

RIKEN clone ID: W01A002J18

Vector : pENTR/D-TOPO

Gene	OTX2	
Accession No.	BC032579.1	2220 bp
	<i>CDS</i>	894 bp
		1..2220
		286..1179

●Plasmid DNA purification

Date : 10 | 2 | 20

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

Date : 10 | 2 | 21

Purification : QIAGEN Miniprep kit→dH₂O 100 ul

●Digestion by restriction enzyme / Concentration calibration

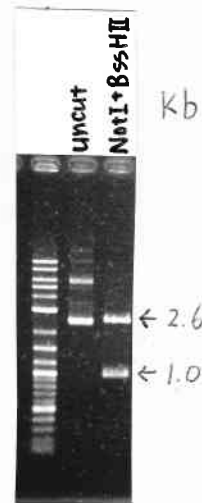
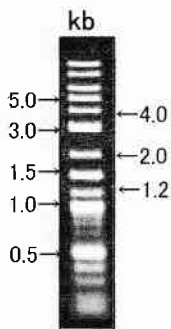
Date : 10 | 2 | 21

DNA concentration (O.D.): 78.28 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 BC032579.1 CDS>

994, 2553 bp

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

Date : 110114

Shipped : 25 ng/ul, 40 ul

Final concentration: 25 ng/ul

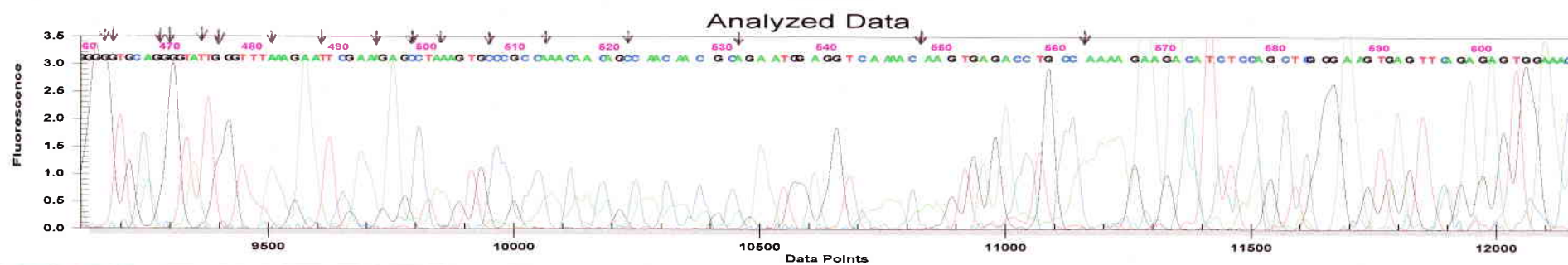
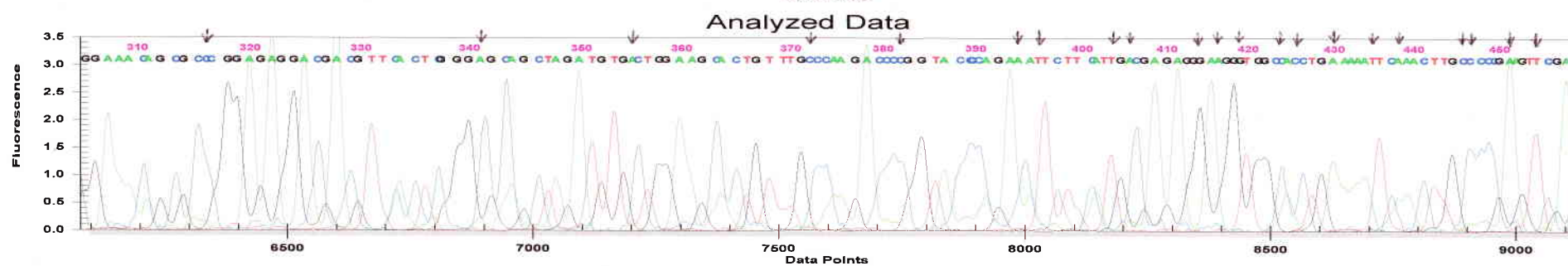
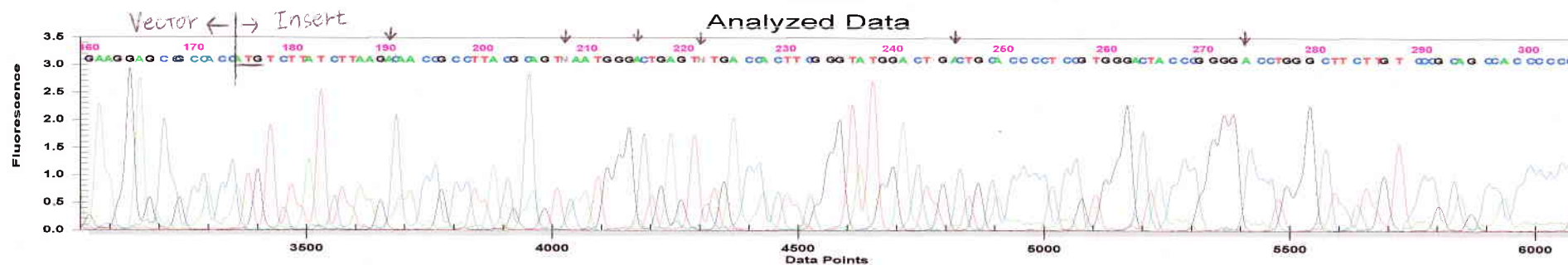
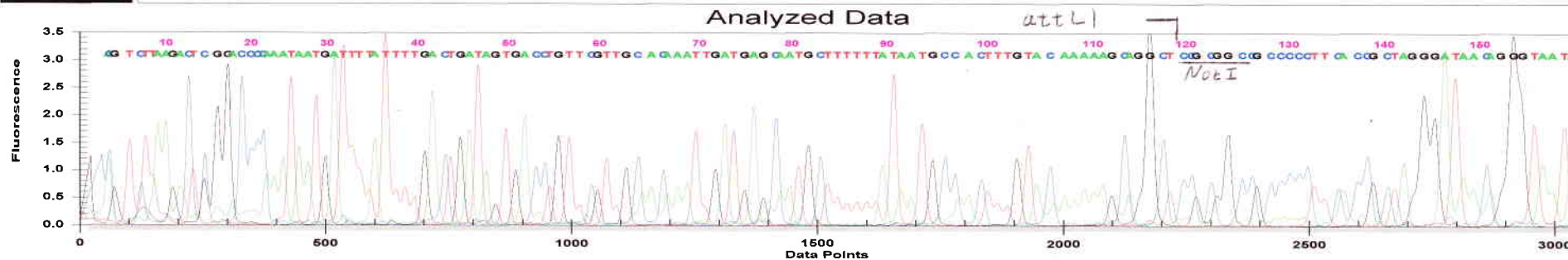
DNA (<u>78.28</u> ng/ul)	<u>79.0</u>	ul
10 × TE	<u>24.7</u>	ul
dH ₂ O	<u>143.6</u>	ul
Total	247.3	ul



Project : GNP
Sample : W01A002J18_M13.A10_10122210AM
Result : W01A002J18_M13.A10_10122210AM

System : CEQ System

Operator : 2.101222.furu
Instrument : CEQ System (Ver. 9.0.25)

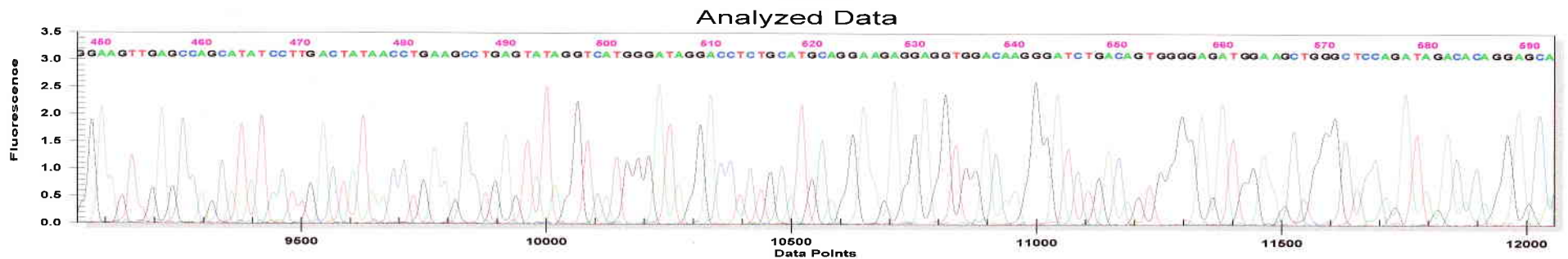
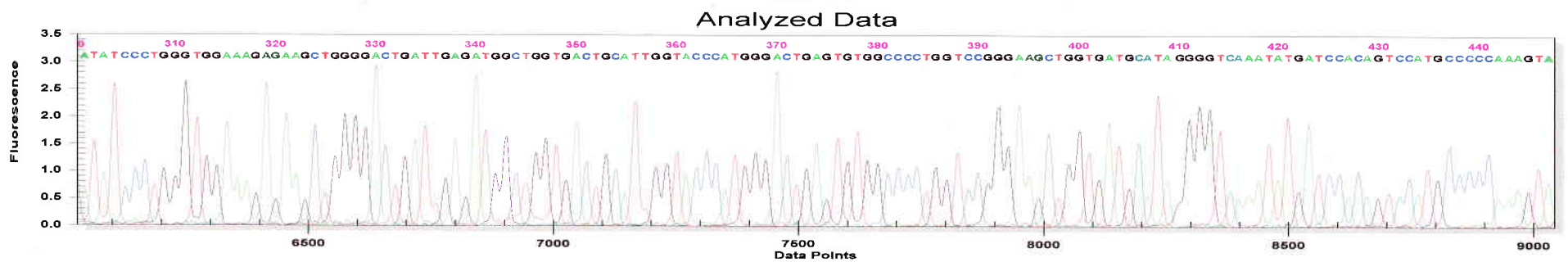
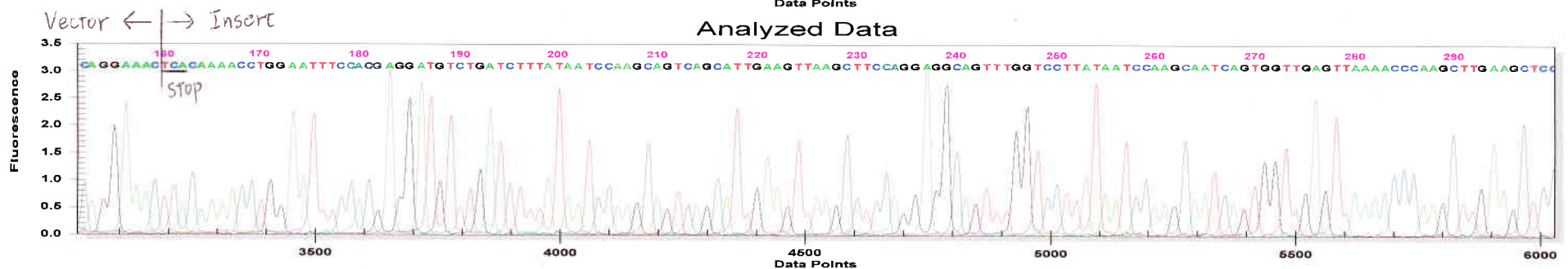
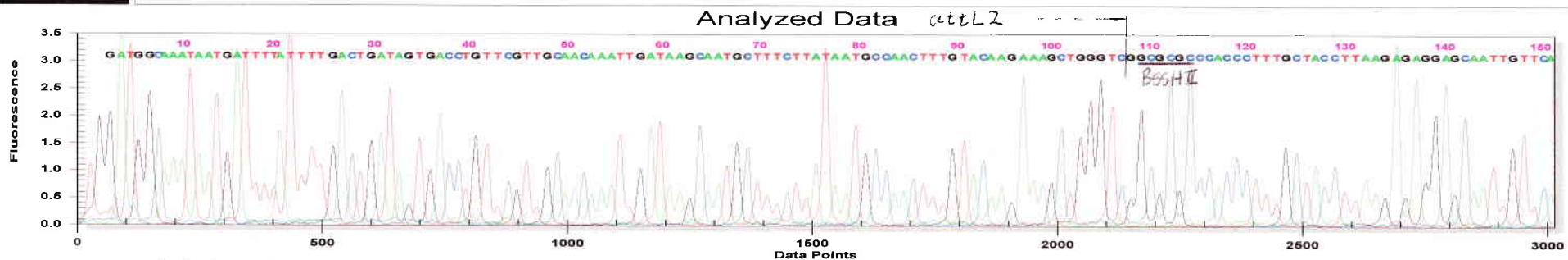




Project : GNP
 Sample : W01A002J18_T7long.B05_110113142M
 Result : W01A002J18_T7long.B05_110113142M

System : CEQ System

Operator : 2.110113.furu
 Instrument : CEQ System (Ver. 9.0.25)



[GENETYX : Homology Data]

Date : 2010.12.24

Query Sequence

File Name :
 Sequence Name : BC032579.1_CDS(286..1179)
 Sequence Size : 894

Target Sequence

File Name : W01A002J18_M13.A10_10122210AM
 Sequence Name : W01A002J18_M13.A10_10122210AM
 Sequence Size : 745

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

Query Range: 4 - 525
 Sbjct Range: 174 - 734
 567 bp, INT.Score: 346, OPT.Score: 1279
 Identity: 474 / 567 (83%)
 Strand: Plus / Plus

Query	4	ATGTC	TATC	TTAAG-CAAC	CGCCTTACGC	AGTCAATGGG	-CTGAGTCTG	ACCACTTCGG	61	
Sbjct	174	ATGTC	TATC	TTAAGACAAC	CGCCTTACGC	AGTNAATGGG	ACTGAGTNTG	ACCACTTCGG	233	
Query	62	GTATG	GACTT	GCTGCACCCC	TCCGTGGG-C	TACCCGGGGC	CCTGGGCTTC	TTGTCCCGCA	120	
Sbjct	234	GTATG	GACTG	ACTGCACCCC	TCCGTGGGAC	TACCCGGGGA	CCTGGGCTTC	TTGTCCCGCA	293	
Query	121	GCCAC	CCCCC	GGAAACAGCG	CCGGGAGAGG	ACGACGTTCA	CTCGGGCGCA	GCTAGATGTG	180	
Sbjct	294	GCCAC	CCCCC	GGAAACAGCG	CCCGGAGAGG	ACGACGTTCA	CTCGGGAGCA	GCTAGATGTG	353	
Query	181	-CTG	GAAAGCA	CTGTTTG-CC	AAGA-CCCGG	TA-CCCAGAC	A-TCTTCA-T	G-CGAGA--G	231	
Sbjct	354	ACTG	GAAAGCA	CTGTTTGCCC	AAGACCCCGG	TACCCAGAA	ATTCTTCATT	GACGAGAGGG	413	
Query	232	GA-G	GGTGG-C	A-CTG--AAA	ATC-AACTTG	--CCCG-AG-	TCGA--GGGT	GCA--GGTA-	276	
Sbjct	414	AAG	GGTGGCC	ACCTGAAAAA	TTCAA	ACTTG	CCCCCGAAGT	TCGAGGGGGT	GCAGGGGTAT	473
Query	277	-TGG	TTT-AA	GAA-TCG-AA	GAG-CT-AAG	TG-CCGCC-A	ACAACAG-CA	ACAACAGCAG	327	
Sbjct	474	TGG	TTTAAA	GAATTGAAA	GAGCCTAAG	TGCCCGCAA	ACAACAGCCA	ACAAC-GCAG	532	
Query	328	AATG	GAGGTC	AAAACAAAGT	GAGACCTGCC	AAAAGAAGA	CATCTCCAGC	TCGGGAAGTG	387	
Sbjct	533	AATG	GAGGTC	AAAAC-AAGT	GAGACCTGCC	-AAAAGAAGA	CATCTCCAGC	TCGGGAAGTG	590	
Query	388	AGTT	CAGAGA	GTGG-AACAA	GTGGCCAATT	-CA-CT-CCC	CCCTCTAGC-	-ACCTCAG-T	440	
Sbjct	591	AGTT	CAGAGA	GTGGAAACAA	GTGGCCAATT	CCACCTCCCC	CCCTCTAGNA	AACCTCAGTT	650	
Query	441	CCCG	-ACCA-	TTGCCAGCAG	CAGTGCTCCT	GTGICTATCT	GGAGCCCAGC	TTCCATCTCC	498	
Sbjct	651	CCCG	AACCAT	TTGCCAGNAG	CCAGNGCCTC	CCGTGTCTAT	CGGAGCCCAGC	CTTCATCTCC	710	
Query	499	CCACT	GTTCAG	ATCCCTTGTC	CACCTCC	525				
Sbjct	711	CC--	CGTC-G	ATCCTGTAC	TCTCTAC	734				

[GENETYX : Homology Data]

Date : 2011.01.17

Query Sequence

File Name :
 Sequence Name : BC032579.1_CDS(286..1179)
 Sequence Size : 894

Target Sequence

File Name : W01A002J18_T7long.B05_110113142M
 Sequence Name : W01A002J18_T7long.B05_110113142M (complement)
 Sequence Size : 763

Unit Size to Compare = 6

Pick up Location No. = 1

Query Range: 286 - 894
 Sbjct Range: 1 - 605
 609 bp, INT.Score: 2296, OPT.Score: 2357
 Identity: 602 / 609 (98%)
 Strand: Plus / Minus

Query	286	AATCGAAGAG	CTAAGTGCCG	CCAACAACAG	CAACAACAGC	AGAATGGAGG	TCAAAACAAA	345
Sbjct	1	AATCG-AGAG	CT-AGTGCCG	CC-ACAACAG	-NACAACAGC	AGAATGGAGG	TCAAAACAAA	56
Query	346	GTGAGACCTG	CCAAAAAGAA	GACATCTCCA	GCTCGGGAAG	TGAGTTCAGA	GAGTGGAAACA	405
Sbjct	57	GTGAGACCTG	CCAAAAAGAA	GACATCTCCA	GCTCGGGGAG	TGAGTTCAGA	GAGTGGGACA	116
Query	406	AGTGGCCAAT	TCACTCCCCC	CTCTAGCACC	TCAGTCCCGA	CCATTGCCAG	CAGCAGTGCT	465
Sbjct	117	AGTGGCCAAT	TCACTCCCCC	CTCTAGCACC	TCAGTCCCGA	CCATTGCCAG	CAGCAGTGCT	176
Query	466	CCTGTGTCTA	TCTGGAGCCC	AGCTTCCATC	TCCCCACTGT	CAGATCCCTT	GTCCACCTCC	525
Sbjct	177	CCTGTGTCTA	TCTGGAGCCC	AGCTTCCATC	TCCCCACTGT	CAGATCCCTT	GTCCACCTCC	236
Query	526	TCTTCCTGCA	TGCAGAGGTC	CTATCCCATG	ACCTATACTC	AGGCTTCAGG	TTATAGTCAA	585
Sbjct	237	TCTTCCTGCA	TGCAGAGGTC	CTATCCCATG	ACCTATACTC	AGGCTTCAGG	TTATAGTCAA	296
Query	586	GGATATGCTG	GCTCAACTTC	CTACTTTGGG	GGCATGGACT	GTGGATCATA	TTTGACCCCT	645
Sbjct	297	GGATATGCTG	GCTCAACTTC	CTACTTTGGG	GGCATGGACT	GTGGATCATA	TTTGACCCCT	356
Query	646	ATGCATCACC	AGCTTCCCGG	ACCAGGGGCC	ACACTCAGTC	CCATGGGTAC	CAATGCAGTC	705
Sbjct	357	ATGCATCACC	AGCTTCCCGG	ACCAGGGGCC	ACACTCAGTC	CCATGGGTAC	CAATGCAGTC	416
Query	706	ACCAGCCATC	TCAATCAGTC	CCCAGCTTCT	CTTTCCACCC	AGGGATATGG	AGCTTCAAGC	765
Sbjct	417	ACCAGCCATC	TCAATCAGTC	CCCAGCTTCT	CTTTCCACCC	AGGGATATGG	AGCTTCAAGC	476
Query	766	TTGGGTTTTA	ACTCAACCAC	TGATTGCTTG	GATTATAAGG	ACCAAACCTGC	CTCCTGGAAG	825
Sbjct	477	TTGGGTTTTA	ACTCAACCAC	TGATTGCTTG	GATTATAAGG	ACCAAACCTGC	CTCCTGGAAG	536
Query	826	CTTAACTTCA	ATGCTGACTG	CTTGGATTAT	AAAGATCAGA	CATCCTCGTG	GAAATTCCAG	885
Sbjct	537	CTTAACTTCA	ATGCTGACTG	CTTGGATTAT	AAAGATCAGA	CATCCTCGTG	GAAATTCCAG	596
Query	886	GTTTTGTGA	894					
Sbjct	597	GTTTTGTGA	605					