

RIKEN clone ID: W01A002A12

Vector : pENTR/D-TOPO

Gene	SFRS1		
Accession No.	BC010264.1	2708 bp	1..2708
	<i>CDS</i>	747 bp	36..782

●Plasmid DNA purification

Date : 101027

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

Date : 101028

Purification : QIAGEN Miniprep kit→dH₂O 100 ul

●Digestion by restriction enzyme / Concentration calibration

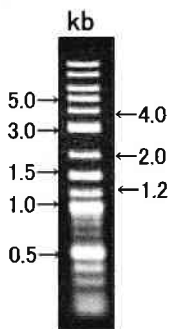
Date : 101028

DNA concentration (O.D.): 73.77 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 BC010264.1 CDS>

2553, 847 bp

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

Date : 101029

Shipped : 25 ng/ul, 40 ul

Final concentration: 25 ng/ul

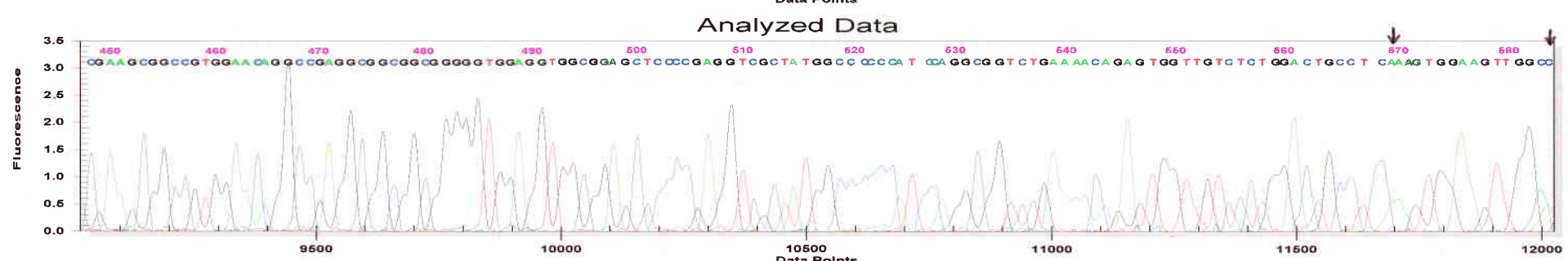
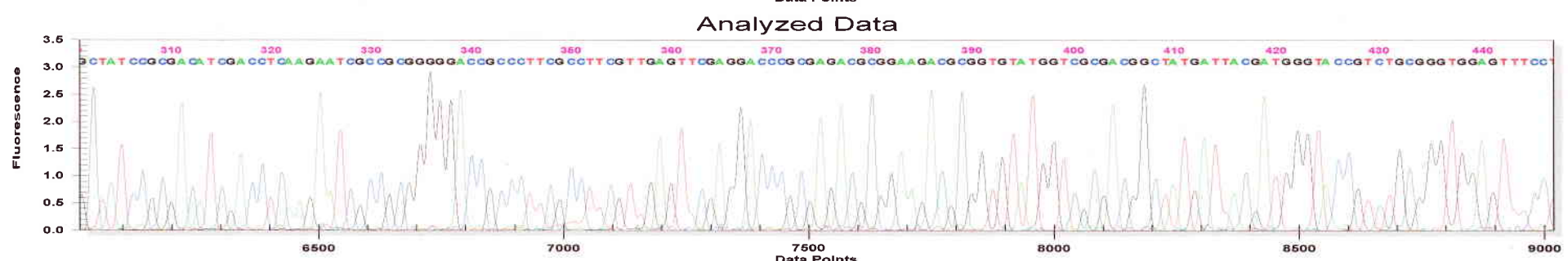
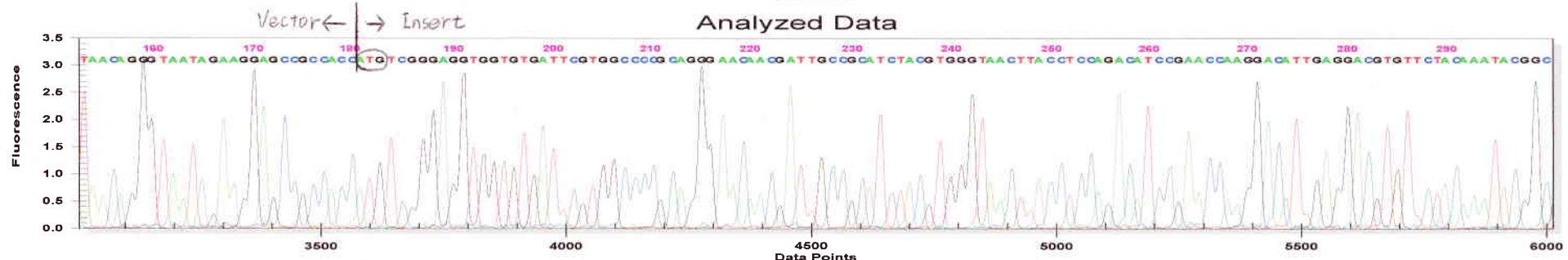
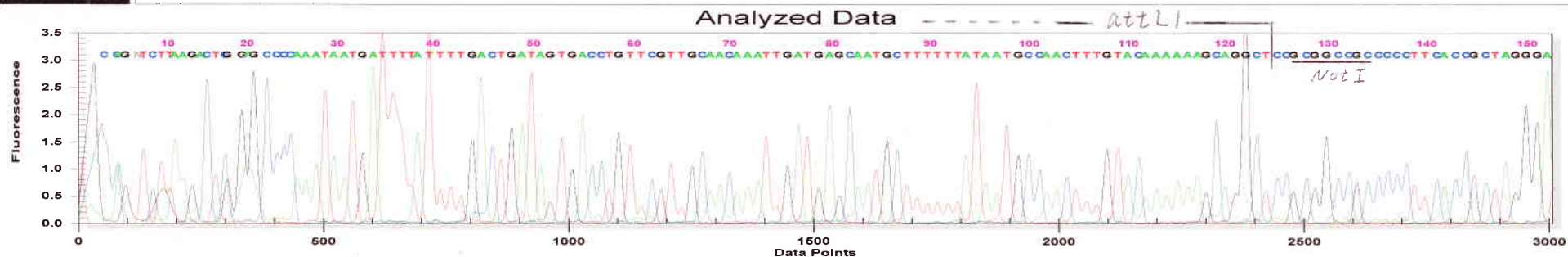
DNA (73.77 ng/ul)	79.0 ul
10 × TE	23.3 ul
dH ₂ O	130.8 ul
Total	233.1 ul



Project : GNP
Sample : W01A002A12_M13.A04_10102910EH
Result : W01A002A12_M13.A04_10102910EH

System : CEQ System

Operator : 2.101029.furu
Instrument : CEQ System (Ver. 9.0.25)

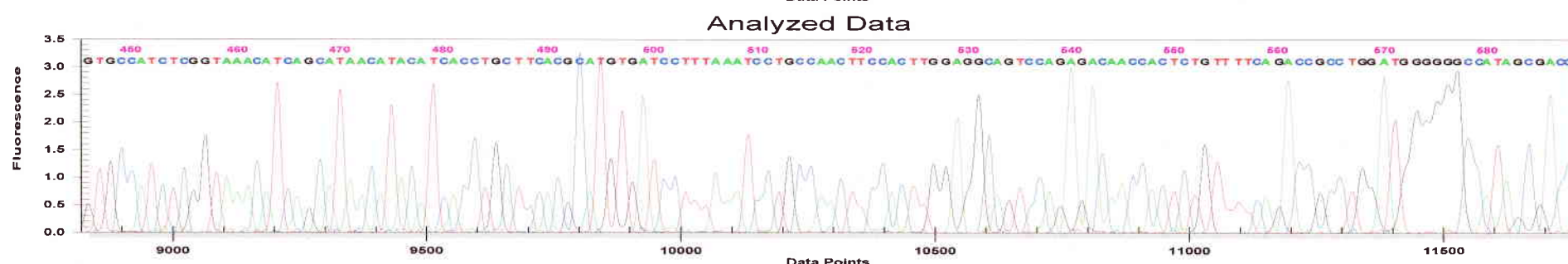
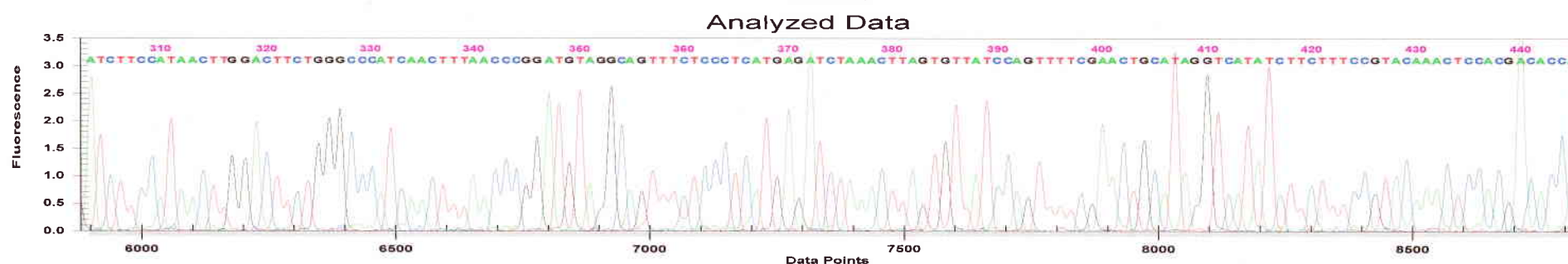
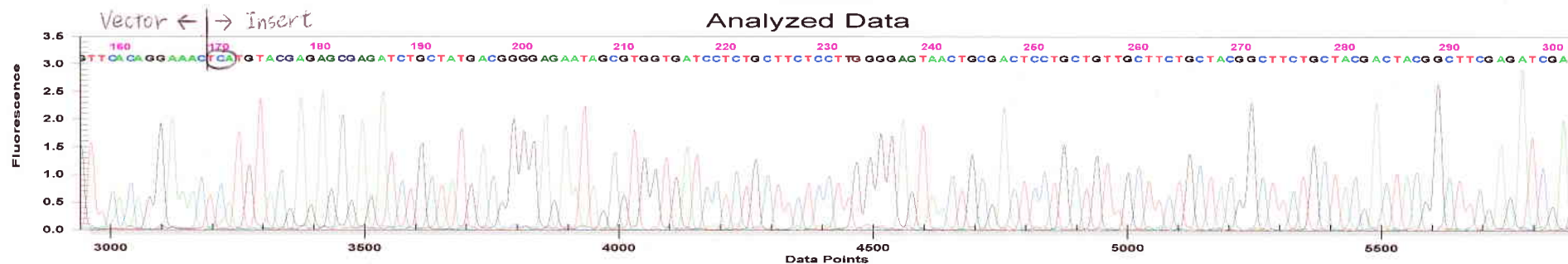
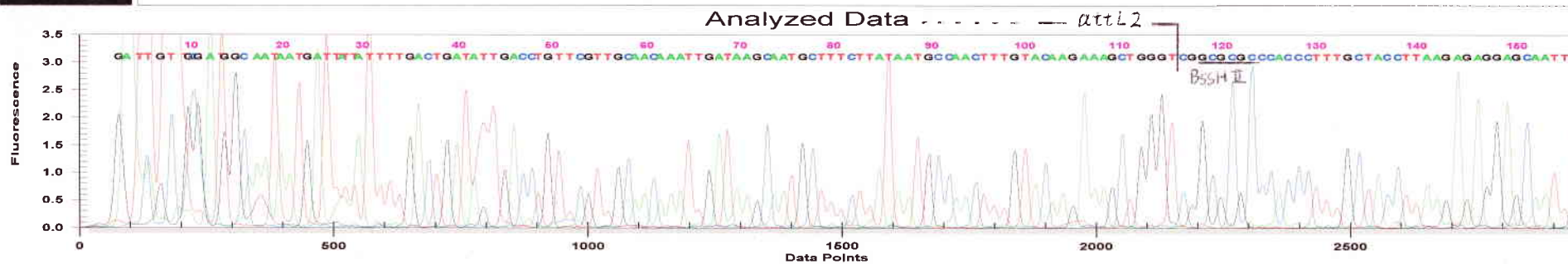




Project : GNP
Sample : W01A002A12_T7.B04_10102910EH
Result : W01A002A12_T7.B04_10102910EH

System : CEQ System

Operator : 2.101029.furu
Instrument : CEQ System (Ver. 9.0.25)



[GENETYX : Homology Data]

Date : 2010.10.29

Query Sequence
File Name :
Sequence Name : BC010264.1(cds_36..782)
Sequence Size : 747

Target Sequence
File Name : W01A002A12_M13.A04_10102910EH.seq
Sequence Name : W01A002A12_M13.A04_10102910EH
Sequence Size : 770

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

Query Range: 1 - 582
Sbjct Range: 180 - 770
593 bp, INT.Score: 1868, OPT.Score: 2015
Identity: 552 / 593 (93%)
Strand: Plus / Plus

Query 1 ATGTCCGGGAG GTGGTGTGAT TCGTGGCCCC GCAGGGAACA ACGATTGCCG CATCTACGTG 60
Sbjct 180 ATGTCCGGGAG GTGGTGTGAT TCGTGGCCCC GCAGGGAACA ACGATTGCCG CATCTACGTG 239
Query 61 GGTAACCTTAC CTCCAGACAT CCGAACCAAG GACATTGAGG ACGTGTCTCA CAAATACGGC 120
Sbjct 240 GGTAACCTTAC CTCCAGACAT CCGAACCAAG GACATTGAGG ACGTGTCTCA CAAATACGGC 299
Query 121 GCTATCCGGG ACATCGACCT CAAGAATCGC CGCGGGGGAC CGCCCTTCGC CTTCGTTGAG 180
Sbjct 300 GCTATCCGGG ACATCGACCT CAAGAATCGC CGCGGGGGAC CGCCCTTCGC CTTCGTTGAG 359
Query 181 TTCGAGGACC CGCGAGACGC GGAAGACCGG GTGTATGCTC GCGACGGCTA TGATTACGAT 240
Sbjct 360 TTCGAGGACC CGCGAGACGC GGAAGACCGG GTGTATGCTC GCGACGGCTA TGATTACGAT 419
Query 241 GGGTACCGGTC TGCGGGTGGG GTTTCCTCGA AGCGGCCGTG GAACAGGCCS AGCGCGGGGC 300
Sbjct 420 GGGTACCGGTC TGCGGGTGGG GTTTCCTCGA AGCGGCCGTG GAACAGGCCS AGCGCGGGGC 479
Query 301 GGGGGTGGAG GTGGCGGAGC TCCCGGAGT CGCTATGGCC CCCCATCCAG GCGGTCTGAA 360
Sbjct 480 GGGGGTGGAG GTGGCGGAGC TCCCGGAGT CGCTATGGCC CCCCATCCAG GCGGTCTGAA 539
Query 361 AACAGAGTGG TTGTCTCTGG ACTGCCTCCA AGTGGAAAGT GGCAGGATTT AAAGGATCAC 420
Sbjct 540 AACAGAGTGG TTGTCTCTGG ACTGCCTCAA AGTGGAAAGT GGCAGGATTT AAAGGATCAC 599
Query 421 ATGCGTGAAG CAGGTGATGT ATGTTATGCT GAIGTTTACC GAGATGGCA- CTGGTCTCCT 479
Sbjct 600 ATGCGTGAAG CAGGTGATGT ATGTTATGCT GATGTTTACC GAGATGGCAC CTGGTGTGNT 659
Query 480 -GGAGTTTGT A-CGGAAAAG AG-ATATGAC C-TATGCA-G TTCGAAA-C T-6GA--TAA 530
Sbjct 660 GGGAGTTTGT ACCGAAAAGA AGAATATGAC CTTATGCAGG TTCGAAAACC TGGGATTAAA 719
Query 531 CACTAA-GTT TAGATCTCAT GAGGGAGAAA CTGCCTACAT CCGGGTTAAA GTT 582
Sbjct 720 CCTTAAGGTT TAAGAATCTT CA--TTGAAG GGGAAAGAAA CTGGCTTAA ATT 770

Query Sequence
File Name :
Sequence Name : BC010264.1(cds_36..782)
Sequence Size : 747

Target Sequence
File Name : W01A002A12_T7.B04_10102910EH.seq
Sequence Name : W01A002A12_T7.B04_10102910EH (complement)
Sequence Size : 781
Unit Size to Compare = 6
Pick up Location No. = 1

Query Range: 138 - 747
Sbjct Range: 5 - 614
611 bp, INT.Score: 2111, OPT.Score: 2373
Identity: 602 / 611 (98%)
Strand: Plus / Minus

Query 138 CCTCAAGAAT CGCCGCGGGG GACCGCCCTT C-GCCTTCGT TGAGTTCGAG GACCCGCGAG 196
Sbjct 5 CCTCAAGATT CGCCGCGGGG GACCGCCCTT CGGCTTCGCG TGAGTTCGAG ACCCGCGAG 64
Query 197 ACGCGGAAGA CGCGGTGTAT GGTCCGACAG GCTATGATTA CGATGGGTAC CGTCTGCGGG 256
Sbjct 65 ACGCGGANA CGCGGTGTAT GGTCCGACAG GCTATGA-TA CGATGGGTAC CGTCTGCGGG 123
Query 257 TGGAGTTTCC TCGAAGCGGC CGTGGAACAG GCCGAGGCGG CGGCGGGGGT GGAGTGGCG 316
Sbjct 124 TGGAGTTTCC TCGAAGCGGC CGTGGAACAG GCCGAGGCGG CGGCGGGGGT GGAGTGGCG 183
Query 317 GAGCTCCCCG AGTCCGTAT GCGCCCCCAT CCAGGCGGTC TGAABACAGA GTGGTGTCT 376
Sbjct 184 GAGCTCCCCG AGTCCGTAT GCGCCCCCAT CCAGGCGGTC TGAABACAGA GTGGTGTCT 243
Query 377 CTGGACTGCC TCCAAGTGGG AGTGGCAGG ATTTAAAGGA TCACATCGCT GAAGCAGGTG 436
Sbjct 244 CTGGACTGCC TCCAAGTGGG AGTGGCAGG ATTTAAAGGA TCACATCGCT GAAGCAGGTG 303
Query 437 ATGTATGTTA TGCTGATGTT TACCGAGATG GCACTGGTGT CGTGGAGTTT GTACGGAAA 496
Sbjct 304 ATGTATGTTA TGCTGATGTT TACCGAGATG GCACTGGTGT CGTGGAGTTT GTACGGAAA 363
Query 497 AAGATATGAC CTATGCAGTT CGAAAACGTT ATAACACTAA GTTTAGATCT CATGAGGGAG 556
Sbjct 364 AAGATATGAC CTATGCAGTT CGAAAACGTT ATAACACTAA GTTTAGATCT CATGAGGGAG 423
Query 557 AAAGTGCCTA CATCCGGGTT AAAGTTGATG GGCCGAGAAG TCCAAGTTAT GGAAGATCTC 616
Sbjct 424 AAAGTGCCTA CATCCGGGTT AAAGTTGATG GGCCGAGAAG TCCAAGTTAT GGAAGATCTC 483
Query 617 GATCTCGAAG CCGTAGTCGT AGCAGAAGCC GTAGCAGAAG CAACAGCAGG AGTCCGAGTT 676
Sbjct 484 GATCTCGAAG CCGTAGTCGT AGCAGAAGCC GTAGCAGAAG CAACAGCAGG AGTCCGAGTT 543
Query 677 ACTCCCCAAG GAGAAGCAGA GGATCACCAC GCTATTCTCC CCGTCATAGC AGATCTCGCT 736
Sbjct 544 ACTCCCCAAG GAGAAGCAGA GGATCACCAC GCTATTCTCC CCGTCATAGC AGATCTCGCT 603
Query 737 CTCGTACATA A 747
Sbjct 604 CTCGTACATG A 614