

RIKEN_clone ID: IRAK047019

Vector : pBluescriptR

Gene	FOXA1	2874
Accession No.	BC033890.1	2445 bp
	<i>CDS</i>	1419 bp
		63..1481

● Plasmid DNA purification

Date : 10/2/13 Culture : LB (100 ug/ml Ampicillin) 3 ml → 37°C O/N

Date : 10/2/14 Purification : QIAGEN Miniprep kit → dH₂O 100 ul

● Digestion by restriction enzyme / Concentration calibration

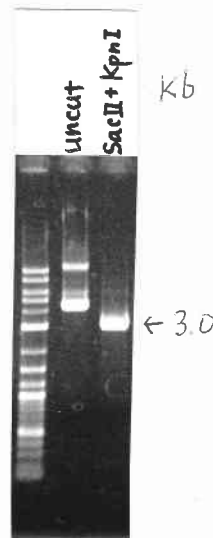
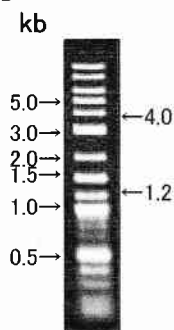
Date : 10/2/14

DNA concentration (O.D.): 207.48 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 BC033890.1 >

2862, 3002 bp

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

Date : 10/2/16

Shipped : 25 ng/ul, 40 ul

Final concentration: 25 ng/ul

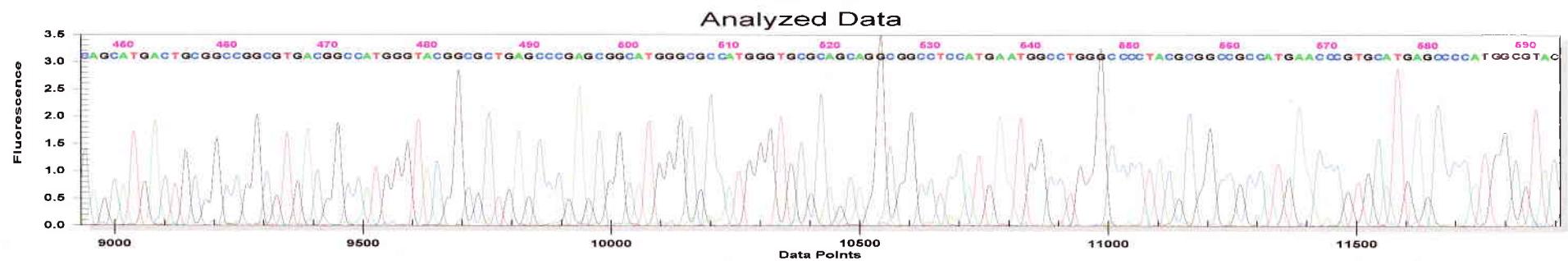
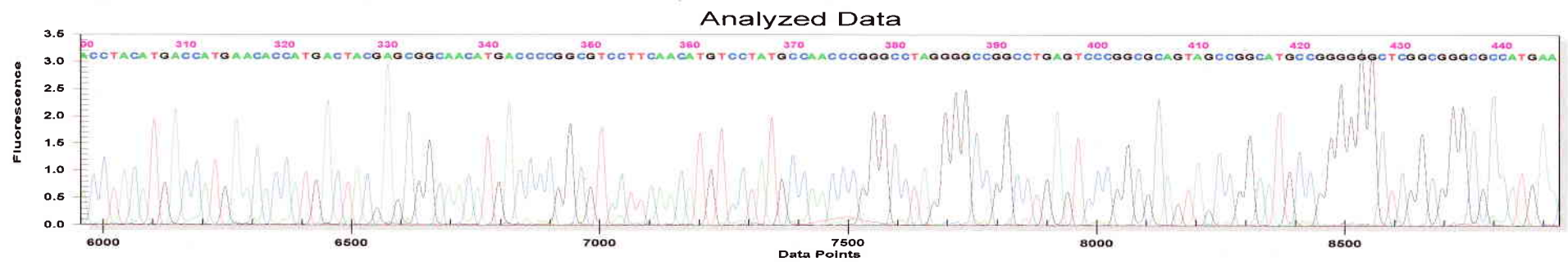
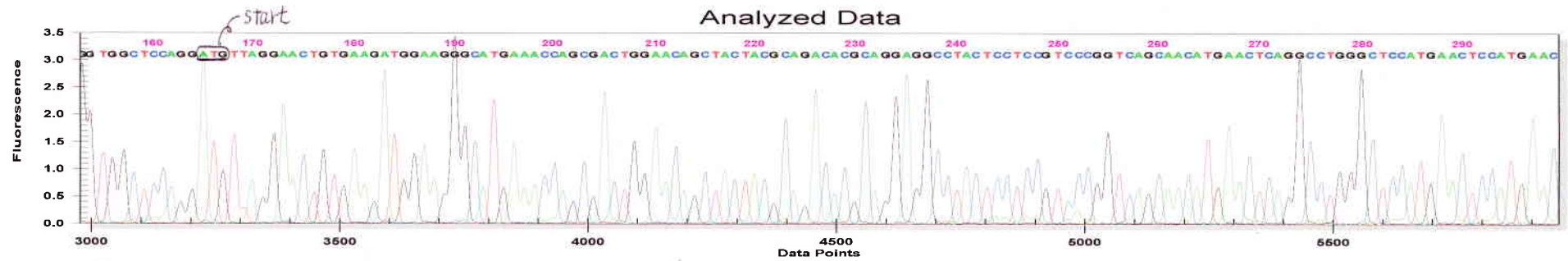
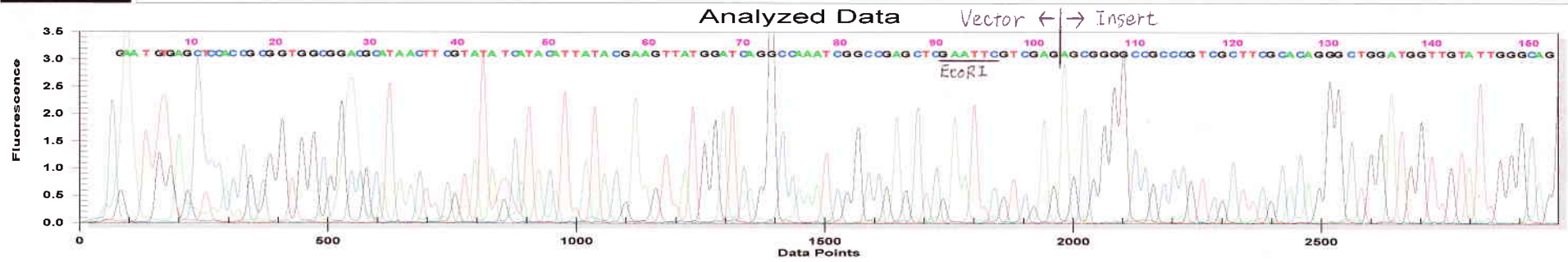
DNA (<u>207.48</u> ng/ul)	<u>88.0</u>	ul
10 × TE	<u>73.0</u>	ul
dH ₂ O	<u>569.3</u>	ul
Total	<u>730.3</u>	ul



Project : GNP
Sample : IRAK047O19_T7.G02_10121512GA
Result : IRAK047O19_T7.G02_10121512GA

System : CEQ System

Operator : 2.101215.furu
Instrument : CEQ System (Ver. 9.0.25)

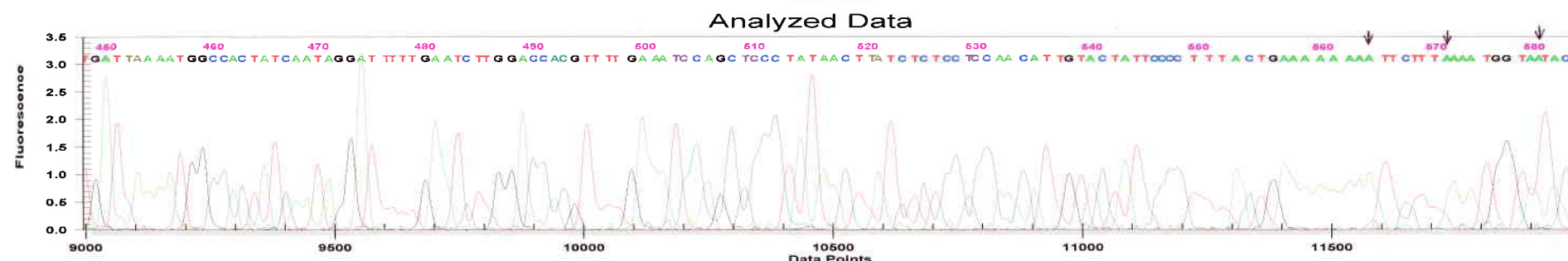
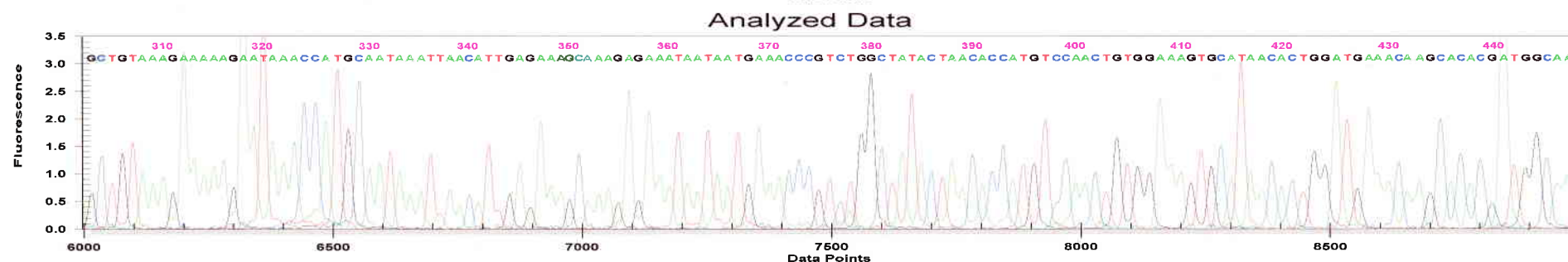
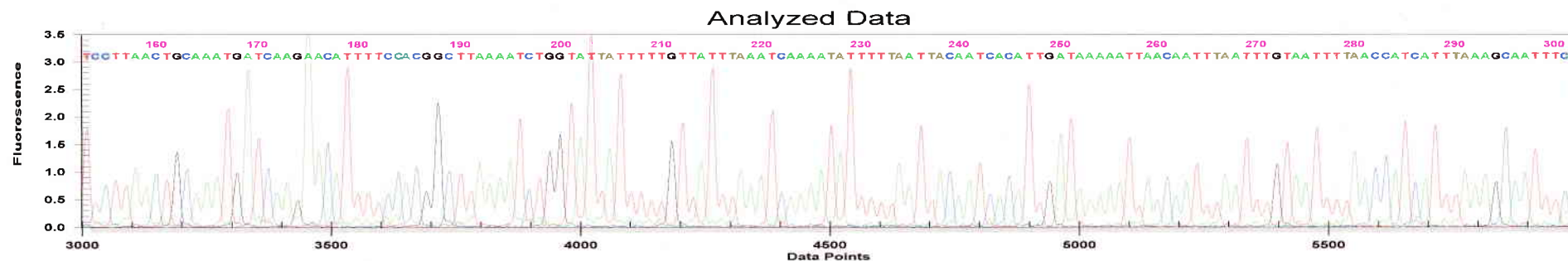
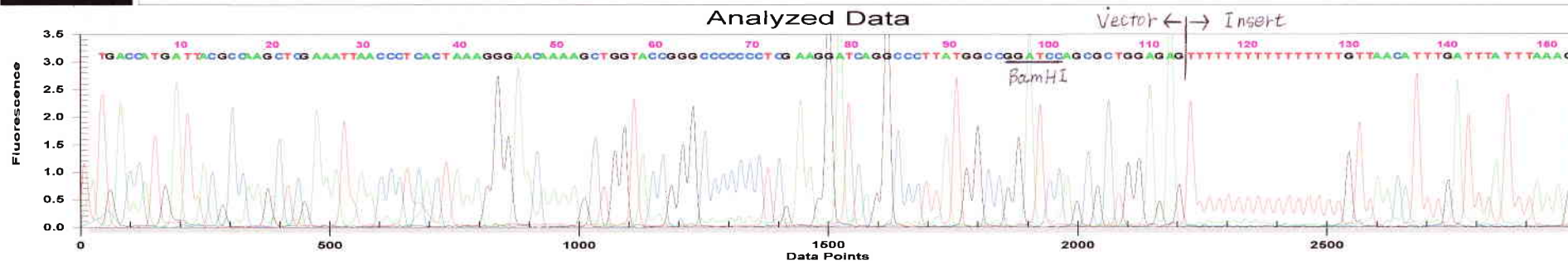




Project : GNP
Sample : IRAK047O19_Reverse2.H02_10121512GA
Result : IRAK047O19_Reverse2.H02_10121512GA

System : CEQ System

Operator : 2.101215.furu
Instrument : CEQ System (Ver. 9.0.25)



[GENETYX : Homology Data]

Date : 2010.12.17

Query Sequence

File Name :
 Sequence Name : BC033890.1
 Sequence Size : 2874

Target Sequence

File Name : IRAK047019_T7.G02_10121512GA.seq
 Sequence Name : IRAK047019_T7.G02_10121512GA
 Sequence Size : 741

Unit Size to Compare = 6

Pick up Location No. = 1

Query Range: 1 - 642

Sbjct Range: 102 - 739

642 bp, INT.Score: 2287, OPT.Score: 2378

Identity: 615 / 642 (95%)

Strand: Plus / Plus

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Query  1   AGCGGGGGCCG CCCGTCGCTT CGCACAGGGC TGGATGGTTG TATTGGGCAG GGTGGCTCCA 60
          |||
Sbjct 102  AGCGGGGGCCG CCCGTCGCTT CGCACAGGGC TGGATGGTTG TATTGGGCAG GGTGGCTCCA 161

Query  61   GGATGTTAGG AACTGTGAAG ATGGAAGGGC ATGAAACCAG CGACTGGAAC AGCTACTACG 120
          |||
Sbjct 162  GGATGTTAGG AACTGTGAAG ATGGAAGGGC ATGAAACCAG CGACTGGAAC AGCTACTACG 221

Query 121   CAGACACGCA GGAGGCCTAC TCCTCCGTCC CGGTCAGCAA CATGAACTCA GGCCTGGGCT 180
          |||
Sbjct 222  CAGACACGCA GGAGGCCTAC TCCTCCGTCC CGGTCAGCAA CATGAACTCA GGCCTGGGCT 281

Query 181   CCATGAACTC CATGAACACC TACATGACCA TGAACACCAT GACTACGAGC GGCAACATGA 240
          |||
Sbjct 282  CCATGAACTC CATGAACACC TACATGACCA TGAACACCAT GACTACGAGC GGCAACATGA 341

Query 241   CCCC GGCGTC CTTCAACATG TCCTATGCCA ACCCGGGCCT AGGGGCCGGC CTGAGTCCC G 300
          |||
Sbjct 342  CCCC GGCGTC CTTCAACATG TCCTATGCCA ACCCGGGCCT AGGGGCCGGC CTGAGTCCC G 401

Query 301   GCGCAGTAGC CGGCATGCCG GGGGGCTCGG CGGGCGCCAT GAACAGCATG ACTGCGGCCG 360
          |||
Sbjct 402  GCGCAGTAGC CGGCATGCCG GGGGGCTCGG CGGGCGCCAT GAACAGCATG ACTGCGGCCG 461

Query 361   GCGTGACGGC CATGGGTACG GCGCTGAGCC CGAGCGGCAT GGGCGCCATG GGTGCGCAGC 420
          |||
Sbjct 462  GCGTGACGGC CATGGGTACG GCGCTGAGCC CGAGCGGCAT GGGCGCCATG GGTGCGCAGC 521

Query 421   AGGCGGCCTC CATGAATGGC CTGGGCCCCT ACGCGGCCGC CATGAACCCG TGCATGAGCC 480
          |||
Sbjct 522  AGGCGGCCTC CATGAATGGC CTGGGCCCCT ACGCGGCCGC CATGAACCCG TGCATGAGCC 581

Query 481   CCATGGCGTA CGCGCCGTCC AACCTGGGCC GCAGCCGCGC GGGCGGGGGC GCGCAGCCCA 540
          |||
Sbjct 582  CCATGGCGTA CGCGCCGTCC AACCTGGGCC GCAGCCGCGC GGGCGGGGGN GNGACGGCC 641

Query 541   AGACGTTCAA GCGCAGCTAC CCGCACGCCA AGCCGCCCTA CTCGTACATC TCGCTCATCA 600
          .|||
Sbjct 642  NGACGTTAAA GCGCAGCTAC CCGCCC GCCC CGCCGCCCTA CTCCTTCATN TCGCTAATCC 701

Query 601   CCATGGCCAT CCAGCAGGCG CCCAGCAAGA TGCTCAGCT GA 642
          |||
Sbjct 702  CCTTGG-CAT -AAACACGC- CCCCCCGA TGCTC-CCCT GA 739
  
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[GENETYX : Homology Data]

Date : 2010.12.17

Query Sequence

File Name :
 Sequence Name : BC033890.1
 Sequence Size : 2874

Target Sequence

File Name : IRAK047019_Reverse2.H02_10121512GA.seq
 Sequence Name : IRAK047019_Reverse2.H02_10121512GA (complement)
 Sequence Size : 814

Unit Size to Compare = 6

Pick up Location No. = 1

Query Range: 2304 - 2874
 Sbjct Range: 128 - 702
 576 bp, INT.Score: 1834, OPT.Score: 1908
 Identity: 520 / 576 (90%)
 Strand: Plus / Minus

Query	2304	TTCCTCAGGA	ATTGCCCTCA	AGAACTCTGC	TTCTTGCTTT	GCAGAGTGCC	ATGGTCAT-G	2362
Sbjct	128	TTTCTTGGGC	TTTTTTGGCA	GGAGGTGGCC	CCAATGGGTT	-CAATGGTTC	ATTTCTTGG	186
Query	2363	TCATTCTGAG	GTCACATA-A	CACATAAAAT	TAG-TTTCTA	T-GAGTGTA-	TACCATTTAA	2418
Sbjct	187	AGGGTCAAAC	ATTAAACACA	AATAAAAATT	TAGTTTTCTA	TGGAGTGTAT	TACCATTTTA	246
Query	2419	AGAATTTTTT	TTTCAGTAA	AGGGAATAGT	ACAATGTTGG	AGGAGAGATA	AGTTATAGGG	2478
Sbjct	247	AAGAATTTTT	TTTCAGTAA	GGGGAATAGT	ACAATGTTGG	AGGAGAGATA	AGTTATAGGG	306
Query	2479	AGCTGGATTT	CAAAACGTGG	TCCAAGATTC	AAAAATCCTA	TTGATAGTGG	CCATTTTAAT	2538
Sbjct	307	AGCTGGATTT	CAAAACGTGG	TCCAAGATTC	AAAAATCCTA	TTGATAGTGG	CCATTTTAAT	366
Query	2539	CATTGCCATC	GTGTGCTTGT	TTCATCCAGT	GTTATGCACT	TTCCACAGTT	GGACATGGTG	2598
Sbjct	367	CATTGCCATC	GTGTGCTTGT	TTCATCCAGT	GTTATGCACT	TTCCACAGTT	GGACATGGTG	426
Query	2599	TTAGTATAGC	CAGACGGGTT	TCATTATTAT	TTCTCTTTCG	TTTCTCAATG	TTAATTTATT	2658
Sbjct	427	TTAGTATAGC	CAGACGGGTT	TCATTATTAT	TTCTCTTTCG	TTTCTCAATG	TTAATTTATT	486
Query	2659	GCATGGTTTA	TTCTTTTTCT	TTACAGCTGA	AATTGCTTTA	AATGATGGTT	AAAATTACAA	2718
Sbjct	487	GCATGGTTTA	TTCTTTTTCT	TTACAGCTGA	AATTGCTTTA	AATGATGGTT	AAAATTACAA	546
Query	2719	ATTAAATTGT	TAATTTTTAT	CAATGTGATT	GTAATTAATA	ATATTTTGAT	TTAAATAACA	2778
Sbjct	547	ATTAAATTGT	TAATTTTTAT	CAATGTGATT	GTAATTAATA	ATATTTTGAT	TTAAATAACA	606
Query	2779	AAAATAATAC	CAGATTTTAA	GCCGTGGAAA	ATGTTCTTGA	TCATTTGCAG	TTAAGGACTT	2838
Sbjct	607	AAAATAATAC	CAGATTTTAA	GCCGTGGAAA	ATGTTCTTGA	TCATTTGCAG	TTAAGGACTT	666
Query	2839	TAAATAAATC	AAATGTTAAC	AAAAAAAAAA	AAAAAA	2874		
Sbjct	667	TAAATAAATC	AAATGTTAAC	AAAAAAAAAA	AAAAAA	702		