Beatrice and Grant Duckett
Duckett Truffieres
400 Lowry's Rd.
Parksville, BC V9P 2B5

September 09, 2009

Fragment Analysis and DNA Sequencing Services
University of British Columbia Okanagan
3333 University Way
Kelowna, BC V1V1V7

Dear Beatrice and Grant Duckett,

I have completed the molecular prep and DNA sequencing for the six fungal samples received on August 27th, 2009. DNA from all six samples was successfully extracted and amplified. Subsequent DNA sequencing was successful on three of the six samples, providing a high degree of confidence in species identification. A second attempt to sequence the three unsuccessful samples using different primer sets for amplification and subsequent sequencing were also unsuccessful. It was observed that the successful samples were those from the fruiting bodies whereas the samples which were not successful appeared to be soil samples. The following is a brief summary of the results. Please see the attached document for more details.

Sample #1-2008- *Tuber melanosporum*; 100% identity over 571bp
Sample #2-2009- *Tuber melanosporum*; 100% identity over 551bp
Sample #3-2009- *Tuber melanosporum*; 100% identity over 240bp
Sample #4-2009- Uncultured fungus genomic DNA sequence, 99% identity over 521bp
Sample #5-2009- unable to sequence
Sample #6-2009- Uncultured mycorrhizal fungus genes, 95% identity over 693bp

Sample 5 showed multiple bands in sequencing which makes it hard to sequence it with regular sequencing methods.

Please do not hesitate to contact me if you have any questions or concerns.

Sincerely,

Mahsa Amirabbasi
FADSS Technician
(250) 807-9610
mahsa.amirabbasi@ubc.ca

Results Summary

Sample #1-2008- *Tuber melanosporum*; 100% identity over 571bp

Sample #2-2009- *Tuber melanosporum*; 100% identity over 551bp

Sample #3-2009- *Tuber melanosporum*; 100% identity over 240bp

Sample #4-2009- Uncultured fungus genomic DNA sequence, 99% identity over 521bp

Sample #5-2009- unable to sequence

Sample #6-2009- Uncultured mycorrhizal fungus genes, 95% identity over 693bp

Sample #1-2008

Contig sequence derived from ITS1 and LR21 primers (891bp)

TTGTGTATTCCCGAACACAAACCTCTCTGCGTATCACTCCATGTTGCTTCCACA
GGTTAAGTGACCATGCTGGCACCTGTGGGAGATCTCTATGTTAACGGAGTATTT
GATTGTGCTGTCTGAGCTGGCCATGTGTCAGATTTAGTAAAGTAAAAACTTTCA
ACAACGGATCTCTTGGCTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAG
GTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACATTGCG
CCCTTTGGTATTCCTTAGGGCATGCCTGTTCGAGCGTCACTACACACCTTATCA
CAAAGTTTGTGGTCTTGGCAGGAGTGAATTGCTAGTCTATCAAAATGTTCCAG
CTGTACACTCTGCTAAAAATTATGAGAAGGTTACCAGGCATGAACGACGGACT
TTATAAACGGTTATAAGACCTGGATCAGTCACAAGTCTTGTCTGGTCCTTACCT
TAAGGACCCCCATCCTAGATGAACTATGGGTTGACCTCGAATCAGGGAGGGAT
ACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAACCAACAGGGA
TTGCCCTAGTAACGGCGAGTGAAGCGGCAAAAGCTCAAATTTGAAATCTGGC
ACCTTTGGTGTCCGAATTGTAATTTGGAGAGGCAACTTCGGGTAGGACCCAGT
CTATGTTCCTTGGAACAGGACGTCATAGAGGGTGAGAATCCCGTTCATGACTG
GATGTTCCTACTAGTACGTAGTGCCTTCTACGAGTCGAGTTGTTTGGGAATGCA
GCTCAAAATGGGTGGTAAATTTCATCTAAAGCTAAATATTGGCGAGAGACCGA
TAGCGCACAAGTAGAGTGATCGAAAGATGAAAGCACT

Blastn top result for percent identity using the Nucleotide Collection (nr/nt) database optimized for highly similar sequences (megablast)

>   gb|U89359.1|TMU89359 Tuber melanosporum internal transcribed spacer
sequence
Length=620

```
 Score = 1055 bits (571),  Expect = 0.0
 Identities = 571/571 (100%), Gaps = 0/571 (0%)
 Strand=Plus/Plus

Query  1     TTGTGTATTCCCGAACACAAACCTCTCTGCGTATCACTCCATGTTGCTTCCACAGGTTAA  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  50    TTGTGTATTCCCGAACACAAACCTCTCTGCGTATCACTCCATGTTGCTTCCACAGGTTAA  109

Query  61    GTGACCATGCTGGCACCTGTGGGAGATCTCTATGTTAACGGAGTATTTGATTGTGCTGTC  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110   GTGACCATGCTGGCACCTGTGGGAGATCTCTATGTTAACGGAGTATTTGATTGTGCTGTC  169

Query  121   TGAGCTGGCCATGTGTCAGATTTAGTAAAGTAAAAACTTTCAACAACGGATCTCTTGGCT  180
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   170   TGAGCTGGCCATGTGTCAGATTTAGTAAAGTAAAAACTTTCAACAACGGATCTCTTGGCT   229

Query   181   CTCGCATCGATGAAGAACGCAGCGAAATGCGATAGGTAATGTGAATTGCAGAATTCAGTG   240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   230   CTCGCATCGATGAAGAACGCAGCGAAATGCGATAGGTAATGTGAATTGCAGAATTCAGTG   289

Query   241   AATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCTTAGGGCATGCCTGTTC   300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   290   AATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCTTAGGGCATGCCTGTTC   349

Query   301   GAGCGTCACTACACACCTTATCACAAAGTTTGTGGTCTTGGCAGGAGTGAATTGCTAGTC   360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   350   GAGCGTCACTACACACCTTATCACAAAGTTTGTGGTCTTGGCAGGAGTGAATTGCTAGTC   409

Query   361   TATCAAAATGTTCCAGCTGTACACTCTGCTAAAAATTATGAGAAGGTTACCAGGCATGAA   420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   410   TATCAAAATGTTCCAGCTGTACACTCTGCTAAAAATTATGAGAAGGTTACCAGGCATGAA   469

Query   421   CGACGGACTTTATAAACGGTTATAAGACCTGGATCAGTCACAAGTCTTGTCTGGTCCTTA   480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   470   CGACGGACTTTATAAACGGTTATAAGACCTGGATCAGTCACAAGTCTTGTCTGGTCCTTA   529

Query   481   CCTTAAGGACCCCCATCCTAGATGAACTATGGGTTGACCTCGAATCAGGGAGGGATACCC   540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   530   CCTTAAGGACCCCCATCCTAGATGAACTATGGGTTGACCTCGAATCAGGGAGGGATACCC   589

Query   541   GCTGAACTTAAGCATATCAATAAGCGGAGGA   571
              |||||||||||||||||||||||||||||||
Sbjct   590   GCTGAACTTAAGCATATCAATAAGCGGAGGA   620
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Sample #2-2009

Contig sequence derived from ITS1 and LR21 primers (869bp)

ACCTCTCTGCGTATCACTCCATGTTGCTTCCACAGGTTAAGTGACCATGCTGGC
ACCTGTGGGAGATCTCTATGTTAACGGAGTATTTGATTGTGCTGTCTGAGCTGG
CCATGTGTCAGATTTAGTAAAGTAAAAACTTTCAACAACGGATCTCTTGGCTCT
CGCATCGATGAAGAACGCAGCGAAATGCGATAGGTAATGTGAATTGCAGAATT
CAGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCTTAGGG
CATGCCTGTTCGAGCGTCACTACACACCTTATCACAAAGTTTGTGGTCTTGGC
AGGAGTGAATTGCTAGTCTATCAAAATGTTCCAGCTGTACACTCTGCTAAAAAT
TATGAGAAGGTTACCAGGCATGAACGACGGACTTTATAAACGGTTATAAGACC
TGGATCAGTCACAAGTCTTGTCTGGTCCTTACCTTAAGGACCCCCATCCTAGAT
GAACTATGGGTTGACCTCGAATCAGGGAGGGATACCCGCTGAACTTAAGCATA
TCAATAAGCGGAGGAAAAGAAACCAACAGGGATTGCCCTAGTAACGGCGAGT
GAAGCGGCAAAAGCTCAAATTTGAAATCTGGCACCTTTGGTGTCCGAATTGTA
ATTTGGAGAGGCAACTTCGGGTAGGACCCAGTCTATGTTCCTTGGAACAGGAC
GTCATAGAGGGTGAGAATCCCGTTCATGACTGGATGTTCCTACTAGTACGTAGT
GCCTTCTACGAGTCGAGTTGTTTGGGAATGCAGCTCAAAATGGGTGGTAAATT
TCATCTAAAGCTAAATATTGGCGAGAGACCGATAGCGCACAAGTAGAGTGATC
GAAAGATGAAAAGCA

Blastn top result for percent identity using the Nucleotide Collection (nr/nt) database optimized for highly similar sequences (megablast)

> gb|U89359.1|TMU89359 Tuber melanosporum internal transcribed spacer sequence
Length=620

```
 Score = 1018 bits (551),  Expect = 0.0
 Identities = 551/551 (100%), Gaps = 0/551 (0%)
 Strand=Plus/Plus

Query  1    ACCTCTCTGCGTATCACTCCATGTTGCTTCCACAGGTTAAGTGACCATGCTGGCACCTGT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  70   ACCTCTCTGCGTATCACTCCATGTTGCTTCCACAGGTTAAGTGACCATGCTGGCACCTGT  129

Query  61   GGGAGATCTCTATGTTAACGGAGTATTTGATTGTGCTGTCTGAGCTGGCCATGTGTCAGA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  130  GGGAGATCTCTATGTTAACGGAGTATTTGATTGTGCTGTCTGAGCTGGCCATGTGTCAGA  189

Query  121  TTTAGTAAAGTAAAAACTTTCAACAACGGATCTCTTGGCTCTCGCATCGATGAAGAACGC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  190  TTTAGTAAAGTAAAAACTTTCAACAACGGATCTCTTGGCTCTCGCATCGATGAAGAACGC  249

Query  181  AGCGAAATGCGATAGGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  250  AGCGAAATGCGATAGGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACG  309

Query  241  CACATTGCGCCCTTTGGTATTCCTTAGGGCATGCCTGTTCGAGCGTCACTACACACCTTA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  310  CACATTGCGCCCTTTGGTATTCCTTAGGGCATGCCTGTTCGAGCGTCACTACACACCTTA  369

Query  301  TCACAAAGTTTGTGGTCTTGGCAGGAGTGAATTGCTAGTCTATCAAAATGTTCCAGCTGT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  370  TCACAAAGTTTGTGGTCTTGGCAGGAGTGAATTGCTAGTCTATCAAAATGTTCCAGCTGT  429

Query  361  ACACTCTGCTAAAAATTATGAGAAGGTTACCAGGCATGAACGACGGACTTTATAAACGGT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  430  ACACTCTGCTAAAAATTATGAGAAGGTTACCAGGCATGAACGACGGACTTTATAAACGGT  489

Query  421  TATAAGACCTGGATCAGTCACAAGTCTTGTCTGGTCCTTACCTTAAGGACCCCCATCCTA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  490  TATAAGACCTGGATCAGTCACAAGTCTTGTCTGGTCCTTACCTTAAGGACCCCCATCCTA  549

Query  481  GATGAACTATGGGTTGACCTCGAATCAGGGAGGGATACCCGCTGAACTTAAGCATATCAA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  550  GATGAACTATGGGTTGACCTCGAATCAGGGAGGGATACCCGCTGAACTTAAGCATATCAA  609

Query  541  TAAGCGGAGGA  551
            |||||||||||
Sbjct  610  TAAGCGGAGGA  620
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Sample #3-2009
Contig sequence derived from ITS1F and ITS2 primers (268bp)
TAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGA
TCATTATGAATGCTTTGGGATACCGTTGTGTATTCCCGAACACAAACCTCTCTG
CGTATCACTCCATGTTGCTTCCACAGGTTAAGTGACCATGCTGGCACCTGTGG
GAGATCTCTATGTTAACGGAGTATTTGATTGTGCTGTCTGAGCTGGCCATGTGT

CAGATTTAGTAAAGTAAAAACTTTCAACAACGGATCTCTTGGCTCTCGCATCG
AT

Blastn top result for percent identity using the Nucleotide Collection (nr/nt) database optimized for highly similar sequences (megablast)

> ☐ [gb|DQ388877.1|](#) Tuber melanosporum isolate Tmel-eu08 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1 and 5.8S ribosomal
RNA gene, complete sequence; and internal transcribed
spacer 2, partial sequence
Length=548

```
 Score =  444 bits (240),  Expect = 1e-121
 Identities = 240/240 (100%), Gaps = 0/240 (0%)
 Strand=Plus/Plus

Query  29    TCCGTAGGTGAACCTGCGGAAGGATCATTATGAATGCTTTGGGATACCGTTGTGTATTCC  88
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     TCCGTAGGTGAACCTGCGGAAGGATCATTATGAATGCTTTGGGATACCGTTGTGTATTCC  60

Query  89    CGAACACAAACCTCTCTGCGTATCACTCCATGTTGCTTCCACAGGTTAAGTGACCATGCT  148
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    CGAACACAAACCTCTCTGCGTATCACTCCATGTTGCTTCCACAGGTTAAGTGACCATGCT  120

Query  149   GGCACCTGTGGGAGATCTCTATGTTAACGGAGTATTTGATTGTGCTGTCTGAGCTGGCCA  208
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   GGCACCTGTGGGAGATCTCTATGTTAACGGAGTATTTGATTGTGCTGTCTGAGCTGGCCA  180

Query  209   TGTGTCAGATTTAGTAAAGTAAAAACTTTCAACAACGGATCTCTTGGCTCTCGCATCGAT  268
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   TGTGTCAGATTTAGTAAAGTAAAAACTTTCAACAACGGATCTCTTGGCTCTCGCATCGAT  240
```

Sample#4-2009
GAAGTAAAAGTCGTAACAAGGTCTCCGTTGGTGAACCAGCGGAGGGATCATT
ACCGAGTTTACAACTCCCAAACCCCTGTGAACATACCTTAATGTTGCCTCGGC
GGATCAGCCCGCGCCCCGTAAAACGGGACGGCCCGCCAGAGGACCCAAACTC
TAATGTTTCTTATTGTAACTTCTGAGTAAAACAAACAAATAAATCAAAACTTTC
AACAACGGATCTCTTGGTTCTGGCATCGATGAAGAACGCAGCAAAATGCGATA
AGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACATTGC
GCCCGCTGGTATTCCGGCGGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAA
GCCCNCGGGTTTGGTGTTGGGGATCGGCTCTGCCTTCTGGCGGTGCCGCCCCC
GAAATACATTGGCGGTCTCGCTGCAGCCTCCATTGCGTAGTAGCTAACACCTC
GCAACTGGAACGCGGCGCGGCCATGCCGTAAAACCCCAACTTCTGAATGTTG
ACCTCGGATCAGGTAGGAATACCCGCTGAACTTAAGCATA
Blast top result for percent identity using the Nucleotide Collection (nr/nt) database optimized for highly similar sequences (megablast)

> ☐ emb|FN397346.1| Uncultured fungus genomic DNA sequence containing 18S rRNA gene,
ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, clone N14_P_4_E7
Length=598

```
 Score = 1048 bits (567),  Expect = 0.0
 Identities = 568/569 (99%), Gaps = 0/569 (0%)
```

```
  Strand=Plus/Minus

Query  1    GAAGTAAAAGTCGTAACAAGGTCTCCGTTGGTGAACCAGCGGAGGGATCATTACCGAGTT   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  584  GAAGTAAAAGTCGTAACAAGGTCTCCGTTGGTGAACCAGCGGAGGGATCATTACCGAGTT   525

Query  61   TACAACTCCCAAACCCCTGTGAACATACCTTAATGTTGCCTCGGCGGATCAGCCCGCGCC   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  524  TACAACTCCCAAACCCCTGTGAACATACCTTAATGTTGCCTCGGCGGATCAGCCCGCGCC   465

Query  121  CCGTAAAACGGGACGGCCCGCCAGAGGACCCAAACTCTAATGTTTCTTATTGTAACTTCT   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  464  CCGTAAAACGGGACGGCCCGCCAGAGGACCCAAACTCTAATGTTTCTTATTGTAACTTCT   405

Query  181  GAGTAAAACAAACAAATAAATCAAAACTTTCAACAACGGATCTCTTGGTTCTGGCATCGA   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  404  GAGTAAAACAAACAAATAAATCAAAACTTTCAACAACGGATCTCTTGGTTCTGGCATCGA   345

Query  241  TGAAGAACGCAGCAAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAA   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  344  TGAAGAACGCAGCAAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAA   285

Query  301  TCTTTGAACGCACATTGCGCCCGCTGGTATTCCGGCGGGCATGCCTGTTCGAGCGTCATT   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  284  TCTTTGAACGCACATTGCGCCCGCTGGTATTCCGGCGGGCATGCCTGTTCGAGCGTCATT   225

Query  361  TCAACCCTCAAGCCCNCGGGTTTGGTGTTGGGGATCGGCTCTGCCTTCTGGCGGTGCCGC   420
            ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  224  TCAACCCTCAAGCCCTCGGGTTTGGTGTTGGGGATCGGCTCTGCCTTCTGGCGGTGCCGC   165

Query  421  CCCCGAAATACATTGGCGGTCTCGCTGCAGCCTCCATTGCGTAGTAGCTAACACCTCGCA   480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  164  CCCCGAAATACATTGGCGGTCTCGCTGCAGCCTCCATTGCGTAGTAGCTAACACCTCGCA   105

Query  481  ACTGGAACGCGGCGCGGCCATGCCGTAAAACCCCAACTTCTGAATGTTGACCTCGGATCA   540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  104  ACTGGAACGCGGCGCGGCCATGCCGTAAAACCCCAACTTCTGAATGTTGACCTCGGATCA   45

Query  541  GGTAGGAATACCCGCTGAACTTAAGCATA   569
            |||||||||||||||||||||||||||||
Sbjct  44   GGTAGGAATACCCGCTGAACTTAAGCATA   16
```

Sample#5-2009

Unable to obtain sequencing results.

Sample#6-2009

AAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTATTGAAT
ACGATTGGTACTGATGCTGGCTCTTCACTGAGCATGTGCTCGTCCATCTATTTAT
CTTCTCTTGTGCACATCTTGTAGTCTTGAATTGAAACCCCTCGCAGTCAAATGC
GGTTTGGGAGGTTGGGCGCGAGCCCTCCTTCTGCTTCTTCAAGGCTATGTTTTC
ATATACACTATAAAGTTACAGAATGTCTTTTAACGATTGTGCTAGTCGCAGTCAT
TAAACCTATACAACTTTCAGCAACGGATCTCTTGGCTCTCCTATCGATGAAGAA
CGCAGCGAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAA
TCTTTGAACGCACCTTGCGCCCTTTGGTATTCCGAAGGGCATGCCTGTTTGAGT
GTCATTAAATTATCAACCTTGCTCTCGCTTTTACCGGCTTGAGTGAGGCTTGGA

TGTGAGGGCTTGCTGGCTTCCTTCAGTGGATGGTCTGCTCCCTTTAAATGCATT
AGTGGAATCCTTTGTGGACCGTCACTTGGTGTGATAATTATCTATGCCATCTTG
ACTTTGAAGCAAAACTTATGGGAATCCGCTCATAACCGTCTTCGGACAATCATT
GACATTTTGACCTCAAATCAGGTAGGACTACCCGCTGAACTTAAG

Blast top result for percent identity using the Nucleotide Collection (nr/nt) database
optimized for highly similar sequences (megablast)

> [dbj|AB454397.1|](#) Uncultured mycorrhizal fungus genes for 18S rRNA, ITS1, 5.8S
rRNA, ITS2, 28S rRNA, partial sequence, clone: Mycena2_M868
Length=649

 Score = 931 bits (504), Expect = 0.0
 Identities = 616/664 (92%), Gaps = 31/664 (4%)
 Strand=Plus/Plus

```
Query  43   CATTATTGAATACGATTGGTACTGATGCTGGCTCTTCACTGAGCATGTGCTCGTC-CA-T  100
            ||||||||||||| |||| |||||||||||||||||||||||||||||||||||| || |
Sbjct  1    CATTATTGAATACGGTTGGGACTGATGCTGGCTCTTCACTGAGCATGTGCTCGTCTCATT  60

Query  101  C-TATTTATCTTCTCTTGTGCACATCTTGTAGTCTTGAATTGAAACCCCTCGCAGTCAAA  159
            | ||||||||||||||||||||||||||||||||||||||| || ||||||||||||||||
Sbjct  61   CTTATTTATCTTCTCTTGTGCACATCTTGTAGTCTTGAA-TG-AACCCCTCGCAGTCAAA  118

Query  160  TGCGGTT-TGGGAGGTTGGGCGCGAGC-C-CTCCTTCTGCT--TC-TTCAAGGCTATGTT  213
            ||||||| ||||||| || ||   | | | ||||| ||   || |||||||||||||
Sbjct  119  TGCGGTTCTGGGAGGCTGAGC-TTAACACGCT-CTTCTCCTGCTCGTTCAAGGCTATGTT  176

Query  214  TTCATATACACTATAAAGTTACAGAATGTCTTTTAACGATTGTGCTAGTCGCAGTCATTA  273
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  177  TTCATATACACTATAAAGTTACAGAATGTCTTTTAACGATTGTGCTAGTCGCAGTCATTA  236

Query  274  AACC-TATACAACTTTCAGCAACGGATCTCTTGGCTCTCCTATCGATGAAGAACGCAGCG  332
            |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  237  AACCTTATACAACTTTCAGCAACGGATCTCTTGGCTCTCCTATCGATGAAGAACGCAGCG  296

Query  333  AAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACC  392
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  297  AAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACC  356

Query  393  TTGCGCCCTTTGGTATTCCGAAGGGCATGCCTGTTTGAGTGTCATTAAATTATCAACCTT  452
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  357  TTGCGCCCTTTGGTATTCCGAAGGGCATGCCTGTTTGAGTGTCATTAAATTATCAACCTT  416

Query  453  -GCTCTCGCTTTTACCGGCTTGAGTGA-GGCTTGGATGTGAGGGCTTGCTGGCTTCCTTC  510
             ||||| || | | |||||| |||||||||| ||||||||||||
Sbjct  417  TGCTCT---TT-----G-C--GAGTGAAGGCTTGGATGTGAGGGTTTGCTGGCTTCCTTC  465

Query  511  AGTGGATGGTCTGCTCCCTTTAAATGCATTAGTGGAATCCTTTGTGGACCGTCACTTGGT  570
            ||| |||||||||||||||||||||||||||||||||| |||||||||| ||||| |||
Sbjct  466  AGTTGATGGTCTGCTCCCTTTAAATGCATTAGTGGATCCTTTGTGGATCGTCACTAGGT  525

Query  571  GTGATAATTATCTATGCCATCTTGACTTTGAAGCAAAACTTATGGGAATCCGCTCATAAC  630
            |||||||||||||||||| | |||||||||||||| || ||||||||||||||||||||
Sbjct  526  GTGATAATTATCTATGCCTT-TTGACTTTGAAGCAAA-CTTATGGGAATCCGCTCATAAC  583

Query  631  CGTCTTCGGACAATCATT-GACATTTTGACCTCAAATCAGGTAGGACTACCCGCTGAACT  689
            ||||||||||| | || |||| |||||||||||||||||||||||||||||||||||||
Sbjct  584  TGTCTTCGGACAA-CTTTTGACAATTTGACCTCAAATCAGGTAGGACTACCCGCTGAACT  642

Query  690  TAAG  693
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            ||||
Sbjct  643  TAAG  646
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