

RIKEN clone ID: IRAK133H20

Vector : pBluescriptR

Gene	NFKBIZ	
Accession No.	BC060800.1	2445 bp
	<i>CDS</i>	2157 bp
		1..3937
		116..2272

● Plasmid DNA purification

Date : 110421 Culture : LB (100 ug/ml Ampicillin) 3 ml →37°C O/N

Date : 110422 Purification : QIAGEN Miniprep kit →dH₂O 100 ul

● Digestion by restriction enzyme / Concentration calibration

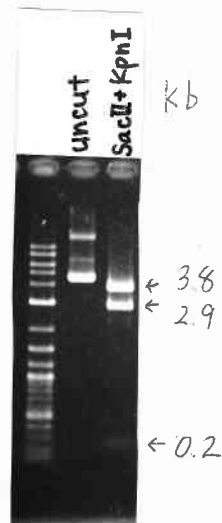
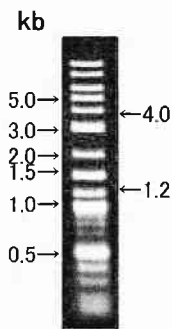
Date : 110422

DNA concentration (O.D.): 134.93 ng/ul

DNA	1 ul
Enzyme (Sac II +KpnI)	0.5+0.5 ul
Buffer L	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 BC060800.1 >

232, 2862, 3833 bp

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

Date : 110511 Shipped : 25 ng/ul, 40 ul

Final concentration: 25 ng/ul

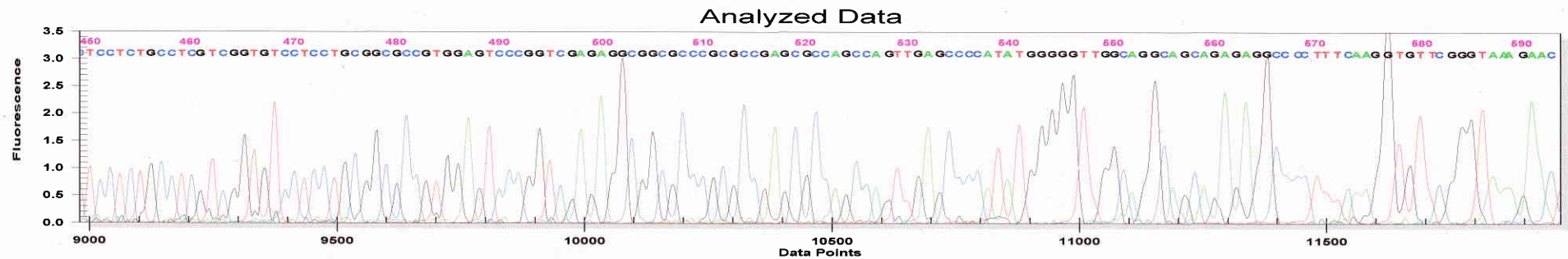
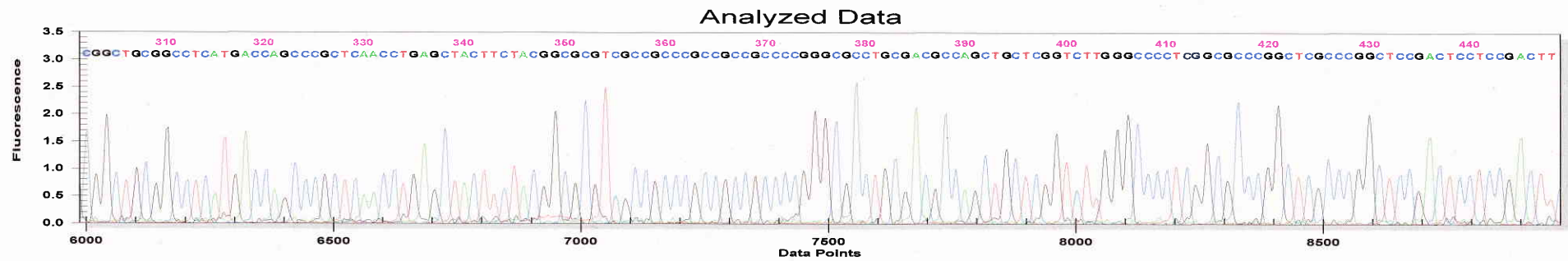
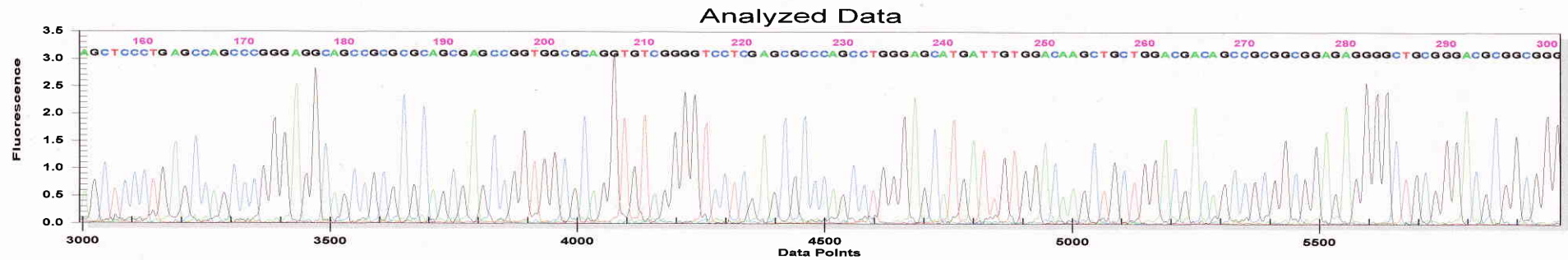
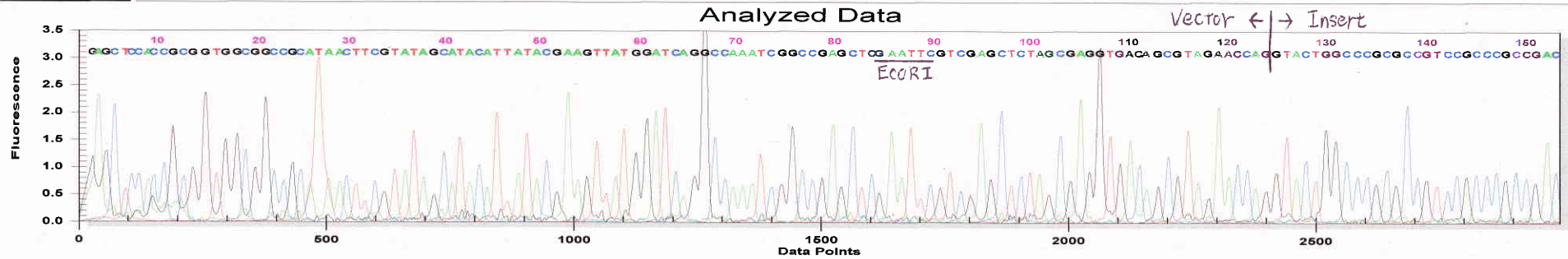
DNA (<u>134.93</u> ng/ul)	<u>87.0</u>	ul
10 × TE	<u>47.0</u>	ul
dH ₂ O	<u>335.6</u>	ul
Total	<u>469.6</u>	ul



Project : GNP
Sample : IRAK133H20_T7long.A12_11051113Q0
Result : IRAK133H20_T7long.A12_11051113Q0

System : CEQ System

Operator : 2.110511-2.furu
Instrument : CEQ System (Ver. 9.0.25)

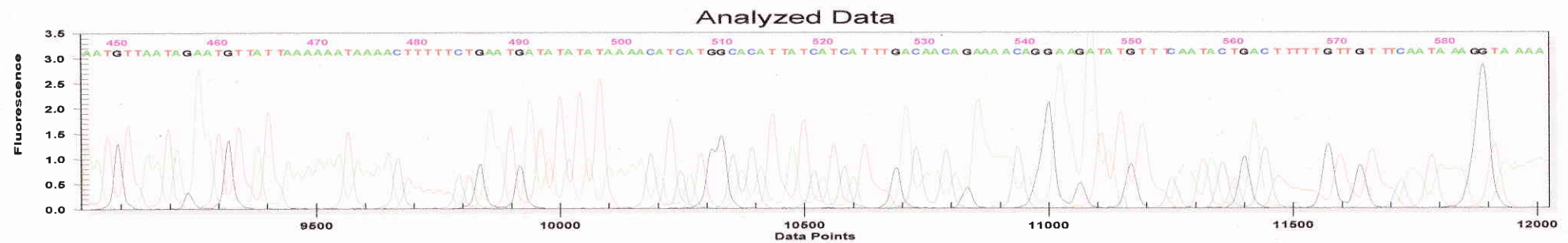
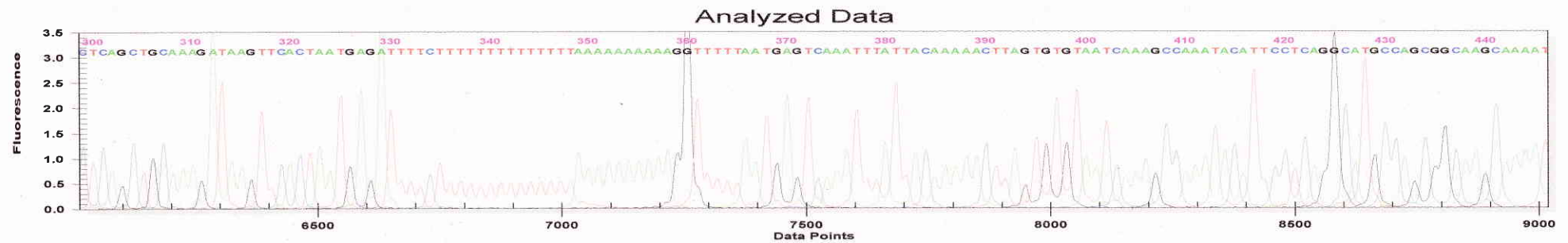
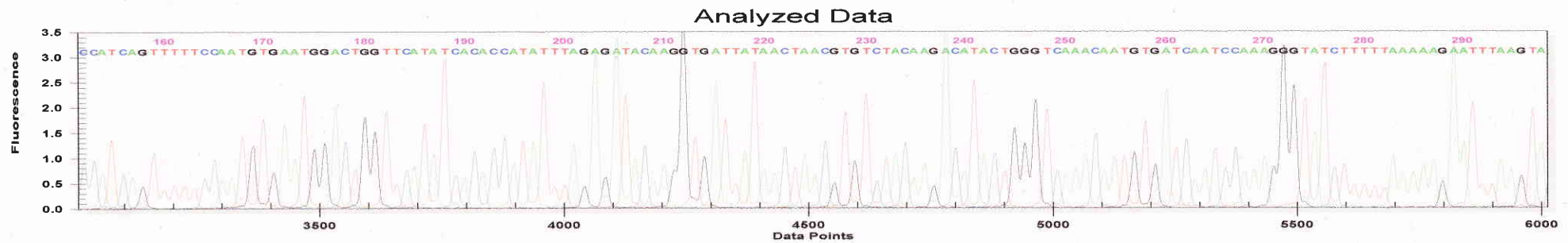
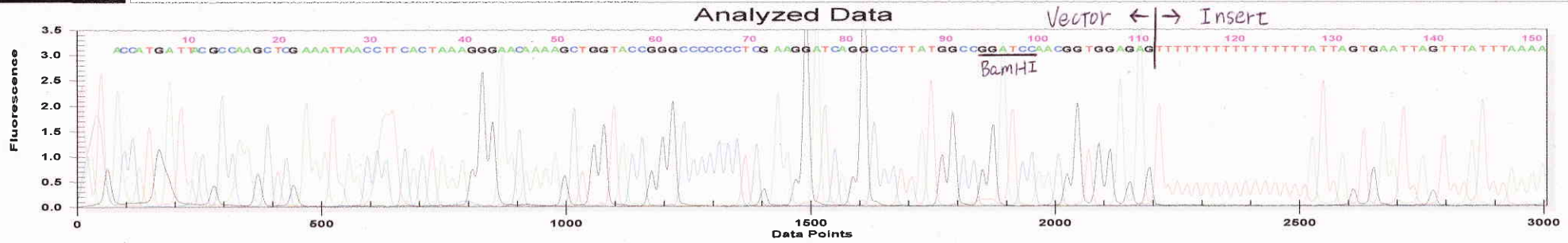




Project : GNP
Sample : IRAK133H20_Reverse2.B08_11042812DC
Result : IRAK133H20_Reverse2.B08_11042812DC

System : System 1

Operator : 1.110428.furu
Instrument : System 1 (Ver. 9.0.25)



[GENETYX : Homology Data]

Date : 2011.05.11

Query Sequence

File Name :
 Sequence Name : BC060800
 Sequence Size : 3937

Target Sequence

File Name : IRAK133H20_T7long.A12_11051113QO
 Sequence Name : IRAK133H20_T7long.A12_11051113QO
 Sequence Size : 719

Unit Size to Compare = 6

Pick up Location No. = 1

Query Range: 1 - 596

Sbjct Range: 124 - 719

596 bp, INT.Score: 2358, OPT.Score: 2360

Identity: 592 / 596 (99%)

Strand: Plus / Plus

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Query 1   GTACTGGCCC GCGCCGTCCG CCCGCCGACA GCTCCCTGAG CCAGCCC GGG AGGCAGCCGC 60
          |||
Sbjct 124 GTACTGGCCC GCGCCGTCCG CCCGCCGACA GCTCCCTGAG CCAGCCC GGG AGGCAGCCGC 183

Query 61   GCGCAGCGAG CCGGTGGCGC AGGTGTCGGG GTCCTCGAGC GCCCAGCCTG GGAGCATGAT 120
          |||
Sbjct 184 GCGCAGCGAG CCGGTGGCGC AGGTGTCGGG GTCCTCGAGC GCCCAGCCTG GGAGCATGAT 243

Query 121  TGTGGACAAG CTGCTGGACG ACAGCCGCGG CGGAGAGGGG CTGCGGGACG CGGCGGGCGG 180
          |||
Sbjct 244 TGTGGACAAG CTGCTGGACG ACAGCCGCGG CGGAGAGGGG CTGCGGGACG CGGCGGGCGG 303

Query 181  CTGCGGCCTC ATGACCAGCC CGCTCAACCT GAGCTACTTC TACGGCGCGT CGCCGCCCGC 240
          |||
Sbjct 304 CTGCGGCCTC ATGACCAGCC CGCTCAACCT GAGCTACTTC TACGGCGCGT CGCCGCCCGC 363

Query 241  CGCCGCCCCG GCGGCCTGCG ACGCCAGCTG CTCGGTCTTG GGCCCTCGG CGCCCGGCTC 300
          |||
Sbjct 364 CGCCGCCCCG GCGGCCTGCG ACGCCAGCTG CTCGGTCTTG GGCCCTCGG CGCCCGGCTC 423

Query 301  GCCCGGCTCC GACTCCTCCG ACTTCTCCTC TGCCTCGTCG GTGTCCTCCT GCGGCGCCGT 360
          |||
Sbjct 424 GCCCGGCTCC GACTCCTCCG ACTTCTCCTC TGCCTCGTCG GTGTCCTCCT GCGGCGCCGT 483

Query 361  GGAGTCCC GAGAGGCG GCGCCCGCGC CGAGCGCCAG CCAGTTGAGC CCCATATGGG 420
          |||
Sbjct 484 GGAGTCCC GAGAGGCG GCGCCCGCGC CGAGCGCCAG CCAGTTGAGC CCCATATGGG 543

Query 421  GGTGGCAGG CAGCAGAGAG GCCCCTTTCA AGGTGTTCGG GTAAAGA AACT CAGTGAAGGA 480
          |||
Sbjct 544 GGTGGCAGG CAGCAGAGAG GCCCCTTTCA AGGTGTTCGG GTAAAGA AACT CAGTGAAGGA 603

Query 481  ACTCCTGTTG CACATCCGAA GTCATAAACA GAAGGCTTCT GGCCAAGCTG TGGATGATTT 540
          |||
Sbjct 604 ACTCCTGTTG CACATCCGAA GTCATAAACA GAAGGCTTCT GGCCAAGCTG TGGATGATTT 663

Query 541  TAAGACACAA GGTGTGAACA TAGAACAGTT CAGAGAATTG AAGAACACAG TATCAT 596
          |||
Sbjct 664 AAAGACACAA GGTGTGAACA TAGAACAGTT CAGAGAATTG AAGAACACAG TATCTT 719

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[GENETYX : Homology Data]

Date : 2011.04.28

Query Sequence

File Name :
 Sequence Name : BC060800
 Sequence Size : 3937

Target Sequence

File Name : IRAK133H20_Reverse2.B08_11042812DC
 Sequence Name : IRAK133H20_Reverse2.B08_11042812DC (complement)
 Sequence Size : 703

Unit Size to Compare = 6

Pick up Location No. = 1

Query Range: 3346 - 3937

Sbjct Range: 1 - 593

594 bp, INT.Score: 2012, OPT.Score: 2316

Identity: 589 / 594 (99%)

Strand: Plus / Minus

Query	3346	GGGATTACAG	GAGTGAGCCA	CCATGCCCGG	CTGGCAGTTG	CATGGAAGAG	AACACCTCTT	3405
Sbjct	1	GGGATTACAG	GAGT-AGCCA	CCATGCCCGG	CTGGCAGTTG	CATGGAGGAG	AACACTTCTT	59
Query	3406	TATGGCTTAC	CC-TCTAGAA	TTTCTAATTT	-ATGTGTTCT	GTTGAAATTT	TTGTTTTTTT	3463
Sbjct	60	TATGGCTTAC	CCTTCTAGAA	TTTCTAATTT	AATGTGTTCT	GTTGAAATTT	TTGTTTTTTT	119
Query	3464	ACCTTTATTG	AAACAACAAA	AAGTCAGTAT	TGAAACATAT	CTTCCTGTTT	TCTGTTGTCA	3523
Sbjct	120	ACCTTTATTG	AAACAACAAA	AAGTCAGTAT	TGAAACATAT	CTTCCTGTTT	TCTGTTGTCA	179
Query	3524	AATGATGATA	ATGTGCCATG	ATGTTTTATA	TATATCATTC	AGAAAAAGTT	TTATTTTTTA	3583
Sbjct	180	AATGATGATA	ATGTGCCATG	ATGTTTTATA	TATATCATTC	AGAAAAAGTT	TTATTTTTTA	239
Query	3584	ATAACATTCT	ATTAACATTA	TTTTGCTTGC	CGCTGGCATG	CCTGAGGAAT	GTATTTGGCT	3643
Sbjct	240	ATAACATTCT	ATTAACATTA	TTTTGCTTGC	CGCTGGCATG	CCTGAGGAAT	GTATTTGGCT	299
Query	3644	TTGATTACAC	ACTAAGTTTT	TGTAATAAAT	TTGACTCATT	AAAAACCTTT	TTTTTTTAAA	3703
Sbjct	300	TTGATTACAC	ACTAAGTTTT	TGTAATAAAT	TTGACTCATT	AAAAACCTTT	TTTTTTTAAA	359
Query	3704	AAAAAAAAAA	AGAAAATCTC	ATTAGTGAAC	TTATCTTTGC	AGCTGAGTAC	TTAAATTCTT	3763
Sbjct	360	AAAAAAAAAA	AGAAAATCTC	ATTAGTGAAC	TTATCTTTGC	AGCTGAGTAC	TTAAATTCTT	419
Query	3764	TTTAAAAAGA	TACCCTTTGG	ATTGATCACA	TTGTTTGACC	CAGTATGTCT	TGTAGACACG	3823
Sbjct	420	TTTAAAAAGA	TACCCTTTGG	ATTGATCACA	TTGTTTGACC	CAGTATGTCT	TGTAGACACG	479
Query	3824	TTAGTTATAA	TCACCTTGTA	TCTCTAAATA	TGGTGTGATA	TGAACCAGTC	CATTCACATT	3883
Sbjct	480	TTAGTTATAA	TCACCTTGTA	TCTCTAAATA	TGGTGTGATA	TGAACCAGTC	CATTCACATT	539
Query	3884	GGAAAAACTG	ATGGTTTTAA	ATAAACTAAT	TCACTAATAA	AAAAAAAAAA	AAAA	3937
Sbjct	540	GGAAAAACTG	ATGGTTTTAA	ATAAACTAAT	TCACTAATAA	AAAAAAAAAA	AAAA	593