

RIKEN clone ID: W01A015C13

Vector : pENTR/D-TOPO

Gene	B4GALT4		
Accession No.	BC004523.2	1714 bp	1..1714
	<i>CDS</i>	1035 bp	169..1203

●Plasmid DNA purification

Date : 110301

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

Date : 110302

Purification : QIAGEN Miniprep kit→dH₂O 100 ul

●Digestion by restriction enzyme / Concentration calibration

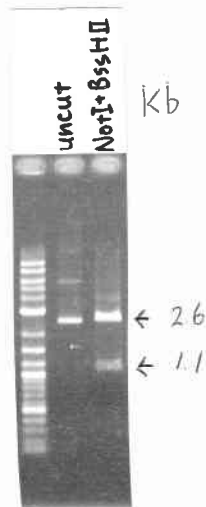
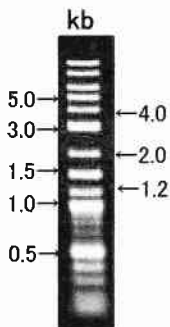
Date : 110302

DNA concentration (O.D.): 50.44 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

Erectrophoresis: 1% agarose gel, 1 × TAE Buffer

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



<Expected digestion pattern from BC004523.2 CDS>

1135, 2553 bp

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

Date : 110304

Shipped : 25 ng/ul, 40 ul

Final concentration: 25 ng/ul

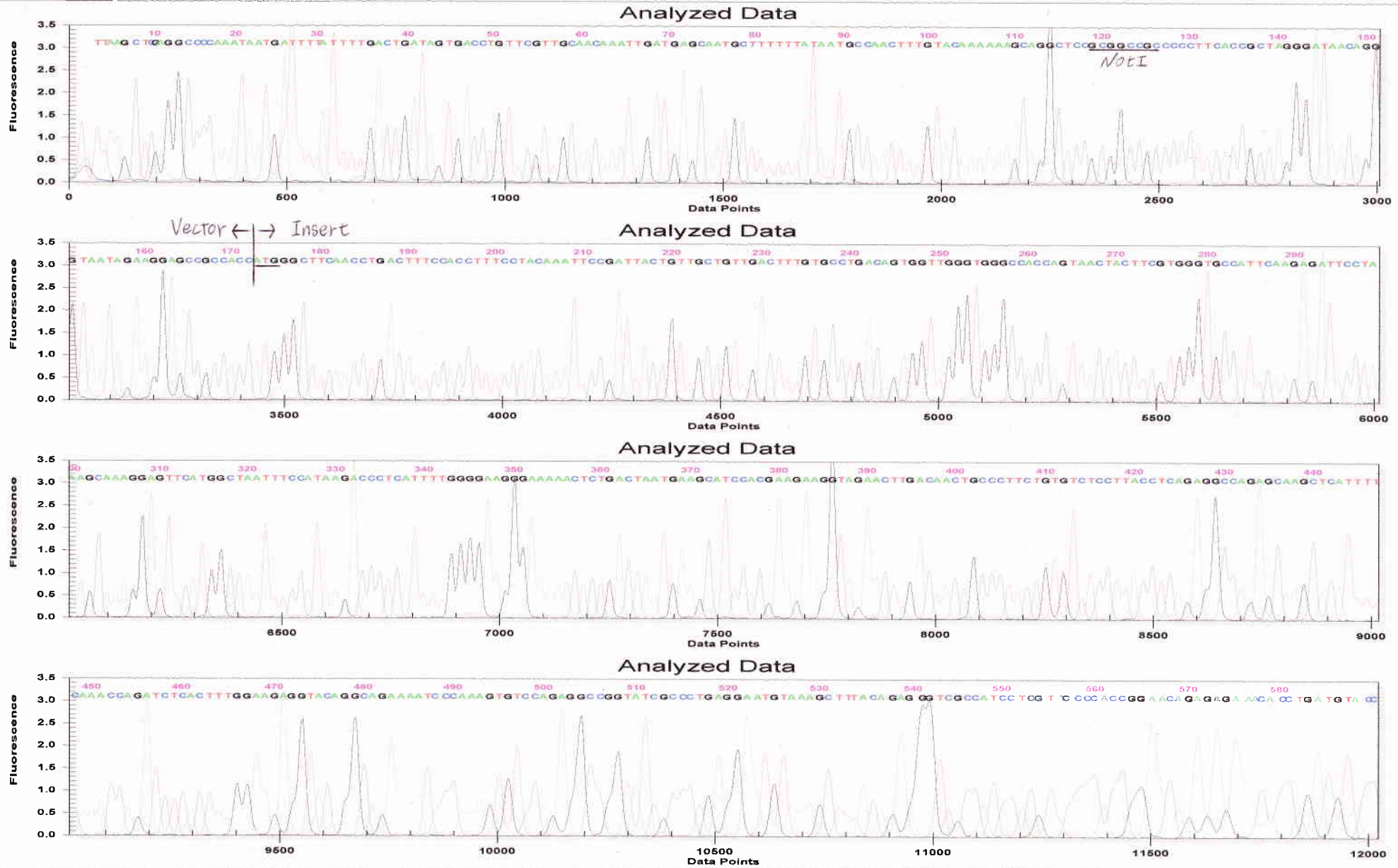
DNA (<u>50.44</u> ng/ul)	<u>84.0</u>	ul
10 × TE	<u>16.9</u>	ul
dH ₂ O	<u>68.5</u>	ul
Total	<u>169.4</u>	ul



Project : GNP
Sample : W01A015C13_M13.B06_11030316JF
Result : W01A015C13_M13.B06_11030316JF

System : System 1

Operator : 1.110303.furu
Instrument : System 1 (Ver. 9.0.25)

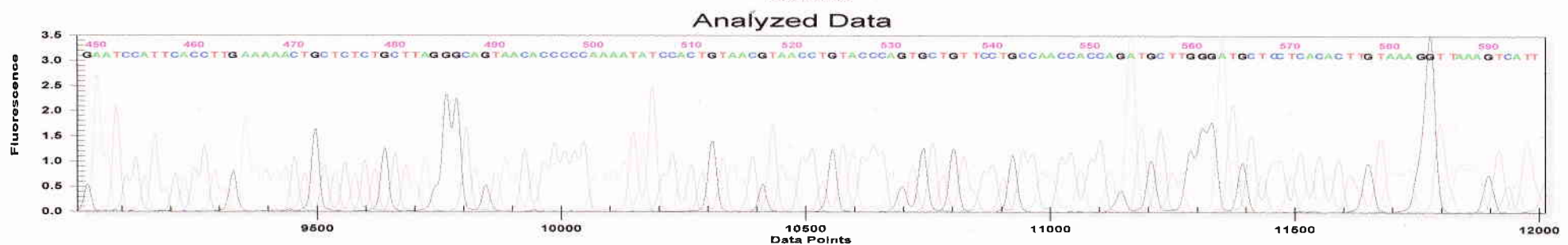
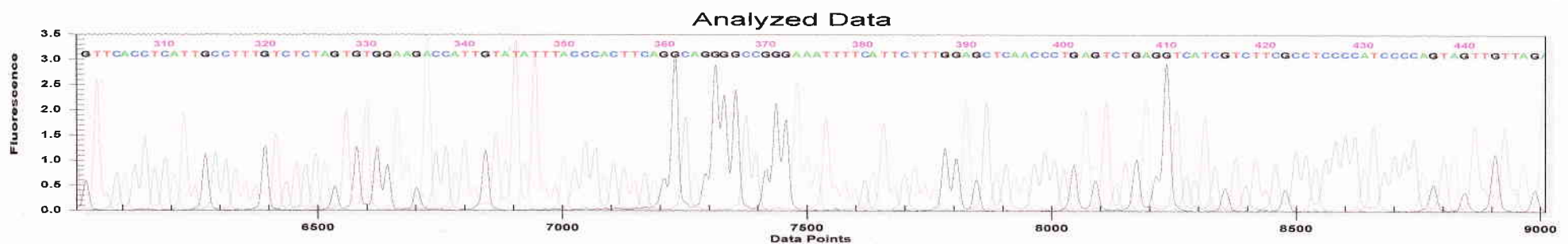
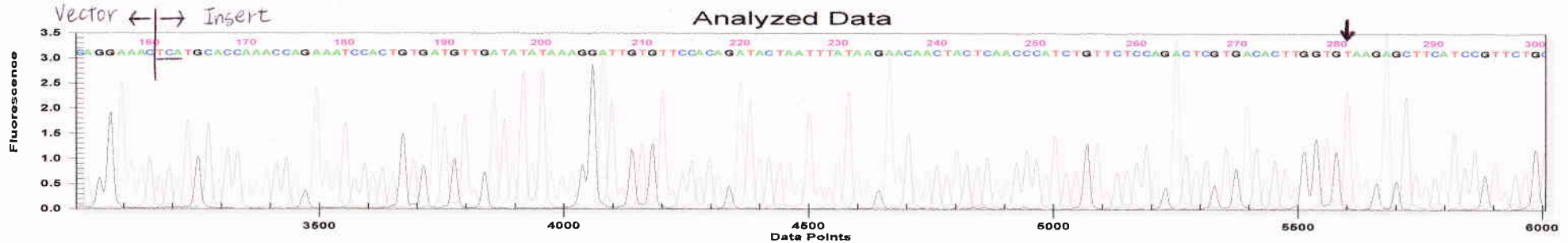
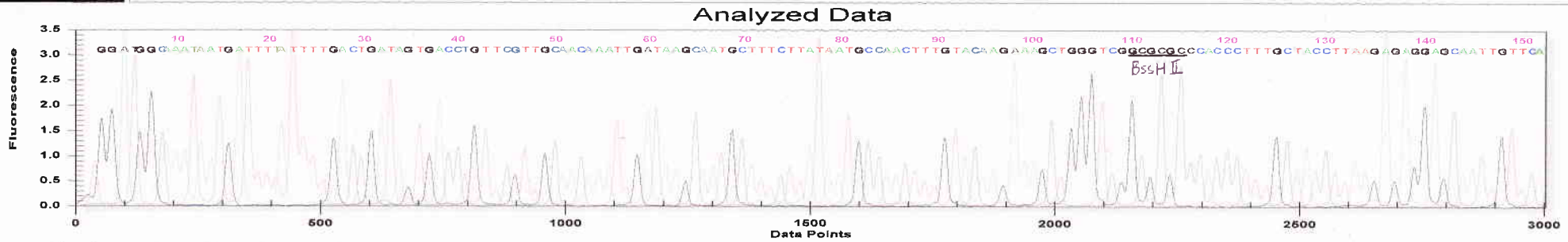




Project : GNP
Sample : W01A015C13_T7long.C06_11030316JF
Result : W01A015C13_T7long.C06_11030316JF

System : System 1

Operator : 1.110303.furu
Instrument : System 1 (Ver. 9.0.25)



[GENETYX : Homology Data]

Date : 2011.03.07

Query Sequence

File Name :
 Sequence Name : BC004523.2_CDS(169..1203)
 Sequence Size : 1035

Target Sequence

File Name : W01A015C13_M13.B06_11030316JF
 Sequence Name : W01A015C13_M13.B06_11030316JF
 Sequence Size : 736

Unit Size to Compare = 6

Pick up Location No. = 1

Query Range: 1 - 563

Sbjct Range: 172 - 735

564 bp, INT.Score: 2116, OPT.Score: 2228

Identity: 561 / 564 (99%)

Strand: Plus / Plus

Query	1	ATGGGCTTCA	ACCTGACTTT	CCACCTTTCC	TACAAATTCC	GATTACTGTT	GCTGTTGACT	60
Sbjct	172	ATGGGCTTCA	ACCTGACTTT	CCACCTTTCC	TACAAATTCC	GATTACTGTT	GCTGTTGACT	231
Query	61	TTGTGCCTGA	CAGTGGTTGG	GTGGGCCACC	AGTAACTACT	TCGTGGGTGC	CATTCAAGAG	120
Sbjct	232	TTGTGCCTGA	CAGTGGTTGG	GTGGGCCACC	AGTAACTACT	TCGTGGGTGC	CATTCAAGAG	291
Query	121	ATTCCTAAAG	CAAAGGAGTT	CATGGCTAAT	TTCCATAAGA	CCCTCATTTT	GGGGAAGGGA	180
Sbjct	292	ATTCCTAAAG	CAAAGGAGTT	CATGGCTAAT	TTCCATAAGA	CCCTCATTTT	GGGGAAGGGA	351
Query	181	AAAACCTCTGA	CTAATGAAGC	ATCCACGAAG	AAGGTAGAAC	TTGACAACCTG	CCCTTCTGTG	240
Sbjct	352	AAAACCTCTGA	CTAATGAAGC	ATCCACGAAG	AAGGTAGAAC	TTGACAACCTG	CCCTTCTGTG	411
Query	241	TCTCCTTACC	TCAGAGGCCA	GAGCAAGCTC	ATTTTCAAAC	CAGATCTCAC	TTTGGGAAGAG	300
Sbjct	412	TCTCCTTACC	TCAGAGGCCA	GAGCAAGCTC	ATTTTCAAAC	CAGATCTCAC	TTTGGGAAGAG	471
Query	301	GTACAGGCAG	AAAATCCCAA	AGTGTCAGAG	GGCCGGTATC	GCCCTGAGGA	ATGTAAAGCT	360
Sbjct	472	GTACAGGCAG	AAAATCCCAA	AGTGTCAGAG	GGCCGGTATC	GCCCTGAGGA	ATGTAAAGCT	531
Query	361	TTACAGAGGG	TCGCCATCCT	CGTTCCCCAC	CGGAACAGAG	AGAAACACCT	GATGTACCTG	420
Sbjct	532	TTACAGAGGG	TCGCCATCCT	CGTTCCCCAC	CGGAACAGAG	AGAAACACCT	GATGTACCTG	591
Query	421	CTGGAACATC	TGCATCCCTT	CCTGCAGAGG	CAGCAGCTGG	ATTATGGCAT	CTACGTCATC	480
Sbjct	592	CTGGAACATC	TGCATCCCTT	CCTGCAGAGG	CAGCAGCTGG	ATTATGGCAT	CTACGTCATC	651
Query	481	CACCAGGCTG	AAGGTAAAAA	GTTTAAATCGA	GCCAAACTCT	TG-AATGTGG	GCTATCTAGA	539
Sbjct	652	CACCAGGCTG	AAGGTAAAAA	GTTTAAATCGA	GCCAAACTCT	TGAAATGTGG	GCTATCTAGA	711
Query	540	AGCCCTCAAG	GAAGAAAATT	GGGA	563			
Sbjct	712	AGCCCTCAAG	GAAGAAATTG	GGGA	735			

[GENETYX : Homology Data]

Date : 2011.03.07

Query Sequence

File Name :
 Sequence Name : BC004523.2_CDS(169..1203)
 Sequence Size : 1035

Target Sequence

File Name : W01A015C13_T7long.C06_11030316JF
 Sequence Name : W01A015C13_T7long.C06_11030316JF (complement)
 Sequence Size : 747

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

Query Range: 448 - 1035
 Sbjct Range: 1 - 588
 589 bp, INT.Score: 1970, OPT.Score: 2312
 Identity: 585 / 589 (99%)
 Strand: Plus / Minus

Query	448	AGGCAGCAGC	TGGATTATGG	CATCTACGTC	ATCCACCAGG	CTGAAGGTAA	AAAGTTTAAT	507
Sbjct	1	AGGCAGCAGC	T-GATTATGG	CATCTACGTC	ATCCACCAGG	CTGAGGGTAA	AAAGTTTAAT	59
Query	508	CGAGCCAAAC	TCTTGAATGT	GGGCTATCTA	GAAG-CCCTC	AAGGAAGAAA	ATTGGGACTG	566
Sbjct	60	CGAGCCAAAC	TC'TTGAATGT	GGGCTATCTA	GAAGCCCTC	AAGGAAGAAA	ATTGGGACTG	119
Query	567	CTTTATATTC	CACGATGTGG	ACCTGGTACC	CGAGAATGAC	TTTAACCTTT	ACAAGTGTGA	626
Sbjct	120	CTTTATATTC	CACGATGTGG	ACCTGGTACC	CGAGAATGAC	TTTAACCTTT	ACAAGTGTGA	179
Query	627	GGAGCATCCC	AAGCATCTGG	TGGTTGGCAG	GAACAGCACT	GGGTACAGGT	TACGTTACAG	686
Sbjct	180	GGAGCATCCC	AAGCATCTGG	TGGTTGGCAG	GAACAGCACT	GGGTACAGGT	TACGTTACAG	239
Query	687	TGGATATTTT	GGGGGTGTTA	CTGCCCTAAG	CAGAGAGCAG	TTTTTCAAGG	TGAATGGATT	746
Sbjct	240	TGGATATTTT	GGGGGTGTTA	CTGCCCTAAG	CAGAGAGCAG	TTTTTCAAGG	TGAATGGATT	299
Query	747	CTCTAACAAC	TACTGGGGAT	GGGGAGGCCA	AGACGATGAC	CTCAGACTCA	GGGTTGAGCT	806
Sbjct	300	CTCTAACAAC	TACTGGGGAT	GGGGAGGCCA	AGACGATGAC	CTCAGACTCA	GGGTTGAGCT	359
Query	807	CCAAAGAATG	AAAATTTCCC	GGCCCCTGCC	TGAAGTGGGT	AAATATACAA	TGGTCTTCCA	866
Sbjct	360	CCAAAGAATG	AAAATTTCCC	GGCCCCTGCC	TGAAGTGGGT	AAATATACAA	TGGTCTTCCA	419
Query	867	CACTAGAGAC	AAAGGCAATG	AGGTGAACGC	AGAACGGATG	AAGCTCTTGC	ACCAAGTGTC	926
Sbjct	420	CACTAGAGAC	AAAGGCAATG	AGGTGAACGC	AGAACGGATG	AAGCTCTTAC	ACCAAGTGTC	479
Query	927	ACGAGTCTGG	AGAACAGATG	GGTTGAGTAG	TTGTTCTTAT	AAATTAGTAT	CTGTGGAACA	986
Sbjct	480	ACGAGTCTGG	AGAACAGATG	GGTTGAGTAG	TTGTTCTTAT	AAATTAGTAT	CTGTGGAACA	539
Query	987	CAATCCTTTA	TATATCAACA	TCACAGTGGA	TTTCTGGTTT	GGTGCATGA	1035	
Sbjct	540	CAATCCTTTA	TATATCAACA	TCACAGTGGA	TTTCTGGTTT	GGTGCATGA	588	