Genome Network Project_Full -Length cDNA clone

RIKEN clone ID: IRAK069P16

Vector : pCMV-SPORT6

Gene	TLR7		
Accession No.	BC033651.1	3595 bp	1..3595
	CDS	3150 bp	151..3300

●Plasmid DNA purification

Date : 100621 Culture : LB (100 ug/ml Ampicillin) 3 ml →37°C O/N

Date : 100622 Purification : QIAGEN Miniprep kit→dH_2O 100 ul

●Digestion by restriction enzyme / Concentrarion calibration

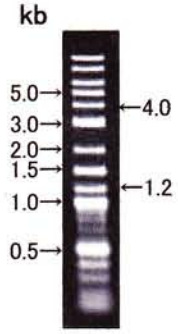
Date : 100622

DNA concentration (O.D.): 113.8 ng/ul

DNA	1 ul
Enzyme (EcoRI+XhoI)	0.5+0.5 ul
Buffer H	1 ul
dH_2O	7 ul
Total	10 ul

Erectrophoresis: 1% agarose gel, 1 × TAE Buffer

Marker: 2-Log DNA Ladder (NEB#N3200L)



<Expected digestion pattern from BC033651.1>

4339, 1781, 264, 909, 684 bp

●Adjust plasmid DNA solution to 25 ng/ul ～preparation for shipping～

Date : 100623 Shipped : 25 ng/ul, 40 ul

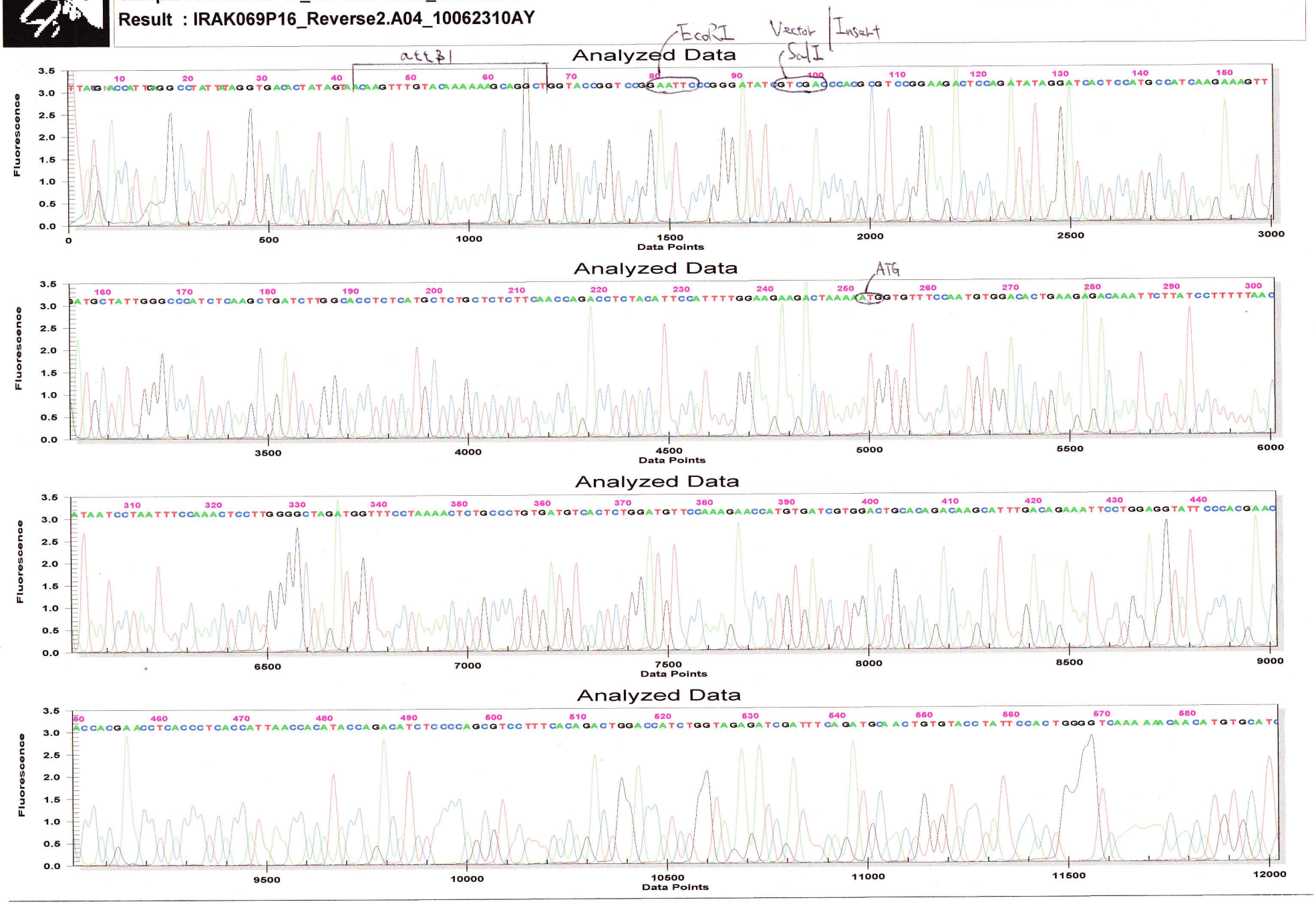
Final concentration: 25 ng/ul

DNA (113.8 ng/ul)	89 ul
10 × TE	40.5 ul
dH_2O	275.6 ul
Total	405.1 ul

Project : GNP
Sample : IRAK069P16_Reverse2.A04_10062310AY
Result : IRAK069P16_Reverse2.A04_10062310AY

System : CEQ System

Operator : 2.100623.furu
Instrument : CEQ System (Ver. 9.0.25)

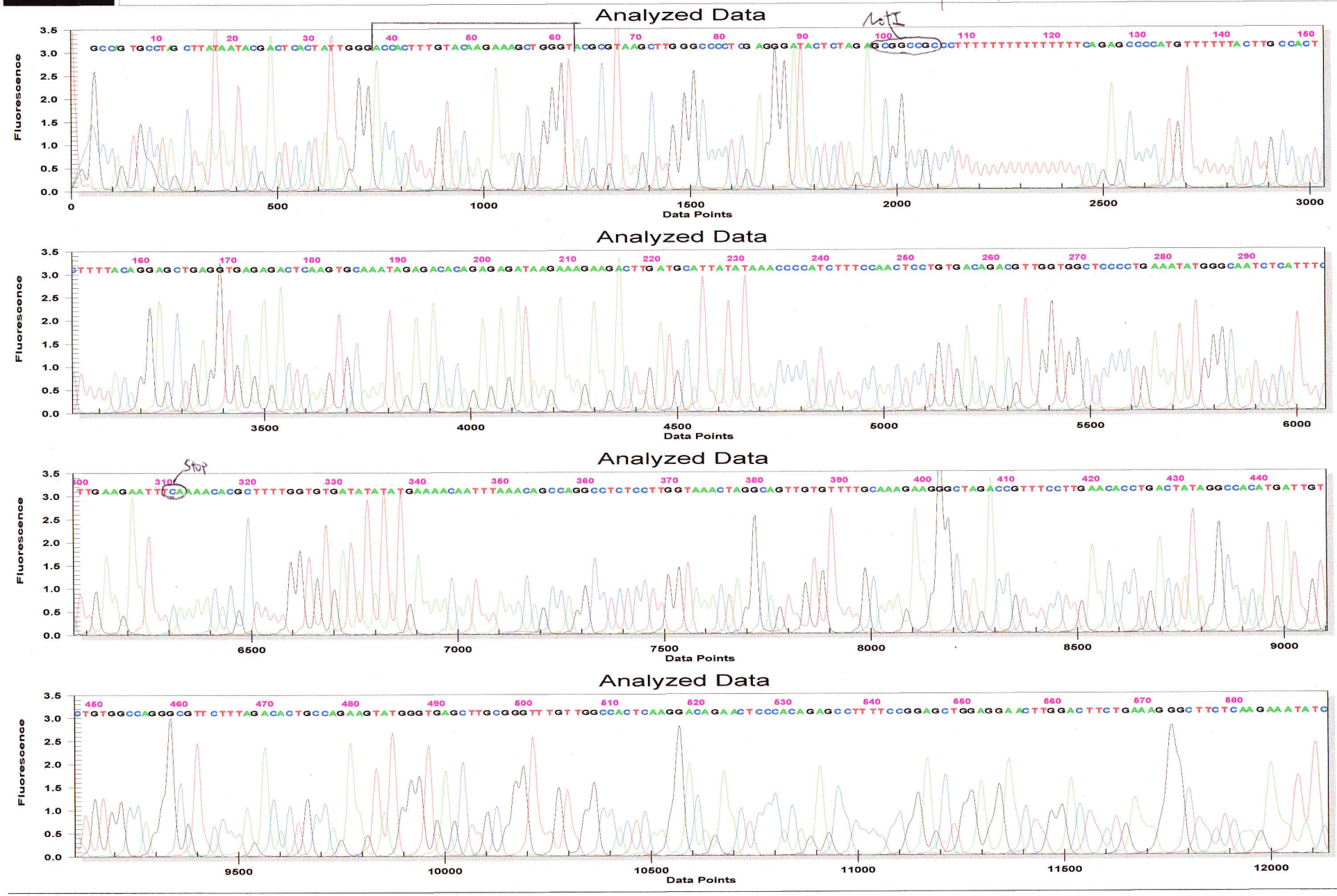


Project : GNP
Sample : IRAK069P16_M13.B04_10062310AY
Result : IRAK069P16_M13.B04_10062310AY

System : CEQ System

Operator : 2.100623.furu
Instrument : CEQ System (Ver. 9.0.25)

Vector | Insert



[GENETYX : Nucleotide Sequence Homology Data]

Date : 2010.06.23

1st Nucleotide Sequence
File Name : BC033651.1.gnu
Sequence Size : 3595

2nd Nucleotide Sequence
File Name : IRAK069P16_Reverse2.A04_10062310AY.fasta
Sequence Size : 685

Unit Size to Compare = 6
Pick up Location No. = 1

[578 / 584 bp] INT/OPT.Score : < 2024/ 2293 >

```
     1'                                                  CCACGCGTCC GGAAGACTCC
                                                         ********** **********
    61" CAGGCTGGTA CCGGTCCGGA ATTCCCGGGA TATCGTCGAC CCACGCGTCC GGAAGACTCC

    21' AGATATAGGA TCACTCCATG CCATCAAGAA AGTTGATGCT ATTGGGCCCA TCTCAAGCTG
        ********** ********** ********** ********** ********** **********
   121" AGATATAGGA TCACTCCATG CCATCAAGAA AGTTGATGCT ATTGGGCCCA TCTCAAGCTG

    81' ATCTTGGCAC CTCTCATGCT CTGCTCTCTT CAACCAGACC TCTACATTCC ATTTTGGAAG
        ********** ********** ********** ********** ********** **********
   181" ATCTTGGCAC CTCTCATGCT CTGCTCTCTT CAACCAGACC TCTACATTCC ATTTTGGAAG

   141' AAGACTAAAA ATGGTGTTTC CAATGTGGAC ACTGAAGAGA CAAATTCTTA TCCTTTTTAA
        ********** ********** ********** ********** ********** **********
   241" AAGACTAAAA ATGGTGTTTC CAATGTGGAC ACTGAAGAGA CAAATTCTTA TCCTTTTTAA

   201' CATAATCCTA ATTTCCAAAC TCCTTGGGGC TAGATGGTTT CCTAAAACTC TGCCCTGTGA
        ********** ********** ********** ********** ********** **********
   301" CATAATCCTA ATTTCCAAAC TCCTTGGGGC TAGATGGTTT CCTAAAACTC TGCCCTGTGA

   261' TGTCACTCTG GATGTTCCAA AGAACCATGT GATCGTGGAC TGCACAGACA AGCATTTGAC
        ********** ********** ********** ********** ********** **********
   361" TGTCACTCTG GATGTTCCAA AGAACCATGT GATCGTGGAC TGCACAGACA AGCATTTGAC

   321' AGAAATTCCT GGAGGTATTC CCACGAACAC CACGAACCTC ACCCTCACCA TTAACCACAT
        ********** ********** ********** ********** ********** **********
   421" AGAAATTCCT GGAGGTATTC CCACGAACAC CACGAACCTC ACCCTCACCA TTAACCACAT

   381' ACCAGACATC TCCCCAGCGT CCTTTCACAG ACTGGACCAT CTGGTAGAGA TCGATTTCAG
        ********** ********** ********** ********** ********** **********
   481" ACCAGACATC TCCCCAGCGT CCTTTCACAG ACTGGACCAT CTGGTAGAGA TCGATTTCAG

   441' ATGCAACTGT GTACCTATTC CACTGGGGTC AAAAAACAAC ATGTGCATCA AGAGGCTGCA
        ********** ********** ********** ********** ********** **********
   541" ATGCAACTGT GTACCTATTC CACTGGGGTC AAAAAACAAC ATGTGCATCA AGAGGCTGCA

   501' GATTAAACCC AGAAGCTTTA GTGGACTCAC TTATTTAAAA TCCCTTTACC TGGATGGAAA
        **** ***** ********** ********** ********** ********** ** ******
   601" GATT-AACCC AGAAGCTTTA GTGGACTCAC TTATTTAAAA TCCCTTTACC TGAATGGAAC

   561' CCAGCTACTA GAGATACCGC AGGGCCTCCC GCCTAGCTTA CAGCTTCTCA GCCTTGAGGC
        ********** *****  *** *.**
   660" CCAGCTACTA GAGATTACGC ANGGGG
```

1st Nucleotide Sequence
File Name : BC033651.1.gnu
Sequence Size : 3595

2nd Nucleotide Sequence
File Name : IRAK069P16_M13.B04_10062310AY.fasta (Complementary)
Sequence Size : 596

2010/06/23 13:37:33 IRAK069P16 homology.txt

Unit Size to Compare = 6
Pick up Location No. = 1

[487 / 488 bp] INT/OPT.Score : < 1944/ 1946 >

```
 3061' TTTTACTTGT CCCATCAGAG GCTCATGGAT GAAAAAGTTG ATGTGATTAT CTTGATATTT
                                                          * * **********
    1"                                                    ATTT CTTGATATTT

 3121' CTTGAGAAGC CCTTTCAGAA GTCCAAGTTC CTCCAGCTCC GGAAAAGGCT CTGTGGGAGT
       ********** ********** ********** ********** ********** **********
   15" CTTGAGAAGC CCTTTCAGAA GTCCAAGTTC CTCCAGCTCC GGAAAAGGCT CTGTGGGAGT

 3181' TCTGTCCTTG AGTGGCCAAC AAACCCGCAA GCTCACCCAT ACTTCTGGCA GTGTCTAAAG
       ********** ********** ********** ********** ********** **********
   75" TCTGTCCTTG AGTGGCCAAC AAACCCGCAA GCTCACCCAT ACTTCTGGCA GTGTCTAAAG

 3241' AACGCCCTGG CCACAGACAA TCATGTGGCC TATAGTCAGG TGTTCAAGGA AACGGTCTAG
       ********** ********** ********** ********** ********** **********
  135" AACGCCCTGG CCACAGACAA TCATGTGGCC TATAGTCAGG TGTTCAAGGA AACGGTCTAG

 3301' CCCTTCTTTG CAAAACACAA CTGCCTAGTT TACCAAGGAG AGGCCTGGCT GTTTAAATTG
       ********** ********** ********** ********** ********** **********
  195" CCCTTCTTTG CAAAACACAA CTGCCTAGTT TACCAAGGAG AGGCCTGGCT GTTTAAATTG

 3361' TTTTCATATA TATCACACCA AAAGCGTGTT TTGAAATTCT TCAAGAAATG AGATTGCCCA
       ********** ********** ********** ********** ********** **********
  255" TTTTCATATA TATCACACCA AAAGCGTGTT TTGAAATTCT TCAAGAAATG AGATTGCCCA

 3421' TATTTCAGGG GAGCCACCAA CGTCTGTCAC AGGAGTTGGA AAGATGGGGT TTATATAATG
       ********** ********** ********** ********** ********** **********
  315" TATTTCAGGG GAGCCACCAA CGTCTGTCAC AGGAGTTGGA AAGATGGGGT TTATATAATG

 3481' CATCAAGTCT TCTTTCTTAT CTCTCTGTGT CTCTATTTGC ACTTGAGTCT CTCACCTCAG
       ********** ********** ********** ********** ********** **********
  375" CATCAAGTCT TCTTTCTTAT CTCTCTGTGT CTCTATTTGC ACTTGAGTCT CTCACCTCAG

 3541' CTCCTGTAAA AGAGTGGCAA GTAAAAAACA TGGGGCTCTG AAAAAAAAAA AAAAA
       ********** ********** ********** ********** ********** *****
  435" CTCCTGTAAA AGAGTGGCAA GTAAAAAACA TGGGGCTCTG AAAAAAAAAA AAAAAGGGCG
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