

**RIKEN clone ID: IRAK091F11**

Vector : pBluescriptR

Gene	CA10		
Accession No.	BC047456.1	2717 bp	1..2717
	<i>CDS</i>	987 bp	900..1886

● Plasmid DNA purification

Date : 110516 Culture : LB (100 ug/ml Ampicillin) 3 ml → 37°C O/N

Date : 110517 Purification : QIAGEN Miniprep kit → dH<sub>2</sub>O 100 ul

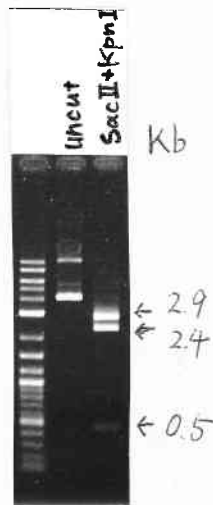
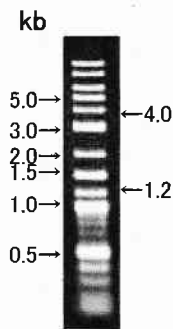
● Digestion by restriction enzyme / Concentration calibration

Date : 110517 DNA concentration (O.D.): 81.61 ng/ul

DNA	1 ul
Enzyme (Sac II +KpnI)	0.5+0.5 ul
Buffer L	1 ul
dH <sub>2</sub> O	7 ul
Total	10 ul

Erectrophoresis: 1% agarose gel, 1 × TAE Buffer

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



<Expected digestion pattern from BC047456.1 >

482, 2363, 2862 bp

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

Date : 110520 Shipped : 25 ng/ul, 40 ul

Final concentration: 25 ng/ul

DNA ( <u>81.61 ng/ul</u> )	<u>84.0</u> ul
10 × TE	<u>27.4</u> ul
dH <sub>2</sub> O	<u>162.8</u> ul
Total	<u>274.2</u> ul

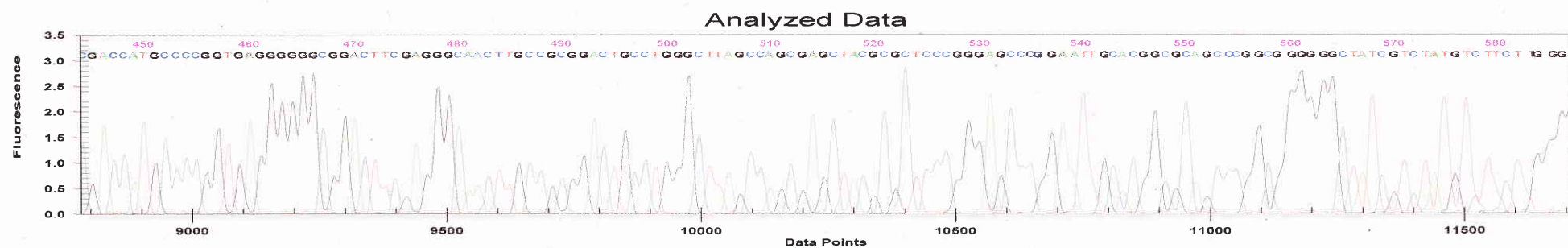
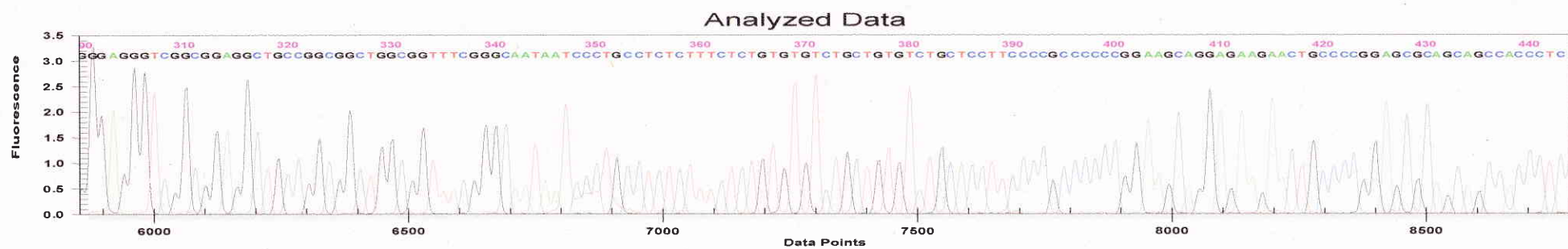
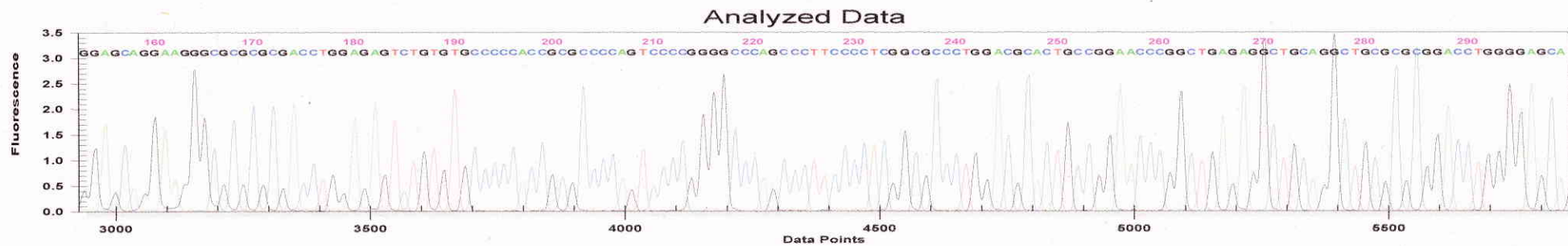
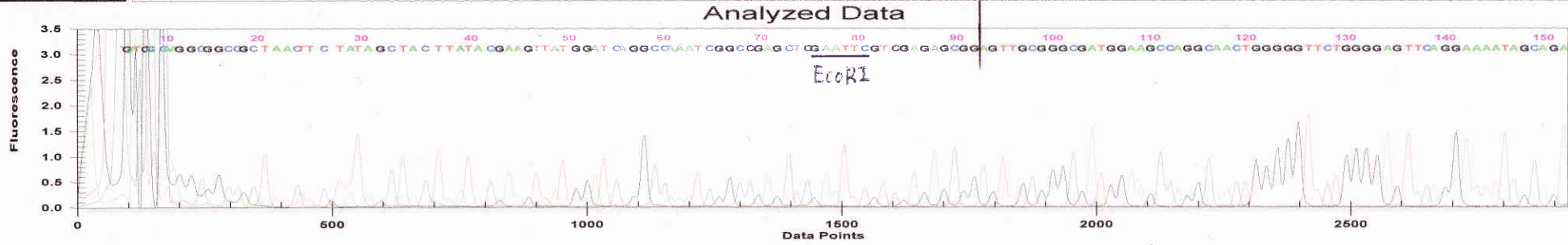


Project : GNP  
Sample : IRAK091F11\_T7.G06\_11051912DW  
Result : IRAK091F11\_T7.G06\_11051912DW

System : System 1

Operator : 1.110519.furu  
Instrument : System 1 (Ver. 9.0.25)

Vector ← → Insert

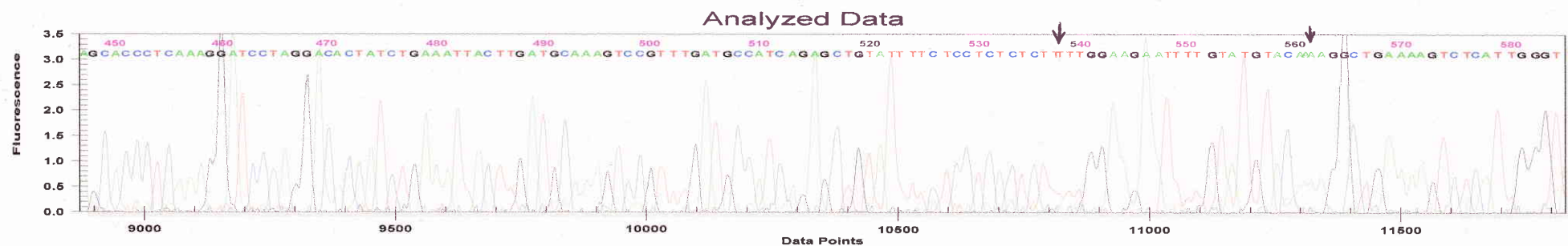
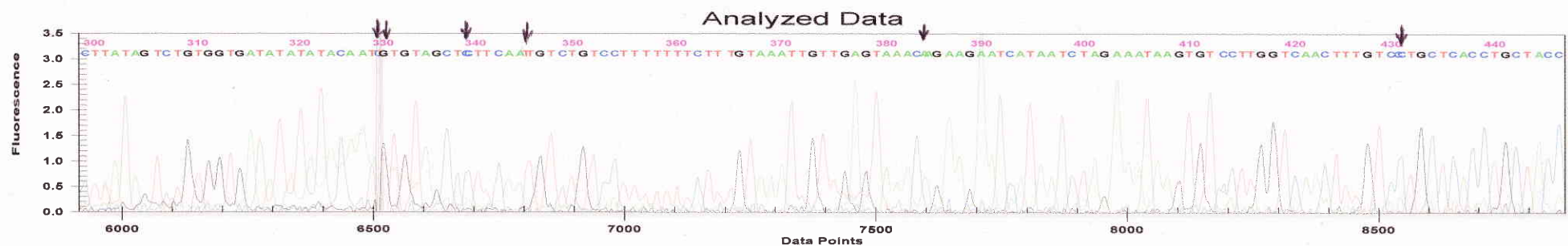
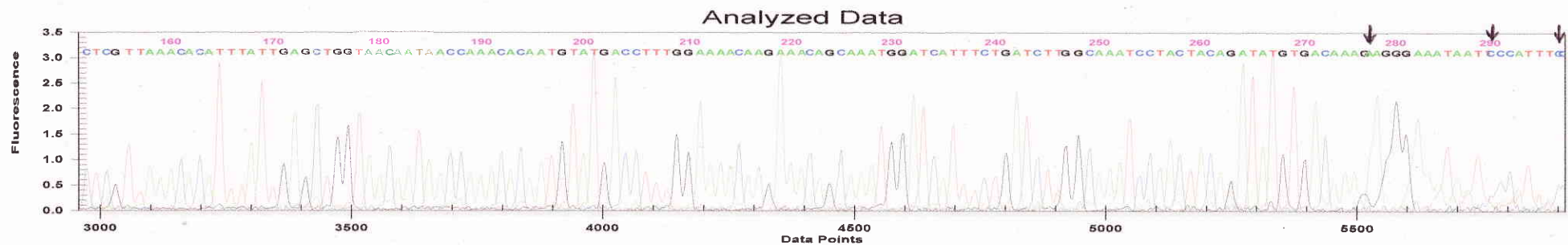
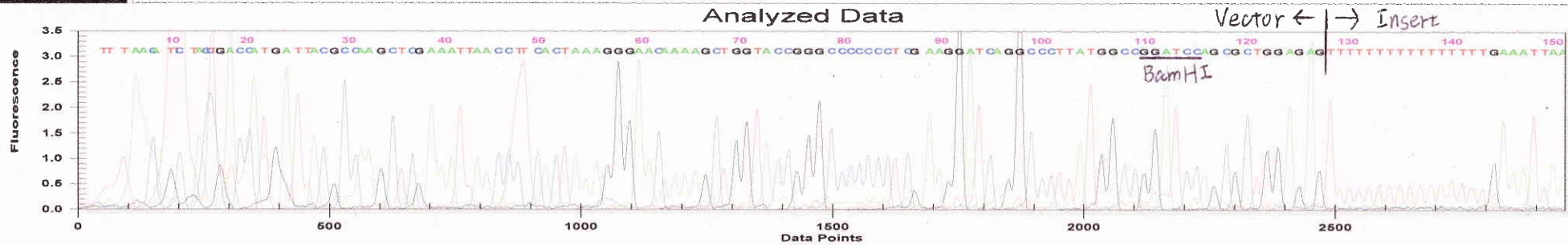




Project : GNP  
Sample : IRAK091F11\_Reverse2.H06\_11051912DW  
Result : IRAK091F11\_Reverse2.H06\_11051912DW

System : System 1

Operator : 1.110519.furu  
Instrument : System 1 (Ver. 9.0.25)



[ GENETYX : Homology Data ]

Date : 2011.05.19

## Query Sequence

File Name :  
 Sequence Name : BC047456  
 Sequence Size : 2717

## Target Sequence

File Name : IRAK091F11\_T7.G06\_11051912DW  
 Sequence Name : IRAK091F11\_T7.G06\_11051912DW  
 Sequence Size : 720

Unit Size to Compare = 6

Pick up Location No. = 1

Query Range: 1 - 630

Sbjct Range: 92 - 718

630 bp, INT.Score: 2256, OPT.Score: 2469

Identity: 626 / 630 (99%)

Strand: Plus / Plus

Query	1	AGTTGCGGGC	GATGGAAGCC	AGGCAACTGG	GGGTTCTGGG	GAGTTCAGGA	AAATAGCAGA	60
Sbjct	92	AGTTGCGGGC	GATGGAAGCC	AGGCAACTGG	GGGTTCTGGG	GAGTTCAGGA	AAATAGCAGA	151
Query	61	GGAGCAGGAA	GGGCGCGCGC	GACCTGGAGA	GTCTGTGTGC	CCCCACCGCG	CCCCAGTCCC	120
Sbjct	152	GGAGCAGGAA	GGGCGCGCGC	GACCTGGAGA	GTCTGTGTGC	CCCCACCGCG	CCCCAGTCCC	211
Query	121	CGGGGCCAG	CCCTTCCCCT	CGGCGCCCTG	GACGCACTGC	CGGAACCCGG	CTGAGAGGCT	180
Sbjct	212	CGGGGCCAG	CCCTTCCCCT	CGGCGCCCTG	GACGCACTGC	CGGAACCCGG	CTGAGAGGCT	271
Query	181	GCAGGCTGCG	CGCGGACCTG	GGGAGCAGGG	AGGGTCGGCG	GAGGCTGCCG	GCGGCTGGCG	240
Sbjct	272	GCAGGCTGCG	CGCGGACCTG	GGGAGCAGGG	AGGGTCGGCG	GAGGCTGCCG	GCGGCTGGCG	331
Query	241	GTTCGGGCA	ATAATCCCTG	CCTCTCTTTC	TCTGTGTGTC	TGCTGTGTCT	GCTCCTTCCC	300
Sbjct	332	GTTCGGGCA	ATAATCCCTG	CCTCTCTTTC	TCTGTGTGTC	TGCTGTGTCT	GCTCCTTCCC	391
Query	301	CGCCCCCGG	AAGCAGGAGA	AGAACTGCCC	CGGAGCGCAG	CAGCCACCCT	CCGACCATGC	360
Sbjct	392	CGCCCCCGG	AAGCAGGAGA	AGAACTGCCC	CGGAGCGCAG	CAGCCACCCT	CCGACCATGC	451
Query	361	CCCGGTGAGG	GGGGCGGACT	TCGAGGGCAA	CTTGCCGCGG	ACTGCCTGGG	CTTAGCCAGC	420
Sbjct	452	CCCGGTGAGG	GGGGCGGACT	TCGAGGGCAA	CTTGCCGCGG	ACTGCCTGGG	CTTAGCCAGC	511
Query	421	GAGCTACGCG	CTCCCGGGAG	CCCGGAATTG	CACGGCGCAG	CCCGGCGGGG	GGCTATCGTC	480
Sbjct	512	GAGCTACGCG	CTCCCGGGAG	CCCGGAATTG	CACGGCGCAG	CCCGGCGGGG	GGCTATCGTC	571
Query	481	TATGTCTTCT	TGGGGCGCCA	GACGAATCGG	GGTCTCGTTT	TTGCTGGAAG	AGCCCAGTGT	540
Sbjct	572	TATGTCTTCT	TGGGGCGCCA	GACGAATCGG	GGTCTCGTTT	TTGCTGGAAG	AGCCCAGTGT	631
Query	541	TGGTGGCTTC	AGGTGGCTGC	TGCCGCCGCC	GCCGCCGCCG	CCGCTGCTAG	TGCGGTTTCC	600
Sbjct	632	TGGTGGCTTC	AGGTGGCTGC	TGCC-CCGCC	GCCGCCGCCG	CCGCTGCTAG	TGCGGTTTCC	690
Query	601	GCCGCTGGTG	CGAAGAGAAG	AGACACGCGA	630			
Sbjct	691	GCCGCTGGTG	CGAAGAGAA-	AGAC-CGCNA	718			

[ GENETYX : Homology Data ]

Date : 2011.05.19

## Query Sequence

File Name :  
 Sequence Name : BC047456  
 Sequence Size : 2717

## Target Sequence

File Name : IRAK091F11\_Reverse2.H06\_11051912DW  
 Sequence Name : IRAK091F11\_Reverse2.H06\_11051912DW (complement)  
 Sequence Size : 723

Unit Size to Compare = 6

Pick up Location No. = 1

Query Range: 2147 - 2717

Sbjct Range: 1 - 597

598 bp, INT.Score: 600, OPT.Score: 1952

Identity: 564 / 598 (94%)

Strand: Plus / Minus

Query	2147	TTACAACC--	TCC--ATCAT	-GGGAA--GT	C-AAGTTTC-	AGAAA-CAAA	A-GTCTCA-T	2194
							.	
Sbjct	1	TTACAACCNT	TCCAATTCAT	GGGGAAGGT	CAAAGTTTCA	AGAAACCAA	AGGTNTCANT	60
Query	2195	TCATAA-GAG	GTCTTA-GAA	GAAAATAACC	A-GTTAACCT	GATTTCAATT	TTGATACC-G	2250
		.				.		
Sbjct	61	TCATNAGGAG	GTCTTAGGAA	GAAAATAACC	AGGTTAACCT	GATTTCNATT	TTGATACCGG	120
Query	2251	TTTTCTGAA	CTAATAAATC	TACCCAATGA	GACTTTTCAG	CC-TTTGTAC	ATACAAAATT	2309
			.					
Sbjct	121	TTTTCTGAA	NTAAT-AATC	TACCCAATGA	GACTTTTCAG	CCTTTTGTAC	ATACAAAATT	179
Query	2310	CTTCC-AAAA	GAGAGAGGAG	AAAATACAGC	TCTGATGGCA	TCAAACGGAC	TTTGCATCAA	2368
Sbjct	180	CTTCCAAAA	GAGAGAGGAG	AAAATACAGC	TCTGATGGCA	TCAAACGGAC	TTTGCATCAA	239
Query	2369	GTAATTTTCAG	ATAGTGTCTT	AGGATCCTTT	GAGGGTGCTG	GTAGCAGGTG	AGCA-GGACA	2427
Sbjct	240	GTAATTTTCAG	ATAGTGTCTT	AGGATCCTTT	GAGGGTGCTG	GTAGCAGGTG	AGCAGGGACA	299
Query	2428	AAGTTGACCA	AGGACACTTA	TTTCTAGATT	ATGATTCTTC	-TGTTTACTC	AACAATTTAC	2486
Sbjct	300	AAGTTGACCA	AGGACACTTA	TTTCTAGATT	ATGATTCTTC	TTGTTTACTC	AACAATTTAC	359
Query	2487	AAAGAAAAAA	AGGACAGAC-	ATTGAA-GAG	CTACAC--AT	TGTATATATA	TCACCACAGA	2542
Sbjct	360	AAAGAAAAAA	AGGACAGACA	ATTGAAGGAG	CTACACAGAT	TGTATATATA	TCACCACAGA	419
Query	2543	CTATAA-GGA	AAT-GGAATT	ATTTCCC-TC	TTGTCACAT	ATCTGTAGTA	GGATTTGCCA	2599
Sbjct	420	CTATAAGGGA	AATGGGAATT	ATTTCCCTTC	TTGTCACAT	ATCTGTAGTA	GGATTTGCCA	479
Query	2600	AGATCAGAAA	TGATCCATTT	GCTGTTTCTT	GTTTTCACAA	GGTCATACAT	TGTGTTTGGT	2659
Sbjct	480	AGATCAGAAA	TGATCCATTT	GCTGTTTCTT	GTTTTCACAA	GGTCATACAT	TGTGTTTGGT	539
Query	2660	TATTGTTACC	AGCTCAATAA	ATGTGTTTAA	CGAGTTAATT	TCAAAAAAAAA	AAAAAAAA	2717
Sbjct	540	TATTGTTACC	AGCTCAATAA	ATGTGTTTAA	CGAGTTAATT	TCAAAAAAAAA	AAAAAAAA	597