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Tue Oct 23, 2018 21:44 CST
953.ape from 1 to 953
Alignment to
76513882-76516982.ape from 1 to 3101

Matches(|):951
Mismatches(#):1
Gaps( ):2150
Unattempted(.):0

                *         *         *         *         *         *         *         *         *         *
     1 ACAGCCTCCTGTCTCGGTGGTTGTCGTGGCCCTGACGCCCTCACTCCCACAAGAAGAAGACACAGCGAAGGAGAAGGGACGGCCCCTCAGGGCGGCTTCT 100
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     1 ACAGCCTCCTGTCTCGGTGGTTGTCGTGGCCCTGACGCCCTCACTCCCACAAGAAGAAGACACAGCGAAGGAGAAGGGACGGCCCCTCAGGGCGGCTTCT 100
                *         *         *         *         *         *         *         *         *         *

                *         *         *         *         *         *         *         *         *         *
   101 GGGCGCGGATGTGCCTGAAATAGTCAACTGAACGGAGGCAGCACCGAGGGGGGGCGACGAGGAAGGAGGCCCAGGGTGCGTGATAATCACGGATGCGGAG 200
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   101 GGGCGCGGATGTGCCTGAAATAGTCAACTGAACGGAGGCAGCACCGAGGGGGGGCGACGAGGAAGGAGGCCCAGGGTGCGTGATAATCACGGATGCGGAG 200
                *         *         *         *         *         *         *         *         *         *

                *         *         *         *         *         *         *         *         *         *
   201 ACTCACTCACTCGGGGGCGGACACCTGGCCCCCCCAGTCTGACACCAAGGAGTAAACAAAACCCCCCCCAACCTAGAGAGGCCCCCAAACGCCACCCAGC 300
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
   201 ACTCACTCACTCGGGGGCGGACACCTGGCCCCCCCAGTCTGACACCAAGGAGTAAACAAAACCCCCCC-AACCTAGAGAGGCCCCCAAACGCCACCCAGC 299
                *         *         *         *         *         *         *         *         *         *

                *         *         *         *         *         *         *         *         *         *
   301 TCTCTTGCGACTGCCACTTATTTTTGCACCGTGTGCCCTTCTCCTGCGTGTCCTGGGCTCTTTCGCAAACCTGTTGATCGAATGTATGGAACATTTCTGT 400
       ||||||||||||||||#|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   300 TCTCTTGCGACTGCCATTTATTTTTGCACCGTGTGCCCTTCTCCTGCGTGTCCTGGGCTCTTTCGCAAACCTGTTGATCGAATGTATGGAACATTTCTGT 399
       *         *         *         *         *         *         *         *         *         *

                *         *         *         *         *         *         *         *         *         *
   401 TCACGACGGCTGAGGATTAATGATTCACCAAGGACACAGGCCCTTTGTACCTATAATTGTCCTGCATTTGTTTGGACTCTCTTTGACCCTTTGTACCCAA 500
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   400 TCACGACGGCTGAGGATTAATGATTCACCAAGGACACAGGCCCTTTGTACCTATAATTGTCCTGCATTTGTTTGGACTCTCTTTGACCCTTTGTACCCAA 499
       *         *         *         *         *         *         *         *         *         *

                *         *         *         *         *         *         *         *         *         *
   501 GTGGTCTGTGGTGGAGCCCTTTGAAAACAATCTCCTGGATAAAGTGTTTATGGGATTTACCGCAAGCCCGTGGCTCTTTTGCTGTGACGCCTGCTGCGTA 600
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   500 GTGGTCTGTGGTGGAGCCCTTTGAAAACAATCTCCTGGATAAAGTGTTTATGGGATTTACCGCAAGCCCGTGGCTCTTTTGCTGTGACGCCTGCTGCGTA 599
       *         *         *         *         *         *         *         *         *         *

                *         *         *         *         *         *         *         *         *
   601 AGAGAGACCAAAACCACCATCTCAACGAGGTCAAACGTGCCGTCACCCCAAGAGCGAGACATTCCTCCTGGGTCCTCCGTAAGCGCCCCG---------- 690
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   600 AGAGAGACCAAAACCACCATCTCAACGAGGTCAAACGTGCCGTCACCCCAAGAGCGAGACATTCCTCCTGGGTCCTCCGTAAGCGCCCCGAGGTGAGATA 699
       *         *         *         *         *         *         *         *         *         *

   691 ---------------------------------------------------------------------------------------------------- 691

   700 TTAAATATTATTTTGAGCAGTGGATGGCCCATCTGTGCCCAAGGGCTGTTACACAAAGTCTGCCTCTCTGCAGAGAACAAGGGTCGGCTGGCCCCAGCTC 799
       *         *         *         *         *         *         *         *         *         *

   691 ---------------------------------------------------------------------------------------------------- 691

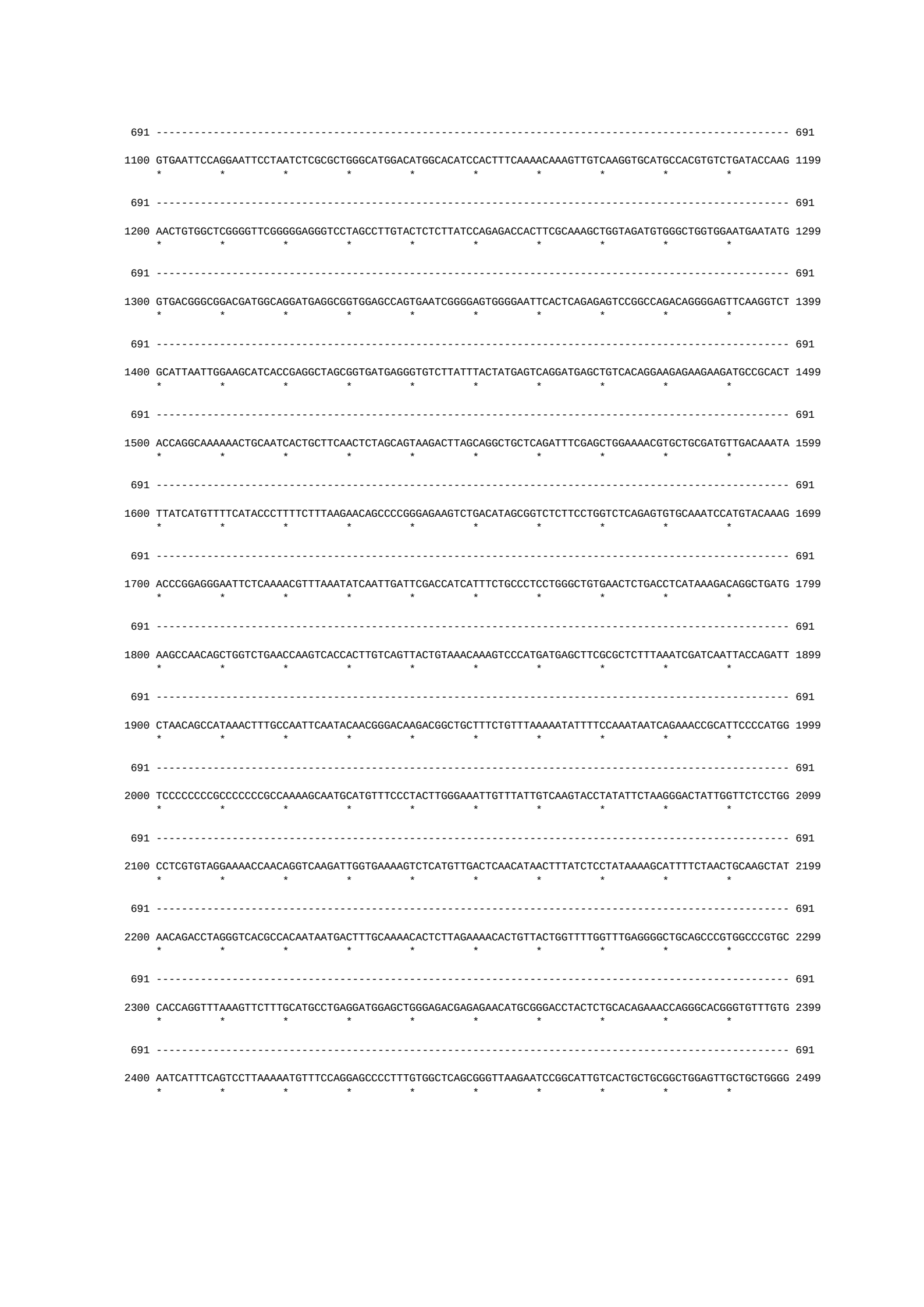
   800 TGTCCTCATTTTTGCTCTGAGCAGGACGGTCAAAGTTCTCGGCAGGTACATCTCGAGGGGCTCTGTCTATACCTCTGATCACGTAGTGACCGAGGAGCCC 899
       *         *         *         *         *         *         *         *         *         *

   691 ---------------------------------------------------------------------------------------------------- 691

   900 AGCTTCCCACCCAACAGCTCAGGTCAAGAGGCAGGACAGAATGTGTCCCCGTGTCGGTTTCCTCTGTCACCCCTCGGACACCTCTTAGCGGAGTGACCGC 999
       *         *         *         *         *         *         *         *         *         *

   691 ---------------------------------------------------------------------------------------------------- 691

  1000 CTCGGCCTTCCTCTCCTCGTCTCCGTTCACACCATCCGCAAACATGCACTGCGGGGCTGCCCTCGGGGAAGCGCCTTGCAGAAATCAAGCAGGGTGACCT 1099
       *         *         *         *         *         *         *         *         *         *
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691 691
2500 CGTGGGTTTGATCCCTGGCCCCAGAAATTCCATATGCTGCAGGCACGGTCAAAAAAAAAAAAAAAAAAAATCCAAATTCCAATATCATTACATTGAAGGCA 2599
691 691
2600 AAGGAAGAAGCTAATTTTAGAAGCTCCCTGGGGTCCTGCTCTGACACCCACATGTCCAAATCCCACGCTTCTGCATGCACGTGTTTACTACACACCCTCA 2699
691 691
2700 TGAACCACTTACCAAGGGTTCCACCGTGAGCTCTTCCTTCAAATTGTATTATCGCAGAGATAAAAGGAGATTTGTGTTATGGCGGTTGAAGGCGCCCATT 2799
691 AGGCATCCCAGGCGCTGGAACATAAAGAAGATGAGAAACGCTCTCTCAGAGAACTTGCTTCC 752
2800 CCGAAAGTGATAACCCATTTAATCCTTCCTTCAACTACAGGCATCCCAGGCGCTGGAACATAAAGAAGATGAGAAACGCTCTCTCAGAGAACTTGCTTCC 2899
753 TGGTCTCGGCTACACCCCAGACTCTCAGAGTCTAGTCTGAGTCTATACGCATCTGTGCTTAGGATCACTCGGCATGGGTTCGAGTAAGCCCATCTGTGAG 852
2900 TGGTCTCGGCTACACCCCAGACTCTCAGAGTCTAGTCTGAGTCTATACGCATCTGTGCTTAGGATCACTCGGCATGGGTTCGAGTAAGCCCATCTGTGAG 2999
853 AGCCTTGTAAAAACATATCTATTGTCATTCCGATTCATCTTATGGATGAGCCCCTTCCGATGTTTGAAAACATGAAATTCCAACACATGTGAAAAAAATC 952
3000 AGCCTTGTAAAAACATATCTATTGTCATTCCGATTCATCTTATGGATGAGCCCCTTCCGATGTTTGAAAACATGAAATTCCAACACATGTGAAAAAAATC 3099
953 A~ 953
3100 AC 3101