plus


Query: 2         atcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 || ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 162034094 atgatcttaaaggtcccttccaacccaaaccattctatgattctat 162034139



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Plus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatcta 46
                 ||| |||||||||||||||||||| |||||||| || | || ||||
Sbjct: 156298413 gatgatcttcaaggtcccttccaagccaaaccattctatgattcta 156298458



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Minus


Query: 2         atcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 |||||||| ||||||||||||||||||||||| |  | || |||||
Sbjct: 137783557 atcatcttaaaggtcccttccaacccaaaccattgtatgattctat 137783512



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Plus
```

```
Query: 2         atcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 || ||||| ||||||||||||||||||||||||||   || |||||
Sbjct: 133605488 atgatcttaaaggtcccttccaacccaaaccactctgtgattctat 133605533



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Minus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatcta 46
                 ||| ||||| ||||||||||||| ||||||||| || | |||||||
Sbjct: 132417525 gatgatctttaaggtcccttccagcccaaaccattctatgaatcta 132417480



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Plus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatcta 46
                 ||| ||||| ||||||||||||||||||||||| || | || ||||
Sbjct: 129861200 gatgatcttaaaggtcccttccaacccaaaccattctatgactcta 129861245



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Plus


Query: 2         atcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 || ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 124517099 atgatcttaaaggtcccttccaacccaaaccattctatgattctat 124517144



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Plus


Query: 2         atcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 || ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 124515886 atgatcttaaaggtcccttccaacccaaaccattctatgattctat 124515931



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Plus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatcta 46
                ||| ||||| |||||||||||||||||||||||||| | |  ||||
Sbjct: 91586790 gatgatcttaaaggtcccttccaacccaaaccactctatgcttcta 91586835



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 54/72 (75%), Gaps = 4/72 (5%)
 Strand = Plus / Plus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatcta----tctcaccccg 56
                ||| ||||||||||||||||||||||||| ||  || |  | ||||    |||| | ||
Sbjct: 73881461 gattatcttcaaggtcccttccaacccaagccgttctatcagtctatgattctcccacca 73881520


Query: 57       aacctggtgttt 68
                ||  | ||||||
Sbjct: 73881521 aatatagtgttt 73881532
```

```
 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 48/60 (80%), Gaps = 2/60 (3%)
 Strand = Plus / Minus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctatct--caccccgaa 58
                |||||||||| |||||||||||||| ||| ||| || | || |||| ||  || || |||
Sbjct: 39723239 gatcatcttcgaggtcccttccaacacaagccattctatgattctaactagcaacctgaa 39723180



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Plus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatcta 46
                ||| |||||||||||||||||||| |||||||| || | || ||||
Sbjct: 25718897 gatgatcttcaaggtcccttccaagccaaaccattctatgattcta 25718942



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 48/60 (80%), Gaps = 2/60 (3%)
 Strand = Plus / Minus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctatct--caccccgaa 58
                |||||||||| |||||||||||||| ||| ||| || | || |||| ||  || || |||
Sbjct: 11817251 gatcatcttcgaggtcccttccaacacaagccattctatgattctaactagcaacctgaa 11817192



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Minus


Query: 1       gatcatcttcaaggtcccttccaacccaaaccactcgaggaatcta 46
               ||| ||||| ||||||||||||||||||||||| || | || ||||
Sbjct: 5799274 gattatcttaaaggtcccttccaacccaaaccattctatgattcta 5799229


>chr6
          Length = 33893787

 Score = 60.2 bits (37), Expect = 3e-007
 Identities = 42/47 (89%)
 Strand = Plus / Minus


Query: 1       gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
               ||||||||| ||||||||||||||| ||||||| || |||| |||||
Sbjct: 2059537 gatcatcttgaaggtcccttccaactcaaaccattctaggattctat 2059491



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 20340623 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 20340577



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Plus


Query: 2       atcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
               || ||||| |||||||||||||| ||||||||||| | || |||||
```

```
Sbjct: 6581103 atgatcttaaaggtcccttccaatccaaaccactctatgattctat 6581148


>chr1_random
          Length = 1356957

 Score = 60.2 bits (37), Expect = 3e-007
 Identities = 42/47 (89%)
 Strand = Plus / Plus


Query: 1      gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
              ||| ||||||||||||||||||||||||||||| || | || |||||
Sbjct: 332938 gatgatcttcaaggtcccttccaacccaaaccattctatgattctat 332984


>chr11
          Length = 19020054

 Score = 60.2 bits (37), Expect = 3e-007
 Identities = 42/47 (89%)
 Strand = Plus / Minus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| |||||||||||||||||||||||||| | || |||||
Sbjct: 18570121 gatgatcttaaaggtcccttccaacccaaaccactccatgattctat 18570075



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Plus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||||||||| ||||||||||||||||||| ||| || | || |||||
Sbjct: 15362728 gatcatctttaaggtcccttccaacccaagccattctatgactctat 15362774


>chr1
          Length = 188239860

 Score = 60.2 bits (37), Expect = 3e-007
 Identities = 42/47 (89%)
 Strand = Plus / Minus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||| ||||| |||||||||||||||||||||||||| | || |||||
Sbjct: 164300722 gatgatcttaaaggtcccttccaacccaaaccactcaatgattctat 164300676



 Score = 60.2 bits (37), Expect = 3e-007
 Identities = 42/47 (89%)
 Strand = Plus / Minus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||| ||||| ||||||||||||||||||||||| || | ||||||||
Sbjct: 156127467 gatgatcttaaaggtcccttccaacccaaaccattctatgaatctat 156127421



 Score = 60.2 bits (37), Expect = 3e-007
 Identities = 42/47 (89%)
 Strand = Plus / Plus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||| ||||| |||||||||||||||||||||||||| | || |||||
Sbjct: 155391379 gatgatcttaaaggtcccttccaacccaaaccactctatgattctat 155391425
```

```
 Score = 60.2 bits (37), Expect = 3e-007
 Identities = 42/47 (89%)
 Strand = Plus / Plus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| |||||||||||||||||||||||||| | || |||||
Sbjct: 57450681 gatgatcttaaaggtcccttccaacccaaaccactctatgattctat 57450727



 Score = 60.2 bits (37), Expect = 3e-007
 Identities = 42/47 (89%)
 Strand = Plus / Minus


Query: 1       gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
               ||| ||||||||||||||||||||||||||||| || | || |||||
Sbjct: 4081958 gatgatcttcaaggtcccttccaacccaaaccattctatgagtctat 4081912



 Score = 58.6 bits (36), Expect = 1e-006
 Identities = 42/48 (87%)
 Strand = Plus / Plus


Query: 5         atcttcaaggtcccttccaacccaaaccactcgaggaatctatctcac 52
                 ||||| ||||||||||||||||||||||| || | || ||||| ||||
Sbjct: 161364843 atcttaaaggtcccttccaacccaaaccattctatgattctatgtcac 161364890



 Score = 58.6 bits (36), Expect = 1e-006
 Identities = 53/70 (75%)
 Strand = Plus / Plus


Query: 5         atcttcaaggtcccttccaacccaaaccactcgaggaatctatctcaccccgaacctggt 64
                 ||||| ||||||||||||||||||||||| || | || | ||| |  | | ||  |||
Sbjct: 151429453 atcttaaaggtcccttccaacccaaaccattctatgactgtatgtttctctgattctgtg 151429512


Query: 65        gtttacagaa 74
                  ||| |||||
Sbjct: 151429513 atttgcagaa 151429522



 Score = 58.6 bits (36), Expect = 1e-006
 Identities = 41/46 (89%)
 Strand = Plus / Plus


Query: 2       atcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
               || ||||| ||||||||||||||||||||||| || | ||||||||
Sbjct: 9903600 atgatcttaaaggtcccttccaacccaaaccattctatgaatctat 9903645



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||| ||||| |||||||||||||||| ||||||||| | || |||||
Sbjct: 182493206 gatgatctttaaggtcccttccaacctaaaccactctatgattctat 182493160



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus
```

```
Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 178639954 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 178639908



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Plus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 175815979 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 175816025



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 169178845 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 169178799



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||| ||||  ||||||||||||||||||||||| || | ||||||||
Sbjct: 167682615 gattatctctaaggtcccttccaacccaaaccattccacgaatctat 167682569



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Plus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 166931689 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 166931735



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 165962026 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 165961980



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 162316185 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 162316139



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 39/43 (90%)
 Strand = Plus / Plus
```

```
Query: 5         atcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||||| |||||||||||||||||||||||||| | || |||||
Sbjct: 160341057 atcttaaaggtcccttccaacccaaaccactctatgattctat 160341099



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 40/45 (88%)
 Strand = Plus / Plus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatct 45
                 ||||||||| ||||||||||||||||||||||| || | || |||
Sbjct: 153968835 gatcatcttaaaggtcccttccaacccaaaccattctatgattct 153968879



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 39/43 (90%)
 Strand = Plus / Minus


Query: 5         atcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||||| |||||||||||||||||||||||||| | || |||||
Sbjct: 132169335 atcttaaaggtcccttccaacccaaaccactctatgattctat 132169293



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 129665941 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 129665895



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Plus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 120849280 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 120849326



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Plus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 116767935 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 116767981



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 108645658 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 108645612



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus
```

```
Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||| ||||| |||||||||||||||||||||||||  | || |||||
Sbjct: 107625429 gatgatcttaaaggtcccttccaacccaaaccactgtatgattctat 107625383



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 ||||||||| |||||||||||||||||||| || || | || |||||
Sbjct: 104828900 gatcatcttaaaggtcccttccaacccaaaacattctatgattctat 104828854



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Plus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| |||||| ||||||||||||||||||| | || |||||
Sbjct: 64198444 gatgatcttaaaggtctcttccaacccaaaccactctatgattctat 64198490



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 55033291 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 55033245



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Plus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 15769414 gatgatcttgaaggtcccttccaacccaaaccattctatgattctat 15769460



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 10740770 gatgatcttaaaggtcccttccaacccaaaccattcaatgattctat 10740724



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Plus


Query: 1       gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
               ||| ||||||||||||||||||||||| ||||| || | || |||||
Sbjct: 2585799 gatgatcttcaaggtcccttccaaccccaaccattctatgattctat 2585845



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
```

```
 Strand = Plus / Minus


Query: 2         atcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 || ||| | |||||||||||||||| ||||||||| |||| |||||
Sbjct: 187335810 atgatccttaaggtcccttccaacctaaaccactccaggattctat 187335765



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Minus


Query: 2         atcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 || ||||| |||||||||||||||| |||||| || |||| |||||
Sbjct: 183093490 atgatctttaaggtcccttccaacctaaaccattctaggattctat 183093445



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Plus


Query: 2         atcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 || |||||||||||||||||||| ||||||||||| | ||  ||||
Sbjct: 181726804 atgatcttcaaggtcccttccagcccaaaccactctatgatactat 181726849



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Plus


Query: 2         atcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 || ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 175086171 atgatcttaaaggtcccttccaacccaaaccattctatgattctat 175086216



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 43/52 (82%)
 Strand = Plus / Plus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctatctcac 52
                 ||| ||||| |||||||||||||||||||| || || | || |||| || ||
Sbjct: 172078866 gatgatcttaaaggtcccttccaacccaaaacattctatgattctacctaac 172078917



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Plus


Query: 2         atcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 || ||||| || ||||||||||||||||||||||| | || |||||
Sbjct: 161462749 atgatcttaaaagtcccttccaacccaaaccactcaatgattctat 161462794



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Minus


Query: 2         atcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 || ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 158040625 atgatcttaaaggtcccttccaacccaaaccattctatgattctat 158040580



 Score = 55.5 bits (34), Expect = 9e-006
```

```
 Identities = 40/46 (86%)
 Strand = Plus / Plus


Query: 2         atcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 || ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 157994978 atgatcttaaaggtcccttccaacccaaaccattctatgattctat 157995023



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Plus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatcta 46
                 ||| ||||| ||||||||||||||||||||||| || | || ||||
Sbjct: 155992721 gatgatcttaaaggtcccttccaacccaaaccattctatgattcta 155992766



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Plus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatcta 46
                 ||| ||||| ||||||||||||||||||||||| || || | ||||
Sbjct: 152859079 gatgatcttaaaggtcccttccaacccaaaccattctagaattcta 152859124



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 42/50 (84%)
 Strand = Plus / Minus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctatctc 50
                 ||| |||||  ||||||||||||||||||||||||| | |  ||||| ||
Sbjct: 151669447 gatgatcttagaggtcccttccaacccaaaccactctatggttctatttc 151669398



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Plus


Query: 2         atcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 |||||||| ||| ||||||||||||||||||| || | || |||||
Sbjct: 150768629 atcatcttaaagatcccttccaacccaaaccattctatgattctat 150768674



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 44/54 (81%)
 Strand = Plus / Plus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctatctcaccc 54
                 ||| ||||| ||||||||||||||||||| ||| || | || |||||   ||||
Sbjct: 149482982 gatgatctttaaggtcccttccaacccaagccattccatgattctatgataccc 149483035



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Minus


Query: 2         atcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 || ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 138868124 atgatcttaaaggtcccttccaacccaaaccattctatgattctat 138868079
```

```
 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Plus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatcta 46
                 |||||||||  |||||||||||||||||||||| || | || ||||
Sbjct: 138462722 gatcatctttgaggtcccttccaacccaaaccattctatgattcta 138462767



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Minus


Query: 2         atcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                 || ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 116318835 atgatcttaaaggtcccttccaacccaaaccattctatgattctat 116318790



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Plus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatcta 46
                 ||| ||||| ||||||||||||||||||||||| |  | |||||||
Sbjct: 110921215 gatgatcttaaaggtcccttccaacccaaaccattttatgaatcta 110921260



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Minus


Query: 1         gatcatcttcaaggtcccttccaacccaaaccactcgaggaatcta 46
                 ||| ||||| ||||||||||||||||||||||| || | || ||||
Sbjct: 107151129 gatgatcttaaaggtcccttccaacccaaaccattctatgattcta 107151084



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 56/74 (75%), Gaps = 2/74 (2%)
 Strand = Plus / Plus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctatctcaccccgaacc 60
                ||| ||||| |||||| |||||||||||||||| || | || ||||| | |   | ||
Sbjct: 57178236 gatgatcttaaaggtctcttccaacccaaaccattctatgattctatgtta-aactaatt 57178294


Query: 61       tgg-tgtttacaga 73
                ||| |||| | |||
Sbjct: 57178295 tggttgttcataga 57178308



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Minus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatcta 46
                ||| ||||| ||||||||||||||||||| |||||| | || ||||
Sbjct: 56978135 gatgatctttaaggtcccttccaacccaagccactccatgattcta 56978090



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Minus
```

```
Query: 2        atcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                || ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 54112010 atgatcttaaaggtcccttccaacccaaaccattctatgattctat 54111965



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Plus


Query: 2        atcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                || ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 53571607 atgatcttaaaggtcccttccaacccaaaccattccatgattctat 53571652



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 59/82 (71%), Gaps = 1/82 (1%)
 Strand = Plus / Minus


Query: 5        atcttcaaggtcccttccaacccaaaccactcgaggaatctatctcaccccgaacctggt 64
                ||||| |||||||||||||||||||| |  || | || | ||||||||   |||  ||
Sbjct: 30078170 atctttaaggtcccttccaacccaaatctttctatgattttatctcacattgaaggtgcg 30078111


Query: 65       gtttacagaacttg-ggtcatc 85
                  | | |||| | |  ||||||
Sbjct: 30078110 tataagagaagtggtagtcatc 30078089



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Minus


Query: 2        atcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                || ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 23212615 atgatcttaaaggtcccttccaacccaaaccattctatgattctat 23212570



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 46/58 (79%)
 Strand = Plus / Plus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctatctcaccccgaa 58
                ||| ||||| || |||||||||||||||| ||| ||   || ||||| ||||  ||||
Sbjct: 11816624 gatgatctttaacgtcccttccaacccaagccattctgtgattctatgtcacttcgaa 11816681



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 54/72 (75%), Gaps = 4/72 (5%)
 Strand = Plus / Plus


Query: 1       gatcatcttcaaggtcccttccaacccaaaccactcgaggaatcta----tctcaccccg 56
               ||| ||||||||||||||||||||||||| ||  || |  | ||||    |||| | ||
Sbjct: 3262694 gattatcttcaaggtcccttccaacccaagccgttctatcagtctatgattctcccacca 3262753


Query: 57      aacctggtgttt 68
               ||  | ||||||
Sbjct: 3262754 aatatagtgttt 3262765


>chr9
          Length = 23409228

 Score = 58.6 bits (36), Expect = 1e-006
 Identities = 58/76 (76%), Gaps = 2/76 (2%)
 Strand = Plus / Plus
```

```
Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctatctcaccccgaacc 60
                || |||||| ||||||||||||||||||||||| || | || ||| ||||| | |    |
Sbjct: 17477044 gaccatcttaaaggtcccttccaacccaaaccattctatgattct-tctcatctcctgtc 17477102


Query: 61       tg-gtgtttacagaac 75
                ||  ||   |||||||
Sbjct: 17477103 tgtctgcccacagaac 17477118



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Minus


Query: 2        atcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                || ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 11222336 atgatcttaaaggtcccttccaacccaaaccattctatgattctat 11222291



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 39/44 (88%)
 Strand = Plus / Plus


Query: 5       atcttcaaggtcccttccaacccaaaccactcgaggaatctatc 48
               ||||| ||||||||||||||||||||||| || | || ||||||
Sbjct: 9540139 atcttaaaggtcccttccaacccaaaccattctatgattctatc 9540182



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Minus


Query: 2       atcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
               || ||||| ||||||||||||||||||||||| |  | ||||||||
Sbjct: 3708179 atgatcttaaaggtcccttccaacccaaaccatttcacgaatctat 3708134


>chr14
          Length = 20603938

 Score = 58.6 bits (36), Expect = 1e-006
 Identities = 58/74 (78%), Gaps = 6/74 (8%)
 Strand = Plus / Minus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat--ctcaccccgaa 58
                ||| ||||| |||||||| |||||||||||||| || | || |||||   ||| ||   |
Sbjct: 15101832 gatgatcttaaaggtcccatccaacccaaaccattctatgattctatgattcagcc---a 15101776


Query: 59       cctggtgtttacag 72
                |||||| || ||||
Sbjct: 15101775 cctggt-ttcacag 15101763



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1       gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
               ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 2438204 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 2438158



 Score = 55.5 bits (34), Expect = 9e-006
```

```
 Identities = 43/52 (82%)
 Strand = Plus / Minus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctatctcac 52
                ||| ||||| ||||||||  |||||||||||||||| | || |||||  |||
Sbjct: 16528773 gatgatcttaaaggtcccccccaacccaaaccactccatgattctataacac 16528722


>chrZ
          Length = 33651169

 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 32990619 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 32990573



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||||| ||| ||||||||||||||||||||||| || | || |||||
Sbjct: 26267215 gatcaacttaaaggtcccttccaacccaaaccattctatgattctat 26267169



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1       gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
               ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 8259071 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 8259025



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Plus


Query: 1       gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
               ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 7077473 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 7077519



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 38/42 (90%)
 Strand = Plus / Plus


Query: 5        atcttcaaggtcccttccaacccaaaccactcgaggaatcta 46
                ||||| |||||||||||||||||||||||||| |  ||||||
Sbjct: 11355695 atcttaaaggtcccttccaacccaaaccactctataaatcta 11355736


>chr8
          Length = 30024636

 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Plus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| ||||||||||||||||||||||| || | || |||||
```

```
Sbjct: 12410795 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 12410841


>chr5
          Length = 56310377

 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 40/45 (88%)
 Strand = Plus / Plus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatct 45
                ||| ||||| |||||||||||||||||||||||||| || | |||
Sbjct: 49173512 gatgatcttaaaggtcccttccaacccaaaccactctagaattct 49173556



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Plus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 38711480 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 38711526



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Plus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 38706843 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 38706889



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 28707874 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 28707828



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Minus


Query: 2        atcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                || ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 24103524 atgatcttgaaggtcccttccaacccaaaccattctatgattctat 24103479



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Plus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatcta 46
                ||| ||||| ||||||||||||||||||||||| || | || ||||
Sbjct: 24071790 gatgatcttaaaggtcccttccaacccaaaccattctacgattcta 24071835



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Plus
```

```
Query: 2        atcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                || ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 23995792 atgatcttgaaggtcccttccaacccaaaccattctatgagtctat 23995837



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Minus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatcta 46
                ||| ||||| ||||||||||||||||||||||| || | || ||||
Sbjct: 18800099 gatgatcttaaaggtcccttccaacccaaaccattctatgactcta 18800054


>chr4
          Length = 90634903

 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 87768767 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 87768721



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 79485532 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 79485486



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Plus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 33786008 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 33786054



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Plus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
                ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 30339974 gatgatcttaaaggtcccttccaacccaaaccattctatgactctat 30340020



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Minus


Query: 1        gatcatcttcaaggtcccttccaacccaaaccactcgaggaatcta 46
                ||| ||||| ||||||||||||||||||||||| || | || ||||
Sbjct: 76890134 gatgatcttaaaggtcccttccaacccaaaccattctatgattcta 76890089



 Score = 55.5 bits (34), Expect = 9e-006
```

```
 Identities = 57/78 (73%), Gaps = 3/78 (3%)
 Strand = Plus / Plus


Query: 1       gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctatctcaccccgaacc 60
               ||| ||| |  ||||||||||||||||||  || || | || ||||| ||| |   |||
Sbjct: 4786174 gatgatccttgaggtcccttccaacccaagacattctatgactctatgtcatc---aaca 4786230


Query: 61      tggtgtttacagaacttg 78
               |  |  |||||||| |||
Sbjct: 4786231 tactcattacagaaattg 4786248


>chr28
          Length = 4731479

 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Plus


Query: 1       gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
               ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 4043341 gatgatcttaaaggtcccttccaacccaaaccattctatgattctat 4043387


>chr20
          Length = 13506680

 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query: 1       gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
               ||| ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 4141564 gataatcttaaaggtcccttccaacccaaaccattctatgattctat 4141518



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 42/50 (84%)
 Strand = Plus / Minus


Query: 1       gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctatctc 50
               ||| ||||| ||||||||||||||||||||||| || | ||  |||| ||
Sbjct: 3227359 gatgatcttaaaggtcccttccaacccaaaccattctatgatcctatttc 3227310



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Minus


Query: 2      atcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
              || ||||| |||||||||||||||| ||||||||| | || |||||
Sbjct: 440936 atgatctttaaggtcccttccaacctaaaccactctatgattctat 440891


>chr15
          Length = 12438626

 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Plus


Query: 1       gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
               ||||||||| | ||||||||||||||||||||||||   || |||||
Sbjct: 9939042 gatcatcttaagggtcccttccaacccaaaccactctgtgattctat 9939088


>chr12
```

```
          Length = 19821895

 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Plus


Query: 1       gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
               ||| ||||| ||||| |||||||||||||||||||| | || |||||
Sbjct: 6828595 gataatcttaaaggtgccttccaacccaaaccactctatgattctat 6828641



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 40/45 (88%)
 Strand = Plus / Plus


Query: 1       gatcatcttcaaggtcccttccaacccaaaccactcgaggaatct 45
               ||||||||| ||||||||||||||||||||||| || | || |||
Sbjct: 4238216 gatcatctttaaggtcccttccaacccaaaccattctatgattct 4238260



 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 41/47 (87%)
 Strand = Plus / Plus


Query: 2       atcatcttcaaggtcccttccaacccaaaccactcgaggaatctatc 48
               || ||||| ||||||||||||||||||||||| || | || ||||||
Sbjct: 2472823 atgatcttaaaggtcccttccaacccaaaccattctatgattctatc 2472869



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Plus


Query: 2       atcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
               || |||||||||||||||||||||||||||||  | | || |||||
Sbjct: 1209182 atgatcttcaaggtcccttccaacccaaaccatcctatgattctat 1209227



 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 40/46 (86%)
 Strand = Plus / Minus


Query: 2      atcatcttcaaggtcccttccaacccaaaccactcgaggaatctat 47
              || ||||| ||||||||||||||||||||||| || | || |||||
Sbjct: 769584 atgatcttaaaggtcccttccaacccaaaccattctatgattctat 769539


>chr22
          Length = 2228820

 Score = 55.5 bits (34), Expect = 9e-006
 Identities = 42/50 (84%)
 Strand = Plus / Plus


Query: 1      gatcatcttcaaggtcccttccaacccaaaccactcgaggaatctatctc 50
              ||| |||||||||||||||  |||||||||||| || | || ||||| ||
Sbjct: 578310 gatgatcttcaaggtccctctcaacccaaaccattctatgattctatgtc 578359


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549
```

```
Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 383,076
Number of Sequences: 54
Number of extensions: 383076
Number of successful extensions: 10521
Number of sequences better than 1.0e-005: 20
Number of HSP's better than  0.0 without gapping: 106
Number of HSP's successfully gapped in prelim test: 6
Number of HSP's that attempted gapping in prelim test: 4466
Number of HSP's gapped (non-prelim): 6078
length of query: 456
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 409
effective length of database: 1,133,627,038
effective search space: 463653458542
effective search space used: 463653458542
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|1432069|gb|U59114.1|PCU59114 Phylloscopus occipitalis
microsatellite Pocc2, complete sequence
         (274 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr3                                                                  112   3e-023

>chr3
          Length = 108638738

 Score =  112 bits (70), Expect = 3e-023
 Identities = 168/264 (63%), Gaps = 26/264 (9%)
 Strand = Plus / Minus


Query: 1       gatcctacttgttcctaggtgt-tagaaattttgtctgttagattt--ttctcctttgtg 57
               |||||| |||     | ||| | | |  || ||||||||||  |||  || |||||| |
Sbjct: 7436985 gatcctgcttaccattgggtttcttgctatcttgtctgttaattttctttttccttttta 7436926


Query: 58      tgaaaaaaccacactgagtaagctgctgctattgnnnnnnnnnnnnnnnnnnngaggaa 117
               |  ||||    |||     ||  |||||  | ||                     | |||
Sbjct: 7436925 tagaaaa----cac-----aa--tgctg--actgctccttatacacacacacacaaagaa 7436879


Query: 118     aaaagccttgaaatatgcttttgtttgaaaactgacagtctcatttc-agtagactttct 176
               |     |||||||| ||| || |||||||||||||||||||  |||| |||||||| |||
Sbjct: 7436878 at----cttgaaatgtgcctt-gtttgaaaactgacagtcttgtttccagtagactctct 7436824


Query: 177     ttcatgctaatgtctgtagcaattaaagttttcagttgcaaggaatatttctgtattagt 236
```

```
               |  ||||| ||||||  ||||||||||| |||  |||   |   | || ||| |  ||||
Sbjct: 7436823 tctatgcttatgtcttcagcaattaaagctttgggttcacatccaaatgtctct-gtagt 7436765


Query: 237     gccatt---tgcaaggtgagctaa 257
               | || |   ||||||||||  |||
Sbjct: 7436764 ggcactggctgcaaggtgacgtaa 7436741


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 306,653
Number of Sequences: 54
Number of extensions: 306653
Number of successful extensions: 4
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 3
Number of HSP's gapped (non-prelim): 1
length of query: 274
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 228
effective length of database: 1,133,627,092
effective search space: 258466976976
effective search space used: 258466976976
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|1432070|gb|U59115.1|PCU59115 Phylloscopus occipitalis
microsatellite Pocc4, complete sequence
         (477 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr3                                                                   90   3e-016
chr2                                                                   57   3e-006
chr1                                                                   57   3e-006

>chr3
          Length = 108638738

 Score = 90.3 bits (56), Expect = 3e-016
 Identities = 115/162 (70%), Gaps = 19/162 (11%)
 Strand = Plus / Plus
```

```
Query: 330      aagataatccaa-tttgtttcttcaaggctgcttataattgcttctgcacacactgaccc 388
                || |||| ||   ||||||||| |||||||| ||| |||  |||||||   |  |||  |
Sbjct: 14052279 aatataacccccctttgtttctgcaaggctgtttacaatcacttctgcctgc--tgattc 14052336


Query: 389      ttcacaaaaataaactgcag-------gcatgggatttccctg---ct-agcct-----t 432
                || ||||||||||||| |||       ||| |||  || |||    || ||| |     |
Sbjct: 14052337 tttacaaaaataaacttcagaacagaggcagggggcttacctcagtctgagcttagtgct 14052396


Query: 433      caggtatttgctttacatctctgaggcatactaagctttttt 474
                ||||| ||||||||||||||| ||||||   || ||||||||
Sbjct: 14052397 caggtgtttgctttacatctcagaggcacgttatgctttttt 14052438


>chr2
          Length = 147590765

 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 48/146 (32%)
 Strand = Plus / Plus


Query: 185       attattaggagcttgattnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 244
                 |||||| |||  |  ||
Sbjct: 141597201 attatttggaattacataaataagacatttgacatgcagtaaatactccaagatattcta 141597260


Query: 245       nnnnacacacacacacacacacacnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 304
                     ||||||||||||||||||||
Sbjct: 141597261 tttcacacacacacacacacacacacaagacctattaaaacaaattaaaaataaagaaaa 141597320


Query: 305       nnngaagaaaacgagaaaataatgaa 330
                     |||||||| |   ||| | |||
Sbjct: 141597321 gagaaagaaaaccaagtaattaggaa 141597346



 Score = 55.5 bits (34), Expect = 1e-005
 Identities = 55/157 (35%), Gaps = 3/157 (1%)
 Strand = Plus / Plus


Query: 198      tgattnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnacacacaca 257
                || ||                                              | |||| ||
Sbjct: 91249570 tgttttactaccaccctgcagaattttactcacaagtttgtttatacataaatacacgca 91249629


Query: 258      cacacacacacnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnngaagaaaacg 317
                |||||||||||                                       ||  ||||
Sbjct: 91249630 cacacacacacaagcttttcttgggctagataatatgcctcagaagtgcagacaaaaaat 91249689


Query: 318      agaaaataatgaaaga-taatccaatttgtttcttca 353
                || |||  || ||||| || | |  ||| ||||||||
Sbjct: 91249690 aggaaaagattaaagagtagtgc--tttatttcttca 91249724



 Score = 55.5 bits (34), Expect = 1e-005
 Identities = 52/153 (33%), Gaps = 1/153 (0%)
 Strand = Plus / Minus


Query: 175      tgattctgctattattaggagcttgattnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 234
                ||||| |  | ||  ||   |  ||||
Sbjct: 26179778 tgattttattttttcctatttgagtgatctgttcacttatagtttttctcctactacaaag 26179719


Query: 235      nnnnnnnnnnnnnnacacacacacacacacacacnnnnnnnnnnnnnnnnnnnnnnnnnn 294
                              ||||||||||||||||||||
Sbjct: 26179718 gtgtagtaacatgcacacacacacacacacacacacacacacacaaaatcaggtttctct 26179659
```

```
Query: 295      nnnnnnnnnnnnngaagaa-aacgagaaaataa 326
                             |||||| ||  | |||||||
Sbjct: 26179658 aattgttttagctgaagaagaaaaaaaaaataa 26179626


>chr1
          Length = 188239860

 Score = 57.1 bits (35), Expect = 3e-006
 Identities = 46/140 (32%), Gaps = 1/140 (0%)
 Strand = Plus / Plus


Query: 202       tnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnacacacacacaca 261
                 |                                              |||||||||||||
Sbjct: 187260083 tcatcgctggctgtctcgtggagatgatctattagcttcacaagcacacacacacacaca 187260142


Query: 262       cacacacnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnngaagaaaacgagaa 321
                 |||||||                                        ||||||| || ||
Sbjct: 187260143 cacacacacacacacacaaagaaaatgtcggtgtcttcattatttataagaaaaagaaaa 187260202


Query: 322       aataatg-aaagataatcca 340
                 || || |  || ||| ||||
Sbjct: 187260203 aaaaaagccaaaatattcca 187260222


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 506,965
Number of Sequences: 54
Number of extensions: 506965
Number of successful extensions: 1697
Number of sequences better than 1.0e-005: 3
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 4
Number of HSP's that attempted gapping in prelim test: 1628
Number of HSP's gapped (non-prelim): 61
length of query: 477
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 430
effective length of database: 1,133,627,038
effective search space: 487459626340
effective search space used: 487459626340
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|1432072|gb|U59117.1|PCU59117 Phylloscopus occipitalis
microsatellite Pocc6, complete sequence
```

```
         (248 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



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

  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 173,413
Number of Sequences: 54
Number of extensions: 173413
Number of successful extensions: 0
Number of sequences better than 1.0e-005: 0
Number of HSP's better than  0.0 without gapping: 0
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 0
length of query: 248
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 202
effective length of database: 1,133,627,092
effective search space: 228992672584
effective search space used: 228992672584
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|1432073|gb|U59118.1|PCU59118 Phylloscopus occipitalis
microsatellite Pocc7, complete sequence
         (193 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chrUn                                                                 166   1e-039
chr13                                                                 163   1e-038

>chrUn
          Length = 165033910

 Score =  166 bits (104), Expect = 1e-039
 Identities = 143/194 (73%), Gaps = 11/194 (5%)
 Strand = Plus / Minus
```

```
Query: 1         gatccttttatccatctttcctnnnnnnnnnnnnnnnntccccacgcccagacaaaagtt 60
                 |||||||||||||||| |||||                           |||||||||||
Sbjct: 122831209 gatccttttatccatccttcctcatacacgtgtgcacag----------agacaaaagtt 122831160


Query: 61        gctttcctctaggcaatcggcagccctgggagagtggcaatttctttgattgcttattgt 120
                   ||||||  |||||| |   |||||||||||| ||||| | ||| ||||||||||||||
Sbjct: 122831159 agtttccttcaggcaacccagagccctgggagaatggcagtatctctgattgcttattgt 122831100


Query: 121       agctggagcactggagataaaagtttaatgcatccttattgtctgggtgcttttaagta- 179
                 ||||| ||| | || |||||||||||||||||| ||||||||||  |||||||||||||
Sbjct: 122831099 agctgtagcgccggggataaaagtttaatgcattcttattgtctcagtgcttttaagtat 122831040


Query: 180       tcagctgctccgag 193
                 | |||||| | |||
Sbjct: 122831039 taagctgcgctgag 122831026


>chr13
          Length = 17279963

 Score =  163 bits (102), Expect = 1e-038
 Identities = 142/194 (73%), Gaps = 11/194 (5%)
 Strand = Plus / Plus


Query: 1       gatccttttatccatctttcctnnnnnnnnnnnnnnnntccccacgcccagacaaaagtt 60
               |||||||||||||||| |||||                           |||||||||||
Sbjct: 8446186 gatccttttatccatccttcctcatacacgtgtgcacag----------agacaaaagtt 8446235


Query: 61      gctttcctctaggcaatcggcagccctgggagagtggcaatttctttgattgcttattgt 120
                 ||||||  |||||| |   |||||||||||| ||||| | ||| ||||||||||||||
Sbjct: 8446236 agtttccttcaggcaacccagagccctgggagaatggcagtatctctgattgcttattgt 8446295


Query: 121     agctggagcactggagataaaagtttaatgcatccttattgtctgggtgcttttaagta- 179
               ||||| ||| | || |||||||||||||||||| ||||||||||  |||||||||| ||
Sbjct: 8446296 agctgtagcgccggggataaaagtttaatgcattcttattgtctcagtgcttttaactat 8446355


Query: 180     tcagctgctccgag 193
               | |||||| | |||
Sbjct: 8446356 taagctgcgctgag 8446369


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 138,080
Number of Sequences: 54
Number of extensions: 138080
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 2
Number of HSP's better than  0.0 without gapping: 2
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 1
Number of HSP's gapped (non-prelim): 2
length of query: 193
length of database: 1,133,629,576
effective HSP length: 45
```

```
effective length of query: 148
effective length of database: 1,133,627,146
effective search space: 167776817608
effective search space used: 167776817608
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|1432074|gb|U59119.1|PCU59119 Phylloscopus occipitalis
microsatellite Pocc8, complete sequence
         (290 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                  Score    E
Sequences producing significant alignments:                       (bits) Value

chr5                                                                    71   9e-011

>chr5
          Length = 56310377

 Score = 71.3 bits (44), Expect = 9e-011
 Identities = 109/194 (56%), Gaps = 18/194 (9%)
 Strand = Plus / Minus


Query: 8        tggcagtcttcagcaaaccatcagctctagcaaccacttccacaccactgcaattcttgc 67
                ||| |||||||||||||||||| || | |||||||| || || | |||  ||   || ||
Sbjct: 12656415 tggaagtcttcagcaaaccatctgcacaagcaaccatttacataacacaacagccctagc 12656356


Query: 68       atgtctcttcagacatctgcaactgcaaggctccaatccacaaggg-------agaattn 120
                |  | |  ||||| |    |||   |||| |||  |||| ||||||        | ||
Sbjct: 12656355 acctttctcagagacacacaa---caagactctcatcc-caagggtagttgctgcataa 12656300


Query: 121      nnnnnnnnnnnnnnnnnnnnnnnnnnnnnttcataagaatagctttggctcctgctgttc 180
                                             | ||| | ||   |||  |||||||||
Sbjct: 12656299 tatccacacacacacacacacacacacagtccatcacaa---cttcagctcctgct---- 12656247


Query: 181      ctctctcttgtaaa 194
                 ||||||||| |||
Sbjct: 12656246 ttctctcttgcaaa 12656233


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 221,184
```

```
Number of Sequences: 54
Number of extensions: 221184
Number of successful extensions: 4
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 3
Number of HSP's gapped (non-prelim): 1
length of query: 290
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 244
effective length of database: 1,133,627,092
effective search space: 276605010448
effective search space used: 276605010448
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|9581812|emb|AJ272374.1|PPI272374 Pica pica microsatellite
DNA, clone Ppi 1
         (289 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr1                                                                  142   3e-032

>chr1
          Length = 188239860

 Score =  142 bits (89), Expect = 3e-032
 Identities = 147/195 (75%), Gaps = 13/195 (6%)
 Strand = Plus / Minus


Query: 105      taagcactcatttgcatgcatgcacacatancacat--atctgc-tcttgtt-------c 154
                |||  || |||||||||||| ||| ||| | | |||  || ||| ||| | |       |
Sbjct: 48127653 taaatacccatttgcatgcacgcaaacacatcgcatgcatatgcctctcggtatctactc 48127594


Query: 155      tctgatgtgtgcacatgaactctctgacagaatgggttccctgtgtctctaccacccca- 213
                ||||| ||||||||| || ||||| | |||  |||| ||||||   ||||  ||||||
Sbjct: 48127593 tctgacgtgtgcacacgagctctcgg-cagggtgggctccctgcagctctcacacccctc 48127535


Query: 214      tctgtnatcacacatctactgggaagagg-attgcacaatgctgctgaaatcattgcagc 272
                || || |||| || | | ||||||||||| |||||||||  |||||||||||| ||| ||
Sbjct: 48127534 tccgtgatcaaacgtttgctgggaagaggcattgcacaacactgctgaaatcactgcggc 48127475


Query: 273      cctttctagtcttgc 287
                ||||||||||| |||
Sbjct: 48127474 cctttctagtcctgc 48127460


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54
```

```
Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 183,004
Number of Sequences: 54
Number of extensions: 183004
Number of successful extensions: 2
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 289
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 243
effective length of database: 1,133,627,092
effective search space: 275471383356
effective search space used: 275471383356
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|9581813|emb|AJ272375.1|PPI272375 Pica pica microsatellite
DNA, clone Ppi 2
         (299 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr9                                                                  194   6e-048

>chr9
          Length = 23409228

 Score =  194 bits (122), Expect = 6e-048
 Identities = 200/281 (71%), Gaps = 23/281 (8%)
 Strand = Plus / Minus


Query: 19       caagggtaggtttggaccctgtaacagaaaccacagaccattcgaagcagaacgcctgat 78
                ||||||||| |||||||||||||||||||||||  | |  | | ||| | |||     ||
Sbjct: 12650281 caagggtagatttggaccctgtaacagaaaccatggcctttccaaaggacaacaggcaat 12650222


Query: 79       gcctctggctttgttctgtagccacttat-acagtttcgagggcactgatatgctcatta 137
                |||| |||||||||  |||   ||||  | |||| |||   |||||||||  ||||||||
Sbjct: 12650221 gcctgtggctttgtcttgt---cactgctcacagcttctgaggcactgatgcgctcatta 12650165


Query: 138      tctaagaaattatgtcccanaggtaaaggcaggaggnnnnnnnnnnnnnnnnnnnnnnnn 197
                |||| ||||| |||||||  ||||||||| |||||
Sbjct: 12650164 tctaggaaatgatgtccccaaggtaaaggtaggag----------------cgcctgtgt 12650121
```

```
Query: 198      nnncgcacatgccctctgctgggtactcaggcgctgttgtgttcagacactgctcacagc 257
                    ||||||||||||||||||||||| || | || ||||| |||||  ||||   ||||
Sbjct: 12650120 gcaggcacatgccctctgctgggtactgagtccctattgtgctcaga-gctgcatgcagc 12650062


Query: 258      cgac--tgacacacatcgacttcattcaccatcggagcctt 296
                | ||  |||||||| ||| |||||||||| ||| |||||||
Sbjct: 12650061 ccactgtgacacacttcgccttcattcactatctgagcctt 12650021


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 160,754
Number of Sequences: 54
Number of extensions: 160754
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 299
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 253
effective length of database: 1,133,627,092
effective search space: 286807654276
effective search space used: 286807654276
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|50404826|gb|AY672128.1| Pachycephala pectoralis clone Ppm1
microsatellite sequence
         (366 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr4                                                                  166   3e-039

>chr4
          Length = 90634903

 Score =  166 bits (104), Expect = 3e-039
 Identities = 204/350 (58%), Gaps = 23/350 (6%)
 Strand = Plus / Minus
```

```
Query: 24       tcaagttttgatagtctt---taagggtgnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 80
                ||||  || |||||  ||   || || |
Sbjct: 15682476 tcaaagttagatagggttacatatggcttaatctatacaagttttgaaaatctttaacga 15682417


Query: 81       nnnnnnntactatgatattatggtgttccttccttccttcctgttcctgtaaagacagac 140
                          | ||||||||| ||        |||||||||| ||||||| |||||||||
Sbjct: 15682416 tggagatgcatctgatattatagt--------cttccttcctattcctgtgaagacagac 15682365


Query: 141      aatcaaggaatatgctcatttangaaaaacaagcttcaagaactgctgattcttgcatac 200
                ||| ||||||||  |||||||| | |||  |   | |||||||||||||||||| |||||
Sbjct: 15682364 aatgaaggaatagactcatttaggcaaagtacagtgcaagaactgctgattctttcatac 15682305


Query: 201      a---gctgaaagaggttatgg-aactcatttcacctgtgaaacaaaaatttttattcaga 256
                |    || | | ||| ||||| |||||||| ||||   ||||||||||||   ||||
Sbjct: 15682304 ataccctttaga-agggtatggaaactcattccacccacgaaacaaaaattaccattcttt 15682246


Query: 257      agttacgggttttgannnnnnnnnnnnnnnaaanggatanaaactttctgactcntttcta 316
                 ||| |   ||||                 |   |||  |||    | | ||| ||||||
Sbjct: 15682245 tgttgcaaatttt---tttctttgttgtttagcagatgaaaa----ccgtctcatttcta 15682193


Query: 317      tctcttanaaaacccnccctctnttttcctgatttgtacanaaccatncc 366
                 |||||| | |  ||  ||||  ||||| ||||   || | || ||| ||
Sbjct: 15682192 cctcttaaagaggccagcctccattttcatgatccataaagaagcatacc 15682143


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 257,070
Number of Sequences: 54
Number of extensions: 257070
Number of successful extensions: 15
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 14
Number of HSP's gapped (non-prelim): 1
length of query: 366
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 320
effective length of database: 1,133,627,092
effective search space: 362760669440
effective search space used: 362760669440
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.
```

```
Query= gi|50404829|gb|AY672131.1| Pachycephala pectoralis clone Ppm8
microsatellite sequence
         (833 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr9                                                                  163   6e-038

>chr9
          Length = 23409228

 Score =  163 bits (102), Expect = 6e-038
 Identities = 145/182 (79%), Gaps = 8/182 (4%)
 Strand = Plus / Plus


Query: 1       agctgatgctcttgccattgctcaagctgtctcctgcctggcaggttagcagcgctccag 60
               |||||||| || |||| ||||||||    ||||||| ||||| ||||||||| ||||| |
Sbjct: 8190626 agctgatgttcctgccgttgctcaacacatctcctgtctggcgggttagcagagctcctg 8190685


Query: 61      gccccacaggaaatcttatctgctgcttctcagccaga------atgcttgaaacacag- 113
               ||||  |||||| ||||||||||| |||| ||||||||       || ||| |||   |
Sbjct: 8190686 gccctgcaggaagtcttatctgct-cttcccagccagagagctgctggttgcaacgtgga 8190744


Query: 114     ctcctgggccaaaagcaccttataggaagaagaaaatctgataagctgtgtgggtggtga 173
               ||| | |||||| ||    || ||||||||||||||||||||||||||||||||||||||
Sbjct: 8190745 ctcttaggccaagagtgagttgtaggaagaagaaaatctgataagctgtgtgggtggtga 8190804


Query: 174     ca 175
               ||
Sbjct: 8190805 ca 8190806



 Score = 87.2 bits (54), Expect = 5e-015
 Identities = 127/190 (66%), Gaps = 16/190 (8%)
 Strand = Plus / Plus


Query: 643     ctgagctgtaatgtagctagtgcttggtttattcagtaagcttcactttcacaggatggc 702
               || | || ||||| ||| |||||||||||||| ||| ||| |    |||||||| |
Sbjct: 8190809 ctcatctataatgcagcaagtgcttggtttatccagcaagttctgttttcacagca---a 8190865


Query: 703     tgactccccacacgttggaaccccaggc-tcagtaccctgttaccccagccctgcacatc 761
               |  || |  |   |   |   ||||||| ||||         |  ||||  |||  || |
Sbjct: 8190866 tttctacatatgtgcctggctcccaggcatcag--------aaaaccagagctgggcacc 8190917


Query: 762     ccatattgcagcccctgcacttcccacaccgcctgtttcttcttagcttctcggttcttg 821
               |   || ||||| ||||||| |||||||| ||| || |||| || || ||| |||||  |
Sbjct: 8190918 c---atggcagctcctgcacatcccacacagcc-gtgtctttttggcctcttggttcccg 8190973


Query: 822     aggctgcaga 831
               ||||||||||
Sbjct: 8190974 aggctgcaga 8190983


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549
```

```
Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 464,814
Number of Sequences: 54
Number of extensions: 464814
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 2
length of query: 833
length of database: 1,133,629,576
effective HSP length: 48
effective length of query: 785
effective length of database: 1,133,626,984
effective search space: 889897182440
effective search space used: 889897182440
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|50404831|gb|AY672133.1| Pachycephala pectoralis clone Ppm11
microsatellite sequence
         (653 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr7                                                                  196   5e-048

>chr7
          Length = 37338262

 Score =  196 bits (123), Expect = 5e-048
 Identities = 281/639 (43%), Gaps = 24/639 (3%)
 Strand = Plus / Plus


Query: 3        gttttctttaagaggccaaaaactctgaaaatgtta--------atcagagtccacttca 54
                |||| |||| ||||  ||| |||    |||| ||||        ||||||| ||||||||
Sbjct: 16438816 gtttcctttgagagaacaacaacaaaaaaaaggttagaactttaatcagagcccacttca 16438875


Query: 55       aagttaatgaaaatgcagcagtaggtttgtaaagattgttttgataaaacaatttgaaga 114
                  ||||||||||||||||||||| ||| |||| ||  ||||    ||| |||||  |||
Sbjct: 16438876 tggttaatgaaaatgcagcagtacgttggtaaggacagtttcaggaaagcaattccaagc 16438935


Query: 115      agctctactcacaatcaagtgcttctctttcagc----ttgttatttaagcttttcacca 170
                ||  || || ||| | ||||  |||| |||||||    ||| | ||||| | || |  |
Sbjct: 16438936 agggctgcttacagtgaagtagttctgtttcagcatttttgctctttaaac-ttccttct 16438994


Query: 171      aggaagtacagagcatgatgtacaaatgtgtttcttcccaaaaagggattatactgagag 230
```

```
                  ||| ||   |  |  ||| |||||||| ||||||||   | ||  ||| |    ||||
Sbjct: 16438995 gagaaata---aataaaatggacaaatgttttcttccatcatagatattttgaatagag 16439051


Query: 231      tcttatttctatccagtgagtgtgttcatagactaaatattagtgtgc-atctccagtat 289
                |    ||   |  |||||||| | |   |||  ||||  || || ||| ||||  |||||
Sbjct: 16439052 tacatttaacacacagtgagtctatctgtaggataaaggttggtatgcaatct-gagtat 16439110


Query: 290      tccccaagtctctgaagaataacagaatgattttaaaagtcacgattttttgtaagactg 349
                 | ||||  ||||||| ||||||   | |   | | ||||||| | |||||| |||||
Sbjct: 16439111 cctccaa-actctgaacaataac--caggggataagaagtcac-agtttttgcaagacca 16439166


Query: 350      ctgaaggtctggacagcacagtctctgggccagcatttctgcttcacacctaaccgnnnn 409
                 ||||||| | |  || ||    | |||| ||||||| ||| |||||| ||||| |
Sbjct: 16439167 gtgaaggtgtag-gag-acgtaatttggggcagcattcctgtttcacatctaacagcatc 16439224


Query: 410      nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 469

Sbjct: 16439225 ttcattctttctttacattggaattgaatgcatagcttttccgacagatattaaggagta 16439284


Query: 470      nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 529

Sbjct: 16439285 ttaagtcataaatcccatcagtgtcattaataactatttcaaaattttcaacaactgttc 16439344


Query: 530      nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 589

Sbjct: 16439345 cagaaaagatgttgagttggttcaatccggatcagcaggctgacaaagcgggcaaagtac 16439404


Query: 590      nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnc 628
                                                      |
Sbjct: 16439405 gtacacagttaaccaagctcgcttctctcctgcgtgctc 16439443


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 443,049
Number of Sequences: 54
Number of extensions: 443049
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 1
length of query: 653
length of database: 1,133,629,576
effective HSP length: 48
effective length of query: 605
effective length of database: 1,133,626,984
effective search space: 685844325320
effective search space used: 685844325320
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
```

```
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|22331932|gb|AY045767.1| Sayornis phoebe microsatellite SAP22
sequence
         (460 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr6                                                                  147   2e-033

>chr6
          Length = 33893787

 Score =  147 bits (92), Expect = 2e-033
 Identities = 271/439 (61%), Gaps = 88/439 (20%)
 Strand = Plus / Minus


Query: 15       gtgggagctttgcagtaaacttgattatgcatttttcatcattttctcnnnnnnnnnnnn 74
                |||||  | |||||| ||||||  || ||| |||||||||| ||| |||
Sbjct: 22975304 gtgggcgttttgcaataaactccatcatgaatttttcatcctttgctctgagtgtgt--- 22975248


Query: 75       nnnnnnnnnncgcatgctttgcagggagtacaggcactgatcctgaacctgcacccagca 134
                           || ||| ||||| |  | |||||| ||| ||||| | ||||| ||||||
Sbjct: 22975247 -----------gcgtgccttgcatgtgggacaggctctggtcctggagctgcatccagca 22975199


Query: 135      caggcgtaaaactcacttgtagtgcaccactgatccaaatccttcacatccccagggtaa 194
                |||| || | |  |||  || |           ||||||||  |  ||||| | ||  |
Sbjct: 22975198 cagg-gtgagagccacccgtggc----------tccaaatctatg-catcctcgggccag 22975151


Query: 195      ctccacttcaagttaccctacatgaaatttgaccctggcatctaatagctagggagctgc 254
                |    | |||||||||||| |||||||| |||||   ||||||
Sbjct: 22975150 ccttgcctcaagttaccctgcatgaaatgtgacc---gcatct----------------- 22975111


Query: 255      tcctgtctttaatctctctgacagtgcctagtcagggctttttgaggaattctgtg-gtc 313
                        ||||||| ||||| |||||| ||||   ||||| ||| | ||||| || |||
Sbjct: 22975110 --------ttaatctgtctgatagtgccaagtccctgctttctgaagcattctctgagtc 22975059


Query: 314      ttttcttccacataagcattagctggggggttttgttgnnnnnnnnnnnnnaatgtgcag 373
                |            || ||| ||        |||| ||               || || ||
Sbjct: 22975058 tg-----------aaacatcag--------ttttcttt--------------atctgaag 22975032


Query: 374      tgttgtactgctatctgacctatttacttggaagcctctgaggagggcttgagttagaag 433
                |  |||| ||||||||||||||||||||||||||||| |||||| |||||  ||| |||
Sbjct: 22975031 ttctgtattgctatctgacctatttacttggaagcctgtgaggaaggcttcggttggaaa 22974972


Query: 434      agagctaagtttgtgatcc 452
                ||||||  |||||||||||
Sbjct: 22974971 agagctgtgtttgtgatcc 22974953


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
```

```
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 324,242
Number of Sequences: 54
Number of extensions: 324242
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 1
Number of HSP's gapped (non-prelim): 2
length of query: 460
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 413
effective length of database: 1,133,627,038
effective search space: 468187966694
effective search space used: 468187966694
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|22331933|gb|AY045768.1| Sayornis phoebe microsatellite SAP32
sequence
         (487 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr12                                                                 148   7e-034

>chr12
          Length = 19821895

 Score =  148 bits (93), Expect = 7e-034
 Identities = 278/464 (59%), Gaps = 61/464 (13%)
 Strand = Plus / Plus


Query: 19      atctg-ttattcaatacttcctcatgctctcagctttcatggag-tctttctctttgaaa 76
               ||||| ||  |||  | ||||||||||||  ||||||||| ||| ||||| ||| |||||
Sbjct: 8521784 atctgattgatcacaa-ttcctcatgctccaagctttcattgagatcttt-tctatgaaa 8521841


Query: 77      ttcgactataatcaagatgcttttcc-aactgcaacagagcaacactccagctcttcaga 135
               || ||||| | | ||| |||  |||| ||||| |  |||  |   |||||  ||||   |
Sbjct: 8521842 tttgactacacttaagctgcccttcctaactgtagaagacga---ctccaagtctttcca 8521898


Query: 136     tttgacaattccattcattnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnaaaac 195
               ||||||||||| ||||||                                     ||||
Sbjct: 8521899 tttgacaattctattcat-------------ccacaagaagaaaaaaaggaaaaaaaaa- 8521944
```

```
Query: 196     cctccgagcagtgaaggctaaaaacatacta--tagttagtaaaatgagaacccttaaga 253
                            ||| | |||| |||| |   ||  |||||    || |||| | ||
Sbjct: 8521945 -------------aagacaaaaaccatatttcttaaatagta----gataaccttaaatg 8521987


Query: 254     gac-attgggtccttaacagcttgtattttccatagattcatccgtnnnnnnnnnnnnnn 312
                || |||  || |||| || |  |   ||| |||  |  ||
Sbjct: 8521988 aactattcagtgcttaccaaccagagctttacatgaaagca---------cacacaatca 8522038


Query: 313     ngggggttacttttaaaaaacaaactggtgaaaaaat-tccattttgcttaactacaata 371
                || | | ||||| |||| |||    | ||| ||||| ||||||||| ||||   ||  |
Sbjct: 8522039 gggtgctaactttaaaaacaca----gttgacaaaatgtccattttg-ttaatggcatga 8522093


Query: 372     attaaatctctctgtgtaaaggtacattgaaaaacaagagtgcagcatcatcttcttaat 431
               ||||||   || | |||||| |||||||||||| |||||| ||||     |||| ||| |
Sbjct: 8522094 attaaaatcctttatgtaaaagtacattgaaaagcaagagcgcag---agtcttattagt 8522150


Query: 432     catcacgattaaataaagtcactgggcttatgttacttttacct 475
                  |  | ||||| || | |||| |||||| ||||| |||| ||
Sbjct: 8522151 -tcctggcttaaacaaggccacttggcttacgttacatttaact 8522193


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 422,028
Number of Sequences: 54
Number of extensions: 422028
Number of successful extensions: 5
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 3
Number of HSP's gapped (non-prelim): 2
length of query: 487
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 440
effective length of database: 1,133,627,038
effective search space: 498795896720
effective search space used: 498795896720
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|4519516|dbj|AB013113.1| Schetba rufa DNA, microsatellite
sequence
         (340 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters
```

```
                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr1                                                                115   5e-024

>chr1
          Length = 188239860

 Score =  115 bits (72), Expect = 5e-024
 Identities = 170/273 (62%), Gaps = 30/273 (10%)
 Strand = Plus / Minus


Query: 9         ggagcaattttggcagctaagataccactgacctctgctgggagtaatcagacacattta 68
                 |||||  || ||||  ||||  |||||||||||||||||||||| ||||   |||||| |
Sbjct: 161076145 ggagccgttctggcgactaacttaccactgacctctgctgggaggaatcgcgcacattca 161076086


Query: 69        gct-tctgtcatgggtcctgtgctgctcg-gatgtggtggagattcctctggcagaggct 126
                 ||| | ||||| ||||||||| ||| | |  ||||| ||||||  ||||||||||    |
Sbjct: 161076085 gctctgtgtcacgggtcctgt-ctggttgctatgtgatggagaagcctctggcag----t 161076031


Query: 127       gacnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnacatacgtacgtatgtatg 186
                 | |                                       ||||  ||  | | ||||
Sbjct: 161076030 gccaaattcacatacgtatttgtg------------------cata--ta--tttatatg 161075993


Query: 187       taagacatgcatacctttgtgcagctgcatacaccttccatccttgctgtcactgcaatt 246
                 ||  | ||||| |||| || || |  |  | |||||||||||||  |||||| ||  | |
Sbjct: 161075992 tagtatatgcacacctatgcgctggagtctgcaccttccatcctcactgtcagtggga-t 161075934


Query: 247       tccccaggggccaagtggtgcaaagaagtaaa 279
                 | ||||   |  ||||  ||  |||  ||||||
Sbjct: 161075933 tacccacatgatcaagctgtataaaagagtaaa 161075901


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 301,243
Number of Sequences: 54
Number of extensions: 301243
Number of successful extensions: 5
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 3
Number of HSP's gapped (non-prelim): 2
length of query: 340
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 294
effective length of database: 1,133,627,092
effective search space: 333286365048
effective search space used: 333286365048
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
```

```
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|4519518|dbj|AB013115.1| Schetba rufa DNA, microsatellite
sequence
         (370 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr2                                                                   76   5e-012

>chr2
          Length = 147590765

 Score = 76.1 bits (47), Expect = 5e-012
 Identities = 60/73 (82%)
 Strand = Plus / Plus


Query: 1        ttcagtgccacaaagcagaactggtaccatagttaaggaagaagcaatactgaatgtttt 60
                |||| ||||||||||||||||||||||  ||||| ||| ||||| | ||||| ||||||
Sbjct: 76398114 ttcaatgccacaaagcagaactggtactgtagttgagggagaagtattactggatgtttc 76398173


Query: 61       tgtctactttctg 73
                | |||  ||| ||
Sbjct: 76398174 tatctgttttttg 76398186


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 359,140
Number of Sequences: 54
Number of extensions: 359140
Number of successful extensions: 9
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 8
Number of HSP's gapped (non-prelim): 1
length of query: 370
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 324
effective length of database: 1,133,627,092
effective search space: 367295177808
effective search space used: 367295177808
T: 0
A: 0
X1: 7 (11.1 bits)
```

```
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|4519519|dbj|AB013116.1| Schetba rufa DNA, microsatellite
sequence
         (380 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr1                                                                  123   2e-026

>chr1
          Length = 188239860

 Score =  123 bits (77), Expect = 2e-026
 Identities = 171/272 (62%), Gaps = 29/272 (10%)
 Strand = Plus / Minus


Query: 9         ggagcaattttggcagctaagataccactgacctctgctgggagtaatcagacacattta 68
                 |||||  || ||||  ||||  |||||||||||||||||||||| ||||   |||||| |
Sbjct: 161076145 ggagccgttctggcgactaacttaccactgacctctgctgggaggaatcgcgcacattca 161076086


Query: 69        gct-tctgtcatgggtcctgtgctgctcg-gatgtggtggagattcctctggcagaggct 126
                 ||| | ||||| ||||||||| ||| | |  ||||| ||||||  ||||||||||    |
Sbjct: 161076085 gctctgtgtcacgggtcctgt-ctggttgctatgtgatggagaagcctctggcag----t 161076031


Query: 127       gacnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnacatacgtacgtatgtatg 186
                 | |                                       ||||  ||  | | ||||
Sbjct: 161076030 gccaaattcacatacgtatttgtg------------------cata--ta--tttatatg 161075993


Query: 187       taagacatgcatacctttgtgcagctgcatacaccttccatccttgctgtcactgcaatt 246
                 ||  | ||||| |||| || || |  |  | |||||||||||||  |||||| ||  |||
Sbjct: 161075992 tagtatatgcacacctatgcgctggagtctgcaccttccatcctcactgtcagtgggatt 161075933


Query: 247       tcccaggtggccaagtggtgcaaagaagtaaa 278
                  ||||  ||  ||||  ||  |||  ||||||
Sbjct: 161075932 acccacatgatcaagctgtataaaagagtaaa 161075901


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 342,645
Number of Sequences: 54
Number of extensions: 342645
```

```
Number of successful extensions: 5
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 3
Number of HSP's gapped (non-prelim): 2
length of query: 380
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 333
effective length of database: 1,133,627,038
effective search space: 377497803654
effective search space used: 377497803654
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|4519521|dbj|AB013118.1| Schetba rufa DNA, microsatellite
sequence
         (273 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr1                                                                  301   6e-080

>chr1
          Length = 188239860

 Score =  301 bits (189), Expect = 6e-080
 Identities = 202/222 (90%)
 Strand = Plus / Minus


Query: 52       ttatacacatacagtatatttctatatacatatctctatctaaagnnnnnnnaaatatta 111
                || |||| ||||||||| |||||||||||||| |||||||||||        ||||||||
Sbjct: 31390491 ttttacatatacagtatgtttctatatacatacctctatctaaaaattccctaaatatta 31390432


Query: 112      cgtttcagcagcaaattcctcctgcatgtccccagccaccctaccttgtaactcctcttt 171
                 |||||||||||||||||||||||||||| ||||| |||||||||||||||| |||||||
Sbjct: 31390431 tgtttcagcagcaaattcctcctgcatgttcccagtcaccctaccttgtaacacctcttt 31390372


Query: 172      ggcaacggtgcttttggttgcacccacttgtagcagtgagtctacagctcctctgtgggc 231
                | ||| |||||||| ||| |||||||||||||||||||||||||||||||||||||||||
Sbjct: 31390371 gacaatggtgctttgggtagcacccacttgtagcagtgagtctacagctcctctgtgggc 31390312


Query: 232      ttttccctacagtagaaactttgagagtgacggccattgatc 273
                ||||||||||||||||||||||||||||||||||||||||||
Sbjct: 31390311 ttttccctacagtagaaactttgagagtgacggccattgatc 31390270


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549
```

```
Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 166,709
Number of Sequences: 54
Number of extensions: 166709
Number of successful extensions: 8
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 7
Number of HSP's gapped (non-prelim): 1
length of query: 273
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 227
effective length of database: 1,133,627,092
effective search space: 257333349884
effective search space used: 257333349884
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|9858727|gb|AF263034.1|AF263034 Troglodytes aedon isolate
TA-C3(B)-2 AC microsatellite sequence
         (237 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr23                                                                 112   3e-023

>chr23
          Length = 5666127

 Score =  112 bits (70), Expect = 3e-023
 Identities = 132/215 (61%), Gaps = 11/215 (5%)
 Strand = Plus / Minus


Query: 7       cacacattcagcagccacagcctgtgccagtgcttttcttttgactgctgaaatagatac 66
               |||||| | ||||  |||||||  |||    ||||| ||||     ||||||||| |||
Sbjct: 2327926 cacacactgagcacacacagcccatgcagcagcttt-ctttcctgagctgaaataaata- 2327869


Query: 67      nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnttgacacaactgtgtcagcaaacc 126
                                                   |||||||||||||||||  |||||
Sbjct: 2327868 -------tgtgtatgtgtgtatgtgttgggattttttgacacaactgtgtcaagaaacc 2327816


Query: 127     aaga-tgagcagctcacaggctccaatggtgctttgggctttgttctaggatgagctg-c 184
               ||||   ||||||| |       ||||| ||||||||||||  | | ||||| ||||| |
Sbjct: 2327815 aagagatagcagcttatgaatgacaatgctgctttgggcttaataccaggatcagctgcc 2327756


Query: 185     tggtttagaataaactcataattttgttatgtgat 219
```

```
               ||||||||| | | ||| | || ||| | | ||||
Sbjct: 2327755 tggtttagagtgagctcgtgatattggtgtctgat 2327721


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 212,016
Number of Sequences: 54
Number of extensions: 212016
Number of successful extensions: 5
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 0
Number of HSP's successfully gapped in prelim test: 1
Number of HSP's that attempted gapping in prelim test: 4
Number of HSP's gapped (non-prelim): 1
length of query: 237
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 191
effective length of database: 1,133,627,092
effective search space: 216522774572
effective search space used: 216522774572
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|9858729|gb|AF263036.1|AF263036 Troglodytes aedon isolate
TA-C6-7 AC microsatellite sequence
         (368 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr14                                                                 404   e-111

>chr14
          Length = 20603938

 Score =  404 bits (254), Expect = e-111
 Identities = 302/366 (82%), Gaps = 10/366 (2%)
 Strand = Plus / Minus


Query: 1        aatgcagtagaagacagagagtagcatgaaacacgtnnnnnnnnnnnnnnntatccctaa 60
                |||||| |  || |||||||  | ||| || ||||                      |||
Sbjct: 17151426 aatgcaatgcaatacagagaccaacataaagcacgcacacacacacact--------taa 17151375
```

```
Query: 61       catgctgactttttatcacagaggttgctcatttcccatgctaggaacaacctttggagc 120
                |||||||||| |||||||  ||||||||| ||||||||||||| ||||||||| |||| |
Sbjct: 17151374 catgctgactctttatcatggaggttgctaatttcccatgctaagaacaacctctggaac 17151315


Query: 121      taaaatgaattattcgtctcattctgagtgcatcaaagagcagacagcctttttaaagga 180
                ||||||||||||| || ||||||||||||||||||||||| ||||||||||||||||| |
Sbjct: 17151314 taaaatgaattatgcgcctcattctgagtgcatcaaagagtagacagcctttttaaagta 17151255


Query: 181      gtcaagatcacctcagctgtgcttttgttatctagcccaaggttaaggatttggccttgg 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 17151254 gtcaagatcacctcagctgtgcttttgttatctagcccaaggttaaggatttggccttgg 17151195


Query: 241      gctaacaattggctcagaaaaccaggatcatgaaataagagttctaggaagagagaaaaa 300
                |||||||||||||||||||||||||||||||  ||| ||||||| ||||||| |||||||
Sbjct: 17151194 gctaacaattggctcagaaaaccaggatcatataatgagagttccaggaagacagaaaaa 17151135


Query: 301      ccaaagcttggtaaaggcacgctcttcaaagtgtcccagtagttgacc--tccnnnnnnn 358
                ||||||||||||||| ||||  ||||||||||||||||| |  |||||  | |
Sbjct: 17151134 ccaaagcttggtaaaagcacattcttcaaagtgtcccagcatctgaccctttcttcccat 17151075


Query: 359      cccccct 364
                 |||||
Sbjct: 17151074 tcccct 17151069


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 283,526
Number of Sequences: 54
Number of extensions: 283526
Number of successful extensions: 4
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 3
Number of HSP's gapped (non-prelim): 1
length of query: 368
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 322
effective length of database: 1,133,627,092
effective search space: 365027923624
effective search space used: 365027923624
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|4049626|gb|AF036263.1|AF036263 Telespiza cantans
```

```
microsatellite Tc.11A4D repeat sequence
         (217 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr1                                                                  161   4e-038

>chr1
          Length = 188239860

 Score =  161 bits (101), Expect = 4e-038
 Identities = 123/143 (86%), Gaps = 2/143 (1%)
 Strand = Plus / Minus


Query: 77       ttgtttgtatacgcatgg--ttcagcattgccattcatcttcactctccaaatcaacaat 134
                |||| |||  |||  ||   ||||| |||||||||||||| ||  |||||||||||||||
Sbjct: 48904809 ttgtgtgtgcacgtgtgtgcttcagaattgccattcatctccagcctccaaatcaacaat 48904750


Query: 135      tatctggagtcccccaggagggaaatgcactcctctcataagcttgcagtaatgactagg 194
                ||| |||||||||||||||||||||||   |||| |||||||| || |||||||||| ||
Sbjct: 48904749 tatatggagtcccccaggagggaaatgtgttcctgtcataagcatggagtaatgacttgg 48904690


Query: 195      aagcagtggtgtgtaacaggatc 217
                |||||||||||||||||||||||
Sbjct: 48904689 aagcagtggtgtgtaacaggatc 48904667


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 130,310
Number of Sequences: 54
Number of extensions: 130310
Number of successful extensions: 2
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 2
length of query: 217
length of database: 1,133,629,576
effective HSP length: 45
effective length of query: 172
effective length of database: 1,133,627,146
effective search space: 194983869112
effective search space used: 194983869112
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]
```

```
Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|4049629|gb|AF036266.1|AF036266 Telespiza cantans
microsatellite Tc.11B4E repeat sequence
         (441 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr11_random                                                          239   4e-061

>chr11_random
          Length = 1153135

 Score =  239 bits (150), Expect = 4e-061
 Identities = 252/451 (55%), Gaps = 23/451 (5%)
 Strand = Plus / Plus


Query: 1      gatcggccccattcatctccctggtgatagcagtgaatgtaggataaatctctg-ctg-c 58
              ||||||||||||||||||||||||||||||||||||||||| |||||||||||| ||| |
Sbjct: 836684 gatcggccccattcatctccctggtgatagcagtgaatgta-gataaatctctgactgcc 836742


Query: 59     tgcttgctgctccagtatgatttttattttgtcttccgtgtaca-ctaggtcaaaaagtg 117
              |||||||||||  ||||||||||||||||||||||||||||| | |||||||||||||||
Sbjct: 836743 tgcttgctgctggagtatgatttttattttgtcttccgtgtatacctaggtcaaaaagtg 836802


Query: 118    ggatgtatactgacggtgggtgannnnnnnnnnnnnnnnnnnnnnnncttcttcagtccc 177
              |||||||| || ||  || |||                         || |      | |
Sbjct: 836803 ggatgtatgctcacactgtgtggatgcgtgtgtgtgtgaatttgtctctcccaagcacac 836862


Query: 178    tgtcattc-tctcgcactgaggcacacaaacacacatctccctgcgtg-agtnnnnnnnn 235
                 | | | |||| | |  | |   |   || || || | | |||||| |
Sbjct: 836863 aaacgtacatctc-ctcacacgtgtatgtacgcatat-tacatgcgtgcacacagatata 836920


Query: 236    nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnntctcctcac---------ccc 286
                                                     ||||| |||         | |
Sbjct: 836921 tatccccgcacatgtatgtgtgcacacagtacacacacatctccgcacacacgcacacac 836980


Query: 287    actgacacagctcctgtgcaccgacccgaggc---gnnnnnnnnnnnnnnnnnnnnnnnn 343
              ||| | ||  ||  | ||||   | | |||||   |
Sbjct: 836981 actcatacttctaatctgcaattatctgaggcattgtgtgcatgtgtgtatgtgtgtcca 837040


Query: 344    nnnnnnnnnnnnnnnnnnnnnnnnnncatacacaggcatctcgctacaccgtcaaacatt 403
                                        |||||||||||||||||||  | |  ||||||||
Sbjct: 837041 cacgcacactgctctgtgtgtatgtgcatacacaggcatctcgct--atctacaaacatt 837098


Query: 404    ccctctccntcccagcagaggctgtgtgcag 434
              |||||||| ||||||||||||||||||||||
Sbjct: 837099 ccctctcc-tcccagcagaggctgtgtgcag 837128


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
```

```
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 279,813
Number of Sequences: 54
Number of extensions: 279813
Number of successful extensions: 5
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 1
length of query: 441
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 394
effective length of database: 1,133,627,038
effective search space: 446649052972
effective search space used: 446649052972
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|4049630|gb|AF036267.1|AF036267 Telespiza cantans
microsatellite Tc.12B5E repeat sequence
         (332 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr9                                                                  126   2e-027

>chr9
          Length = 23409228

 Score =  126 bits (79), Expect = 2e-027
 Identities = 195/314 (62%), Gaps = 51/314 (16%)
 Strand = Plus / Minus


Query: 24       aaggttaggttcggaccctgtaacagaagccacaaaccattc--aagcacaacgcctggt 81
                |||| ||| || |||||||||||||||| |||    || |||  ||| |||||      |
Sbjct: 12650280 aagggtagatttggaccctgtaacagaaaccatgg-cctttccaaaggacaacaggcaat 12650222


Query: 82       gcctctggatttgtcctgcagccactgataccgttttgggcactgatatgctcattatct 141
                |||| ||| |||||| ||   |  || | | | | |  |||||||||  |||||||||||
Sbjct: 12650221 gcctgtggctttgtcttgtcactgctcacagcttctgaggcactgatgcgctcattatct 12650162


Query: 142      aagaaatgatgtcccggaggtacaggcaggannnnnnnnnnnnnnnnnnnnnnnnnnnnnn 201
                | |||||||||||||  ||||| ||| ||||
Sbjct: 12650161 aggaaatgatgtccccaaggtaaaggtaggagcgcctgtgtgcag--------------- 12650117


Query: 202      nnnnnnnnnnnnnnnnnnnnnnnnnnnncgcccangccctctgctgggtacacgggccct 261
                                             || || ||||||||||||||||   | ||||
Sbjct: 12650116 -----------------------------gcacatgccctctgctgggtactgagtccct 12650086
```

```
Query: 262      gttgtgctcagacactgctcacagccgac--tggcacacatcgacttcattcaccatcgg 319
                 |||||||||||  ||||   ||||| ||  || ||||| ||| |||||||||| ||| |
Sbjct: 12650085 attgtgctcaga-gctgcatgcagcccactgtgacacacttcgccttcattcactatctg 12650027


Query: 320      agcctt-ggtgatc 332
                |||||| |||||||
Sbjct: 12650026 agccttcggtgatc 12650013


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 163,348
Number of Sequences: 54
Number of extensions: 163348
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 2
length of query: 332
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 286
effective length of database: 1,133,627,092
effective search space: 324217348312
effective search space used: 324217348312
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|4049624|gb|AF036261.1|AF036261 Telespiza cantans
microsatellite Tc.5A5A repeat sequence
         (264 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr2                                                                 190   1e-046

>chr2
          Length = 147590765

 Score =  190 bits (119), Expect = 1e-046
 Identities = 186/268 (69%), Gaps = 34/268 (12%)
```

```
 Strand = Plus / Plus


Query: 1        gatcacgccgacctagatgctatcagaggctagcaaaaatgactggtcagacctgtcagg 60
                ||||||   |||||||||||||||||||| ||||||||||||| ||||||||||||||||
Sbjct: 91296347 gatcactatgacctagatgctatcagaggttagcaaaaatgacaggtcagacctgtcagg 91296406


Query: 61       actaaacagctgcatcaagcagtnnnnnnnagca----ccaggggaaggagggagcagga 116
                |  |||||||||||||||||| |        |||     | |||| |||||||  |  ||
Sbjct: 91296407 atgaaacagctgcatcaagcaatggggtggggcaggtgtctgggggaggagggcacccga 91296466


Query: 117      attgcaaatagagagacagaggagcaggaggaaaagatggaaactgcgtgtcctgaatac 176
                 ||||||  | |||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct: 91296467 gttgcaa--acagagacagagaagcaggaggaaaagatggaaactgcgtgtcctgaata- 91296523


Query: 177      aaggcatgaactnnnnnnnnnnnnnnnnnnnnnnnnnnnnntctctgcagctgaagctct 236
                                                         | | |||||||| |||||
Sbjct: 91296524 ---------------------------tgtataaatgcgtgtgtgtgcagctgcagctca 91296556


Query: 237      gttctcgtcatttgcatatacacagatc 264
                | |||  ||||||||||| |||||||||
Sbjct: 91296557 ggtcttatcatttgcatacacacagatc 91296584


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 194,405
Number of Sequences: 54
Number of extensions: 194405
Number of successful extensions: 8
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 5
Number of HSP's gapped (non-prelim): 2
length of query: 264
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 218
effective length of database: 1,133,627,092
effective search space: 247130706056
effective search space used: 247130706056
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|21743561|gb|AF477389.1| Terpsiphone mutata clone Tmm02
microsatellite sequence
         (328 letters)
```

```
Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                  Score    E
Sequences producing significant alignments:                       (bits) Value

chr1                                                                  164   8e-039

>chr1
          Length = 188239860

 Score =  164 bits (103), Expect = 8e-039
 Identities = 141/175 (80%), Gaps = 14/175 (8%)
 Strand = Plus / Plus


Query: 154      cttcccagtctgtttatcccaagattcttcattgtgtataaaagagtaattagtccaaat 213
                ||||||||||||||||  |||| ||| |||||| || |||||| ||| ||||||||||||
Sbjct: 76478107 cttcccagtctgtttactccaaaattttcattttgcataaaatagttattagtccaaat 76478166


Query: 214      gatactgacacttgataaatgtgggttaactgatattctaaaactcaaatgaaaatctca 273
                |||| ||||| |||||||||||||||||||| || | ||             | ||||||
Sbjct: 76478167 gatagtgacatttgataaatgtgggttaactcatttcct-------------acatctca 76478213


Query: 274      gccttagggaaagggaacagcaaaaaataatcaccttgggagccttcaacaatat 328
                ||||||||| ||||||| ||| ||||||| |||||||| ||| ||||| ||||||
Sbjct: 76478214 gccttaggggaagggaaaagc-aaaaatattcaccttgagaggcttcagcaatat 76478267


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 220,143
Number of Sequences: 54
Number of extensions: 220143
Number of successful extensions: 4
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 1
length of query: 328
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 282
effective length of database: 1,133,627,092
effective search space: 319682839944
effective search space used: 319682839944
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
```

```
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|21743565|gb|AF477393.1| Terpsiphone mutata clone Tmm06
microsatellite sequence
         (390 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr21                                                                 210   1e-052

>chr21
          Length = 6202554

 Score =  210 bits (132), Expect = 1e-052
 Identities = 133/322 (41%)
 Strand = Plus / Plus


Query: 1       cactgcaaaaacagaaaatgaggggctgcagagccgcaccaatttacttcatccgacctt 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3846281 cactgcaaaaacagaaaatgaggggctgcagagccgcaccaatttacttcatccgacctt 3846340


Query: 61      gattaaaagaaaattaattgccgcatctctcaggatatctcaggcagcagccaatggctc 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3846341 gattaaaagaaaattaattgccgcatctctcaggatatctcaggcagcagccaatggctc 3846400


Query: 121     tctagaatggcacnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 180
               || ||||||||||
Sbjct: 3846401 tccagaatggcacaaaaaaaaagaaaaaagaaaaaaccagggagcgaggcacagagaatc 3846460


Query: 181     nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 240

Sbjct: 3846461 tttgccctttcatctcgtagcgcaactgtcttattggaagcgttggcaggaggagggaga 3846520


Query: 241     nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 300

Sbjct: 3846521 aaacccagtgctcaggaaagcatggagaagggaaggcaacgcgagtttgccaaggtttcc 3846580


Query: 301     nnnnnnnnnnnnnnnnnnnnnc 322
                                    |
Sbjct: 3846581 agccgaaatttcccttctgtgc 3846602



 Score = 77.7 bits (48), Expect = 2e-012
 Identities = 58/68 (85%), Gaps = 1/68 (1%)
 Strand = Plus / Plus


Query: 322     cagggagcaagccacaganaatctttgccctt-catctcatagcacaactgtcttactan 380
               |||||||| || |||||| ||||||||||||| |||||| |||| ||||||||||| |
Sbjct: 3846438 cagggagcgaggcacagagaatctttgccctttcatctcgtagcgcaactgtcttattgg 3846497


Query: 381     aagtgttg 388
               ||| ||||
Sbjct: 3846498 aagcgttg 3846505


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54
```

```
Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 179,983
Number of Sequences: 54
Number of extensions: 179983
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 2
length of query: 390
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 343
effective length of database: 1,133,627,038
effective search space: 388834074034
effective search space used: 388834074034
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|5410417|gb|AF130431.1| Plocepasser mahali microsatellite
WBSW1 sequence
         (333 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr1                                                                  106   4e-021

>chr1
          Length = 188239860

 Score =  106 bits (66), Expect = 4e-021
 Identities = 146/216 (67%), Gaps = 9/216 (4%)
 Strand = Plus / Minus


Query: 1       ttcacatcatctcttattgacccttctaacttgatatatattggaacggcctctgtttgg 60
               ||||||| |||| |||  | | ||| | |||||| |  | | ||  |  | ||| ||  |
Sbjct: 7227781 ttcacattatctgttacgg-ctctttttacttgaaaagtttggggccatcttctcttcag 7227723


Query: 61      tttcactgtcacatataatttaaatatacaaatctttcttcctataaacctttacacact 120
               |||   | || | | |||   || ||   |||| ||||| |||||||  ||||  |  ||
Sbjct: 7227722 ttttcttatctcttctaaa--aagta---aaatatttctgcctataagtctttgtatcct 7227668


Query: 121     tcacttgctggactttattttatgctctgcccagttgccacacttcctaccctttta--t 178
                  ||  ||  || | |||| ||    |||||  ||  |||||||| || |||||||  |
Sbjct: 7227667 ctgctaacttcacctcatttgatttcatgccctatttgcacacttcgtaaccttttaatt 7227608
```

```
Query: 179     tcctagtcattcatcatgttttatggaaagcatata 214
               |||| |||||| || ||||||||||||||| | |||
Sbjct: 7227607 tcct-gtcatttataatgttttatggaaagaagata 7227573


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 262,581
Number of Sequences: 54
Number of extensions: 262581
Number of successful extensions: 4
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 0
Number of HSP's successfully gapped in prelim test: 1
Number of HSP's that attempted gapping in prelim test: 4
Number of HSP's gapped (non-prelim): 1
length of query: 333
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 287
effective length of database: 1,133,627,092
effective search space: 325350975404
effective search space used: 325350975404
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|3347993|gb|AF076665.1|AF076665 Zosterops lateralis
chlorocephala clone ZL04, microsatellite sequence
         (204 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chrZ                                                                   97   1e-018

>chrZ
          Length = 33651169

 Score = 96.7 bits (60), Expect = 1e-018
 Identities = 62/64 (96%)
 Strand = Plus / Plus


Query: 141      aagaccctgaagaaaagcagacagctgctaactagttgtctagctgtctatttgtggaca 200
                || | |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 26966703 aaaaacctgaagaaaagcagacagctgctaactagttgtctagctgtctatttgtggaca 26966762
```

```
Query: 201      tttt 204
                ||||
Sbjct: 26966763 tttt 26966766


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 147,925
Number of Sequences: 54
Number of extensions: 147925
Number of successful extensions: 8
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 6
Number of HSP's gapped (non-prelim): 2
length of query: 204
length of database: 1,133,629,576
effective HSP length: 45
effective length of query: 159
effective length of database: 1,133,627,146
effective search space: 180246716214
effective search space used: 180246716214
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|25266098|emb|AJ517994.1|ZLA517994 Zosterops lateralis
microsatellite DNA, locus ZL41
         (290 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr2                                                                   92   6e-017

>chr2
          Length = 147590765

 Score = 91.9 bits (57), Expect = 6e-017
 Identities = 102/141 (72%), Gaps = 5/141 (3%)
 Strand = Plus / Plus


Query: 91       agcccagatcttgcatcaggagagatttattctgtgcctttttgcttctctgcccttctg 150
                ||| |||  ||||    |  || || ||  | ||||||||| || || ||||| ||||
```

```
Sbjct: 13852424 agcacaggccttgacctaatagtgacttgctatgtgcctttgtggttttctgctcttcct 13852483


Query: 151      actttggtgaggacagtctatctttc--ctgc-cgagagacttttgcctgatatggagaa 207
                 ||||| | |||||  ||||||||    || | |  | |||  || | ||||||| ||||
Sbjct: 13852484 gctttgttaaggac--tctatcttgtggcttctcctgggacacttccttgatatgcagaa 13852541


Query: 208      gtgtaagaaaggctgcctgca 228
                |||||||||||||||||||||
Sbjct: 13852542 gtgtaagaaaggctgcctgca 13852562


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 219,863
Number of Sequences: 54
Number of extensions: 219863
Number of successful extensions: 2
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 0
Number of HSP's successfully gapped in prelim test: 1
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 1
length of query: 290
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 244
effective length of database: 1,133,627,092
effective search space: 276605010448
effective search space used: 276605010448
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|25266101|emb|AJ517996.1|ZLA517996 Zosterops lateralis
microsatellite DNA, locus ZL44
         (243 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr13                                                                  86   4e-015

>chr13
          Length = 17279963

 Score = 85.6 bits (53), Expect = 4e-015
```

```
 Identities = 135/230 (58%), Gaps = 32/230 (13%)
 Strand = Plus / Minus


Query: 15       ctcatcccacnnnnnnnnnnnnnnnnnnnagggtgccgtgtggagccggggaagcagg-g 73
                |||| | | |                     | ||| |  ||||||   | |  | || |
Sbjct: 12065761 ctcacctcccctcttttacagggctgcacgtgctgctgc-tggagcaaagcatcctggag 12065703


Query: 74       atccgccatgcccacattgccaccaccaaccacaccgaggctgcccgccgccccctcgcc 133
                | ||||||||||  |||  |  ||   | ||||||||||||  ||||| |||||||||||
Sbjct: 12065702 agccgccatgcctgcatgtctgcccagacccacaccgaggcctcccgctgccccctcgcc 12065643


Query: 134      ccactgaggctatggannnnnnnnnnnnnnnnncatcaccacaggaattttggcttggca 193
                |||||||||| ||                              || |||| |||| || |
Sbjct: 12065642 ccactgaggccat------------------------------gggatttcggctgggga 12065613


Query: 194      aggggactcttggtgcctctgccatggtgacatgaagcagacggcgaggg 243
                  ||||||||  |  | | ||||||||||||||||||| ||| |||||||
Sbjct: 12065612 cagggactctcagcacgtttgccatggtgacatgaagcggacagcgaggg 12065563


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 100,312
Number of Sequences: 54
Number of extensions: 100312
Number of successful extensions: 2
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 2
length of query: 243
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 197
effective length of database: 1,133,627,092
effective search space: 223324537124
effective search space used: 223324537124
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|25266103|emb|AJ517997.1|ZLA517997 Zosterops lateralis
microsatellite DNA, locus ZL45
         (552 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters
```

```
                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr13_random                                                          76   7e-012

>chr13_random
          Length = 1219686

 Score = 76.1 bits (47), Expect = 7e-012
 Identities = 91/148 (61%), Gaps = 10/148 (6%)
 Strand = Plus / Plus


Query: 185   ggcccggagcaccacg---cacagctcccaggcattnnnnnnnnnnnnnnnnnnnnn- 240
              |||||  |||||| |    |||||||| |||| ||
Sbjct: 43818 ggcccc-agcaccgctgcacacagctctcaggtatcgacagacagacactcagacagaca 43876


Query: 241   ---gtgggcaggctgcagccattcctgctcatccaacatggaagaactcgaggcgcttgg 297
                 |||||||||| |||||||||||||||  ||||      || ||   |||| | ||||
Sbjct: 43877 gacgtgggcaggccgcagccattcctgcttctccaggggacaataaggggaggggtttgg 43936


Query: 298   acccagacc-aagtatttcctcaagtcc 324
              |  |||||| ||||| ||||||||| ||
Sbjct: 43937 attcagaccgaagta-ttcctcaagccc 43963


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 361,740
Number of Sequences: 54
Number of extensions: 361740
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 1
length of query: 552
length of database: 1,133,629,576
effective HSP length: 47
effective length of query: 505
effective length of database: 1,133,627,038
effective search space: 572481654190
effective search space used: 572481654190
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 35 (57.1 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|25266107|emb|AJ517999.1|ZLA517999 Zosterops lateralis
```

```
microsatellite DNA, locus ZL48
         (358 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr16                                                                 87   2e-015

>chr16
          Length = 239457

 Score = 87.2 bits (54), Expect = 2e-015
 Identities = 85/117 (72%)
 Strand = Plus / Plus


Query: 1      actgcagcntgaaggagtcaaaagagccctcagggactctccactggagctccacagagt 60
              |||||| | ||||||||||||| |||||||| ||||| ||||| |  ||||  || ||||
Sbjct: 210057 actgcaccgtgaaggagtcaaaggagccctcggggacgctccattccagctggacggagt 210116


Query: 61     ttggtgtgacactggagaccttcagctcctccagcactgcttgcattgggagtgcct 117
                ||  ||||   |||| || |||||||  ||||   || |||   |||  || |||
Sbjct: 210117 cggggctgacgtgggaggccgtcagctcacccaggcgtggttgggatggcggttcct 210173



 Score = 84.0 bits (52), Expect = 2e-014
 Identities = 82/113 (72%)
 Strand = Plus / Plus


Query: 1      actgcagcntgaaggagtcaaaagagccctcagggactctccactggagctccacagagt 60
              |||||| | ||||||||||||| |||||||| ||||  ||||| |  ||||  || ||||
Sbjct: 212302 actgcaccgtgaaggagtcaaaggagccctcggggatgctccattccagctggacggagt 212361


Query: 61     ttggtgtgacactggagaccttcagctcctccagcactgcttgcattgggagt 113
                ||  ||||   |||| || |||||||  ||||   || |||   ||| |||
Sbjct: 212362 cggggctgacgtgggaggccgtcagctcacccaggcgtggttgggatggcagt 212414



 Score = 82.4 bits (51), Expect = 5e-014
 Identities = 69/88 (78%)
 Strand = Plus / Plus


Query: 1      actgcagcntgaaggagtcaaaagagccctcagggactctccactggagctccacagagt 60
              |||||| | ||||||||||||| |||||||||||||  ||||| |  ||||  || ||||
Sbjct: 210691 actgcaccgtgaaggagtcaaaggagccctcagggatgctccattccagctggacggagt 210750


Query: 61     ttggtgtgacactggagaccttcagctc 88
              | ||  |||||  |||  || |||||||
Sbjct: 210751 tggggctgacatgggatgccgtcagctc 210778



 Score = 71.3 bits (44), Expect = 1e-010
 Identities = 68/93 (73%)
 Strand = Plus / Plus


Query: 1      actgcagcntgaaggagtcaaaagagccctcagggactctccactggagctccacagagt 60
              |||||| | ||||||||||||| |||||||| ||||| ||||| |  ||||  || ||||
Sbjct: 211654 actgcaccgtgaaggagtcaaaggagccctcggggacgctccattccagctggacggagt 211713


Query: 61     ttggtgtgacactggagaccttcagctcctcca 93
                ||   |||   |||  |  |||||||  |||
```

```
Sbjct: 211714 cggggccgacgtgggacgctgtcagctcaccca 211746



 Score = 68.2 bits (42), Expect = 1e-009
 Identities = 85/129 (65%)
 Strand = Plus / Plus


Query: 1      actgcagcntgaaggagtcaaaagagccctcagggactctccactggagctccacagagt 60
              |||||| | ||||||||||||| | ||||||| |||| ||||| |  ||||  |  |||
Sbjct: 213126 actgcaccgtgaaggagtcaaaggtgccctcaaggacactccattccagctggatggagc 213185


Query: 61     ttggtgtgacactggagaccttcagctcctccagcactgcttgcattgggagtgcctgag 120
              | || || ||   ||||||  | |||    ||||    |   ||  |||  || |||
Sbjct: 213186 taggagtcacgtgggagactgtgagcatgcccaggcggggccgctgtggtggttcctcct 213245


Query: 121    atgaagggg 129
               ||| ||||
Sbjct: 213246 ctgatgggg 213254


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 202,820
Number of Sequences: 54
Number of extensions: 202820
Number of successful extensions: 6
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 1
Number of HSP's gapped (non-prelim): 5
length of query: 358
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 312
effective length of database: 1,133,627,092
effective search space: 353691652704
effective search space used: 353691652704
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|25266113|emb|AJ518002.1|ZLA518002 Zosterops lateralis
microsatellite DNA, locus ZL51
         (230 letters)

Database: WholeChickenGenome.txt
          54 sequences; 1,133,629,576 total letters
```

```
                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr5                                                                  301   5e-080

>chr5
          Length = 56310377

 Score =  301 bits (189), Expect = 5e-080
 Identities = 211/231 (91%), Gaps = 3/231 (1%)
 Strand = Plus / Minus


Query: 1        gcaggagcgtcacccagccaggctgggatcctgctggcagcctctccctctgtttgagct 60
                ||||||||||||||| | |||||||||||||||||||||||||||||| || ||||||||
Sbjct: 35072202 gcaggagcgtcacccgggcaggctgggatcctgctggcagcctctcccgctctttgagct 35072143


Query: 61       catgggctaaatgcagcgcttgatgctgctgctgttgctg---ttgctgcgcgagcaacc 117
                || |||||||||||||||| |||||| ||||| |  || |   |||| ||||||||||||
Sbjct: 35072142 cacgggctaaatgcagcgcctgatgccgctgccgccgccgccgttgccgcgcgagcaacc 35072083


Query: 118      tccgttcttagagatctgggccacgggggcgggagaactgggccagctgctatttctgaa 177
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 35072082 tccgttcttagagatctgggccacgggggcgggagaactgggccagctgctatttctgcg 35072023


Query: 178      ctgcccgtcagagcagaggggacagccaaggactgccgcagctcacggccc 228
                ||||||||||| || ||||||||||||||||||||||||||| ||||||||
Sbjct: 35072022 ctgcccgtcagcgccgaggggacagccaaggactgccgcagcgcacggccc 35071972


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 189,419
Number of Sequences: 54
Number of extensions: 189419
Number of successful extensions: 32
Number of sequences better than 1.0e-005: 1
Number of HSP's better than  0.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 29
Number of HSP's gapped (non-prelim): 2
length of query: 230
length of database: 1,133,629,576
effective HSP length: 45
effective length of query: 185
effective length of database: 1,133,627,146
effective search space: 209721022010
effective search space used: 209721022010
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
BLASTN 2.2.8 [Jan-05-2004]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
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Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|25266115|emb|AJ518003.1|ZLA518003 Zosterops lateralis
microsatellite DNA, locus ZL52
         (348 letters)

Database: WholeChickenGenome.txt
           54 sequences; 1,133,629,576 total letters



                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

chr15                                                                 131   9e-029
chr19                                                                  74   1e-011

>chr15
          Length = 12438626

 Score =  131 bits (82), Expect = 9e-029
 Identities = 97/112 (86%)
 Strand = Plus / Plus


Query: 237     agccgagactcacttggaaagggacaccccaccgggcttcccgatgagctcctcgtggtg 296
               |||  | |||||||||||||| ||||| || ||||||||||| |||||||||||||||||
Sbjct: 7126326 agcacacactcacttggaaagagacactccgccgggcttccctatgagctcctcgtggtg 7126385


Query: 297     cagcaccgtgtcgctccaggagatgtccaggaacctcatgatgttgtgcatg 348
               |||||| ||||| |||||||||||  |||||||| ||||||||   ||||||
Sbjct: 7126386 cagcacggtgtcactccaggagatacccaggaacttcatgatggcatgcatg 7126437


>chr19
          Length = 9463882

 Score = 74.5 bits (46), Expect = 1e-011
 Identities = 83/118 (70%), Gaps = 2/118 (1%)
 Strand = Plus / Minus


Query: 222     aaaagccaaggaaaga--gccgagactcacttggaaagggacaccccaccgggcttcccg 279
               |||||  |||  | ||  ||  | |||||||||||||| || || || ||||  || ||
Sbjct: 4694313 aaaagataagagaggaacgctcatactcacttggaaagagaaacaccgccggcttttcca 4694254


Query: 280     atgagctcctcgtggtgcagcaccgtgtcgctccaggagatgtccaggaacctcatga 337
               || |  || |||||||||||||| |  | | |||| | ||||   |||||| | | ||
Sbjct: 4694253 atcatttcttcgtggtgcagcactgcttggttccatgggatgcgaaggaactttaaga 4694196


  Database: WholeChickenGenome.txt
    Posted date:  Jun 15, 2004  1:46 PM
  Number of letters in database: 1,133,629,576
  Number of sequences in database:  54

Lambda     K      H
    1.10    0.333    0.549

Gapped
Lambda     K      H
    1.10    0.333    0.549


Matrix: blastn matrix:1 -1
Gap Penalties: Existence: 2, Extension: 1
Number of Hits to DB: 184,338
Number of Sequences: 54
Number of extensions: 184338
Number of successful extensions: 3
Number of sequences better than 1.0e-005: 2
Number of HSP's better than  0.0 without gapping: 2
```

```
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 1
Number of HSP's gapped (non-prelim): 2
length of query: 348
length of database: 1,133,629,576
effective HSP length: 46
effective length of query: 302
effective length of database: 1,133,627,092
effective search space: 342355381784
effective search space used: 342355381784
T: 0
A: 0
X1: 7 (11.1 bits)
X2: 18 (28.5 bits)
S1: 14 (23.8 bits)
S2: 34 (55.5 bits)
```