

RIKEN clone ID: W01A058H22

Vector : pENTR/D-TOPO

Gene	NR112	
Accession No.	BC017304.2	2718 bp
	<i>CDS</i>	1302 bp
		240..1541

● Plasmid DNA purification

Date : 110117 Culture : LB (25 ug/ml Kanamycin) 3 ml → 37°C O/N

Date : 110118 Purification : QIAGEN Miniprep kit → dH₂O 100 ul

● Digestion by restriction enzyme / Concentration calibration

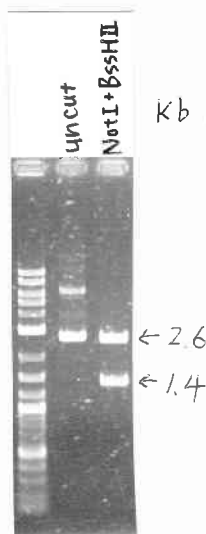
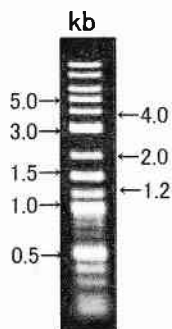
Date : 110118

DNA concentration (O.D.): 106.12 ng/ul

DNA	1 ul
Restriction enzyme (NotI+BssH II)	0.5+0.5 ul
Buffer H	1 ul
dH ₂ O	7 ul
Total	10 ul

Electrophoresis: 1% agarose gel, 1 × TAE Buffer

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



<Expected digestion pattern from BC017304.2 CDS>

1402, 2553 bp

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

Date : 110119 Shipped : 25 ng/ul, 40 ul

Final concentration: 25 ng/ul

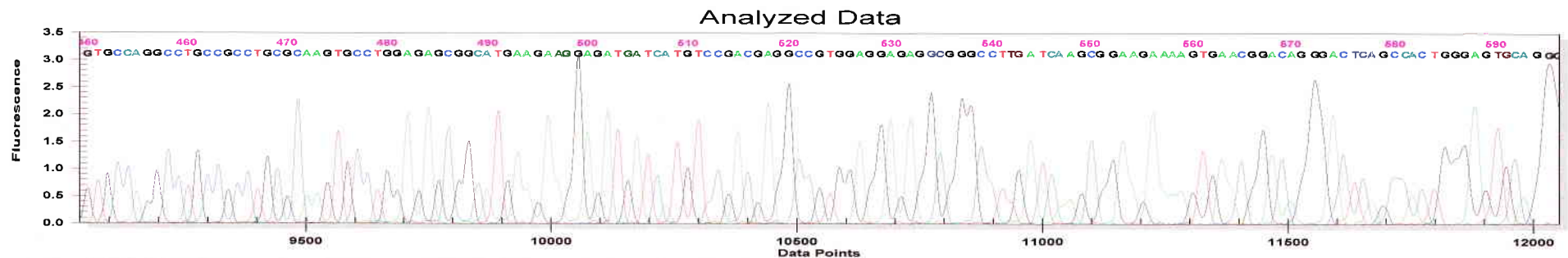
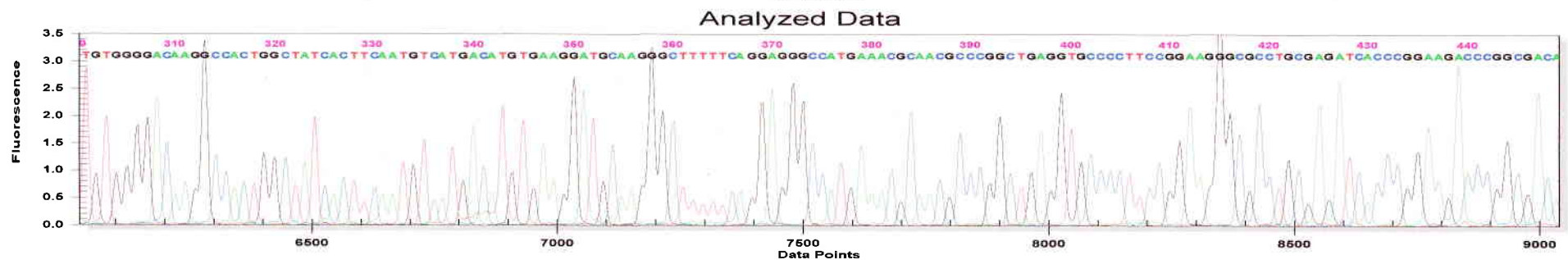
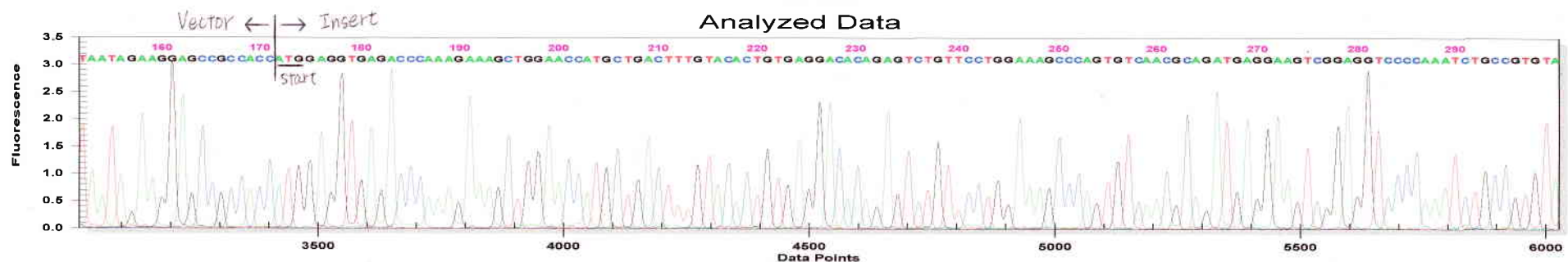
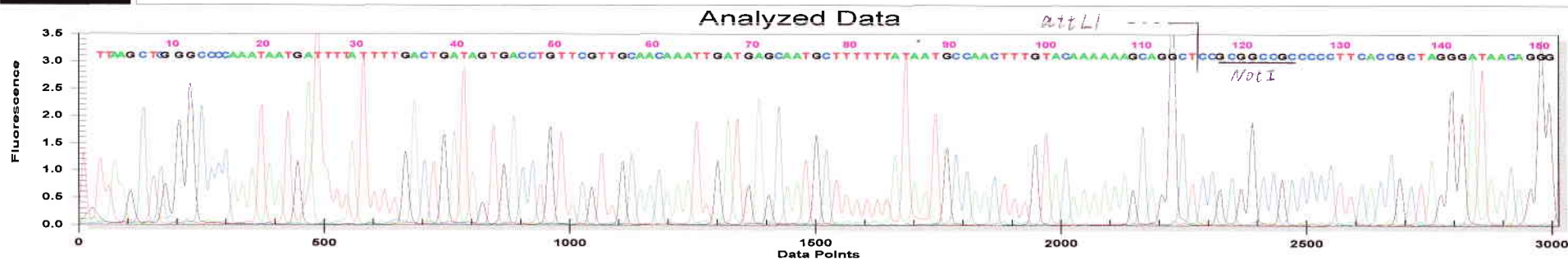
DNA (<u>106.12</u> ng/ul)	<u>85.0</u> ul
10 × TE	<u>36.1</u> ul
dH ₂ O	<u>239.7</u> ul
Total	<u>360.8</u> ul



Project : GNP
Sample : W01A058H22_M13.C08_11011910G7
Result : W01A058H22_M13.C08_11011910G7

System : CEQ System

Operator : 2.110119.furu
Instrument : CEQ System (Ver. 9.0.25)

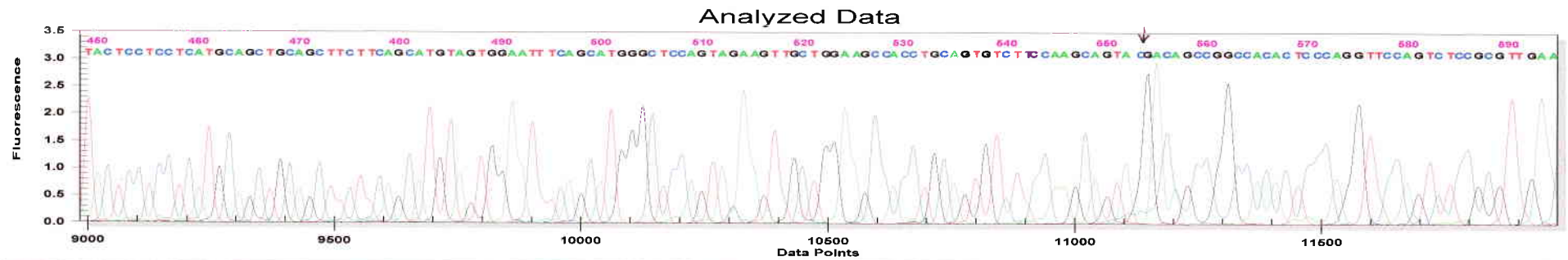
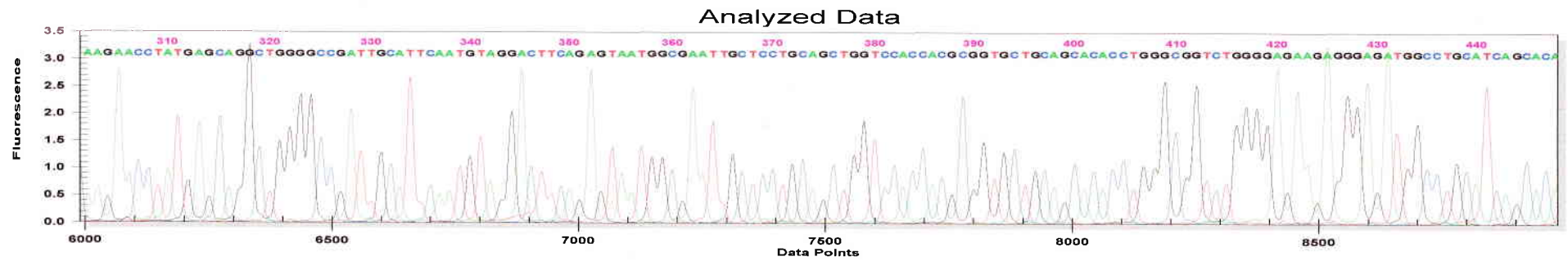
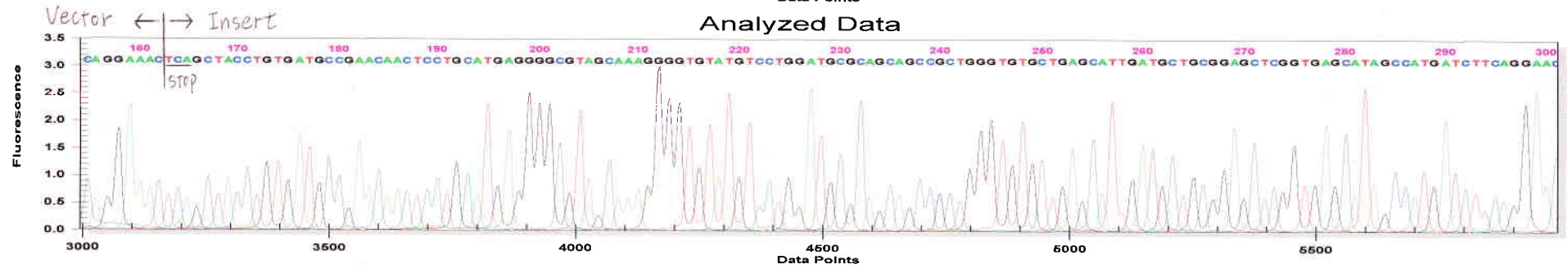
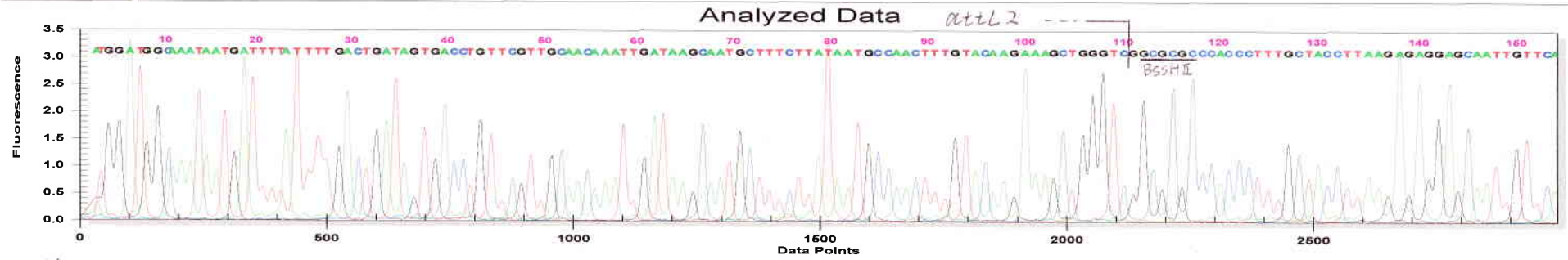




Project : GNP
Sample : W01A058H22_T7long.D08_11011910G7
Result : W01A058H22_T7long.D08_11011910G7

System : CEQ System

Operator : 2.110119.furu
Instrument : CEQ System (Ver. 9.0.25)



[GENETYX : Homology Data]

Date : 2011.01.19

Query Sequence

File Name :
 Sequence Name : BC017304.2_CDS(240..1541)
 Sequence Size : 1302

Target Sequence

File Name : W01A058H22_M13.C08_11011910G7
 Sequence Name : W01A058H22_M13.C08_11011910G7
 Sequence Size : 717

Unit Size to Compare = 6

Pick up Location No. = 1

Query Range: 2 - 546

Sbjct Range: 172 - 717

546 bp, INT.Score: 2074, OPT.Score: 2150

Identity: 541 / 546 (99%)

Strand: Plus / Plus

```

Query  2      TGGAGGTGAG ACCCAAAGAA AGCTGGAACC ATGCTGACTT TGTACACTGT GAGGACACAG 61
          |||
Sbjct 172    TGGAGGTGAG ACCCAAAGAA AGCTGGAACC ATGCTGACTT TGTACACTGT GAGGACACAG 231

Query  62      AGTCTGTTCC TGGAAAGCCC AGTGTCAACG CAGATGAGGA AGTCGGAGGT CCCCAAATCT 121
          |||
Sbjct 232    AGTCTGTTCC TGGAAAGCCC AGTGTCAACG CAGATGAGGA AGTCGGAGGT CCCCAAATCT 291

Query 122      GCCGTGTATG TGGGGACAAG GCCACTGGCT ATCACTTCAA TGTCATGACA TGTGAAGGAT 181
          |||
Sbjct 292      GCCGTGTATG TGGGGACAAG GCCACTGGCT ATCACTTCAA TGTCATGACA TGTGAAGGAT 351

Query 182      GCAAGGGCTT TTTCAGGAGG GCCATGAAAC GCAACGCCCG GCTGAGGTGC CCCTTCCGGA 241
          |||
Sbjct 352      GCAAGGGCTT TTTCAGGAGG GCCATGAAAC GCAACGCCCG GCTGAGGTGC CCCTTCCGGA 411

Query 242      AGGGCGCCTG CGAGATCACC CGGAAGACCC GGCGACAGTG CCAGGCCTGC CGCCTGCGCA 301
          |||
Sbjct 412      AGGGCGCCTG CGAGATCACC CGGAAGACCC GGCGACAGTG CCAGGCCTGC CGCCTGCGCA 471

Query 302      AGTGCCTGGA GAGCGGCATG AAGAAGGAGA TGATCATGTC CGACGAGGCC GTGGAGGAGA 361
          |||
Sbjct 472      AGTGCCTGGA GAGCGGCATG AAGAAGGAGA TGATCATGTC CGACGAGGCC GTGGAGGAGA 531

Query 362      GGCGGGCCTT GATCAAGCGG AAGAAAAGTG AACGGACAGG GACTCAGCCA CTGGGAGTGC 421
          |||
Sbjct 532      GGCGGGCCTT GATCAAGCGG AAGAAAAGTG AACGGACAGG GACTCAGCCA CTGGGAGTGC 591

Query 422      AGGGGCTGAC AGAGGAGCAG CGGATGATGA TCAGGGAGCT GATGGACGCT CAGATGAAAA 481
          |||
Sbjct 592      AGGGGCTGAC AGAGGAGCAG CGGATGATGA TCAGGGAGCT GATGGACGCT CAGATGAAAA 651

Query 482      CCTTTGACAC TACCTTCTCC CATTTC AAGA ATTTCCGG-C CAGGGGTGCT TAGCAGTGGC 540
          |||
Sbjct 652      CCTTTGACAC TACCCTCTCC CATTTC AAGA ATTTCCGGCC CAGGGGTGCC TANCAGTGGC 711

Query 541      TGCGAG      546
          .|||
Sbjct 712      NGCGAG      717
  
```

[GENETYX : Homology Data]

Date : 2011.01.19

Query Sequence

File Name :
 Sequence Name : BC017304.2_CDS(240..1541)
 Sequence Size : 1302

Target Sequence

File Name : W01A058H22_T7long.D08_11011910G7
 Sequence Name : W01A058H22_T7long.D08_11011910G7 (complement)
 Sequence Size : 698

Unit Size to Compare = 6

Pick up Location No. = 1

Query Range: 766 - 1302
 Sbjct Range: 1 - 537
 537 bp, INT.Score: 2103, OPT.Score: 2121
 Identity: 532 / 537 (99%)
 Strand: Plus / Minus

Query	766	TTTGCCAAAG	TCATCTCCTA	CTTCAGGGAC	TTGCCCATCG	AGGACCAGAT	CTCCCTGCTG	825
Sbjct	1	TTTGCCAAAG	TCATCTCCTA	CTTCAGGGAC	TTGCCCATCG	NGACCCAGAT	CTCCCTGCTG	60
Query	826	AAGGGGGCCG	CTTTCGAGCT	GTGTCAACTG	AGATTCAACA	CAGTGTTCAA	CGCGGAGACT	885
Sbjct	61	AAGGGGGCCG	CTTTCGAGCT	GTGTCAACTG	AGATTCAACA	CAGTGTTCAA	CGCGGAGACT	120
Query	886	GGAACCTGGG	AGTGTGGCCG	GCTGTCTTAC	TGCTTGGAAG	ACACTGCAGG	TGGCTTCCAG	945
Sbjct	121	GGAACCTGGG	AGTGTGGCCG	GCTGTCTGAC	TGCTTGGAAG	ACACTGCAGG	TGGCTTCCAG	180
Query	946	CAACTTCTAC	TGGAGCCCAT	GCTGAAATTC	CACTACATGC	TGAAGAAGCT	GCAGCTGCAT	1005
Sbjct	181	CAACTTCTAC	TGGAGCCCAT	GCTGAAATTC	CACTACATGC	TGAAGAAGCT	GCAGCTGCAT	240
Query	1006	GAGGAGGAGT	ATGTGCTGAT	GCAGGCCATC	TCCCTCTTCT	CCCCAGACCG	CCCAGGTGTG	1065
Sbjct	241	GAGGAGGAGT	ATGTGCTGAT	GCAGGCCATC	TCCCTCTTCT	CCCCAGACCG	CCCAGGTGTG	300
Query	1066	CTGCAGCACC	GCGTGGTGGG	CCAGCTGCAG	GAGCAATTCG	CCATTACTCT	GAAGTCCTAC	1125
Sbjct	301	CTGCAGCACC	GCGTGGTGGG	CCAGCTGCAG	GAGCAATTCG	CCATTACTCT	GAAGTCCTAC	360
Query	1126	ATTGAATGCA	ATCGGCCCCA	GCCTGCTCAT	AGGTTCTTGT	TCCTGAAGAT	CATGGCTATG	1185
Sbjct	361	ATTGAATGCA	ATCGGCCCCA	GCCTGCTCAT	AGGTTCTTGT	TCCTGAAGAT	CATGGCTATG	420
Query	1186	CTCACCGAGC	TCCGCAGCAT	CAATGCTCAG	CACACCCAGC	GGCTGCTGCG	CATCCAGGAC	1245
Sbjct	421	CTCACCGAGC	TCCGCAGCAT	CAATGCTCAG	CACACCCAGC	GGCTGCTGCG	CATCCAGGAC	480
Query	1246	ATACACCCT	TTGCTACGCC	CCTCATGCAG	GAGTTGTTTCG	GCATCACAGG	TAGCTGA	1302
Sbjct	481	ATACACCCT	TTGCTACGCC	CCTCATGCAG	GAGTTGTTTCG	GCATCACAGG	TAGCTGA	537