

**RIKEN clone ID: IRAK068E12**

Vector : pCMV-SPORT6

Gene	HNRPA1		
Accession No.	BC033714.1	1738 bp	1..1738
	<i>CDS</i>	963 bp	51..1013

●Plasmid DNA purification

Date : 10/020 Culture : LB (100 ug/ml Ampicillin) 3 ml →37°C O/N

Date : 10/021 Purification : QIAGEN Miniprep kit→dH<sub>2</sub>O 100 ul

●Digestion by restriction enzyme / Concentration calibration

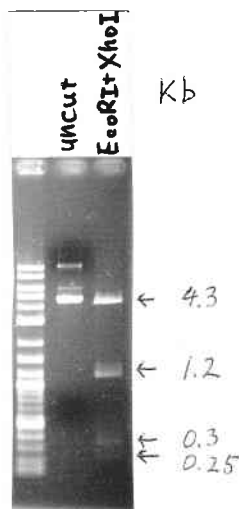
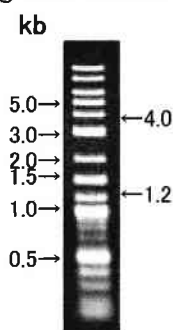
Date : 10/021

DNA concentration (O.D.): 93.81 ng/ul

DNA	i ul
Enzyme (EcoRI+XhoI)	0.5+0.5 ul
Buffer H	1 ul
dH <sub>2</sub> O	7 ul
Total	10 ul

Electrophoresis: 1% agarose gel, 1 × TAE Buffer

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



<Expected digestion pattern from BC033714.1>

4339, 1196, 321, 242 bp

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

Date : 10/022 Shipped : 25 ng/ul, 40 ul

Final concentration: 25 ng/ul

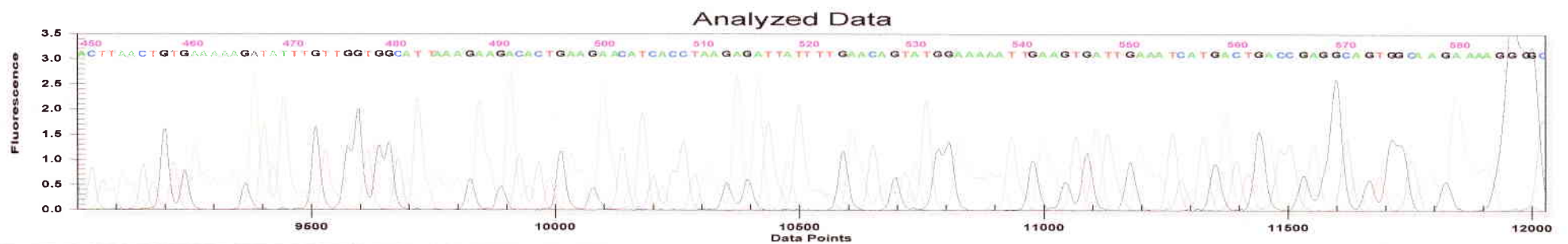
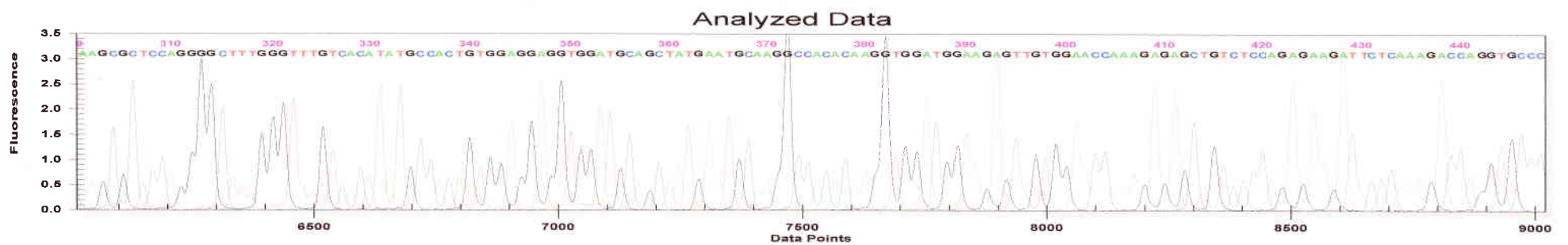
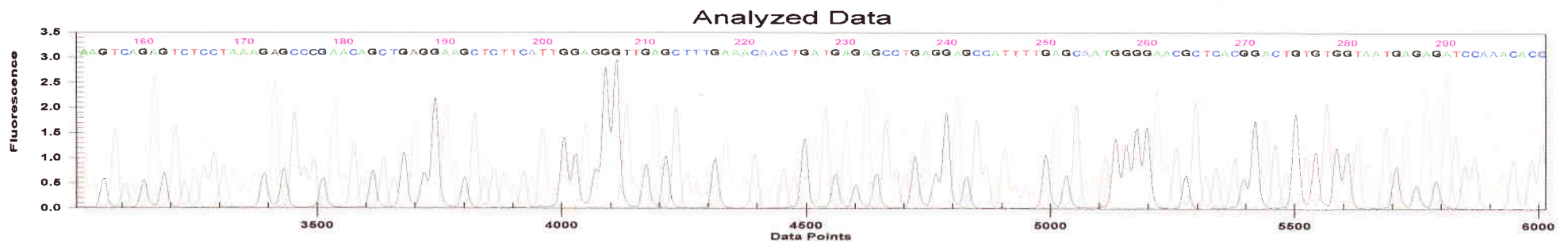
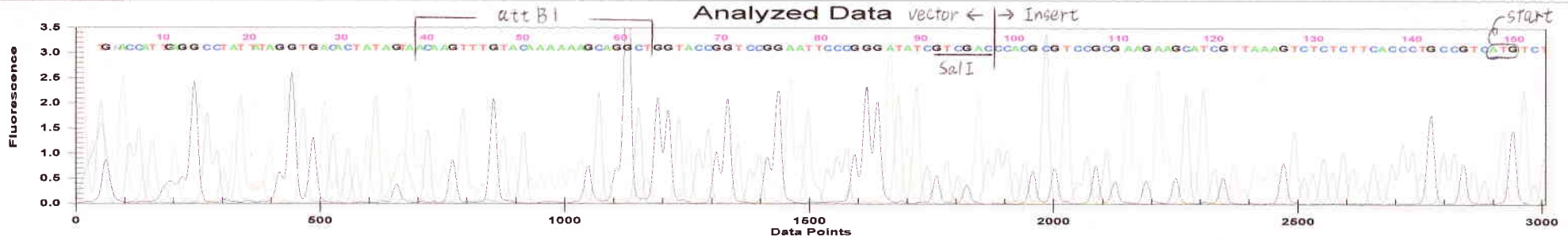
DNA ( <u>93.81</u> ng/ul)	85 ul
10 × TE	31.9 ul
dH <sub>2</sub> O	202.1 ul
Total	319.0 ul



Project : GNP  
Sample : IRAK068E12\_Reverse2.C12\_10102212IK  
Result : IRAK068E12\_Reverse2.C12\_10102212IK

System : System 1

Operator : 1.101022.furu  
Instrument : System 1 (Ver. 9.0.25)

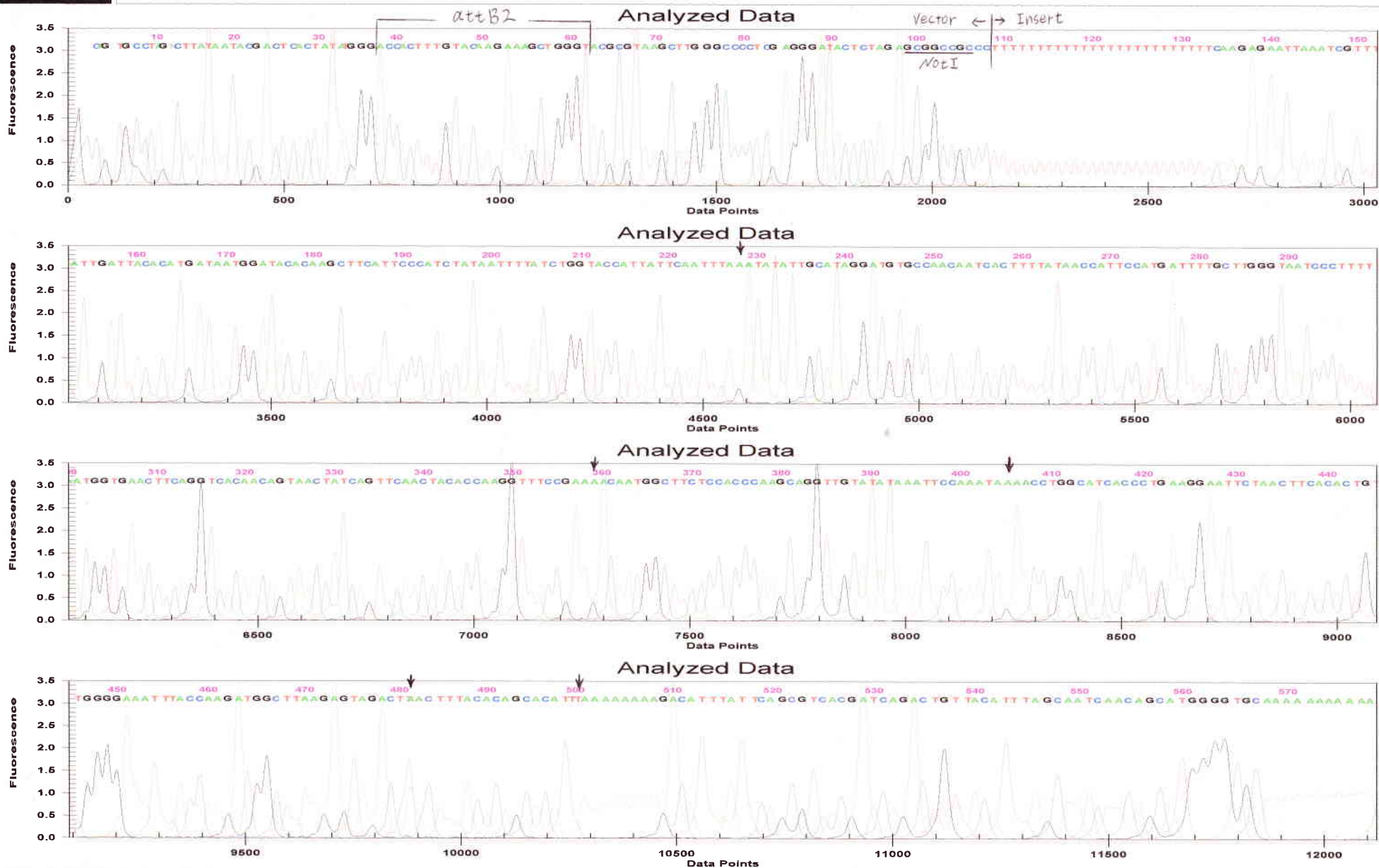




Project : GNP  
Sample : IRAK068E12\_M13.D12\_10102212IK  
Result : IRAK068E12\_M13.D12\_10102212IK

System : System 1

Operator : 1.101022.furu  
Instrument : System 1 (Ver. 9.0.25)



[ GENETYX : Homology Data ]

Date : 2010.10.22

Query Sequence
File Name :
Sequence Name : BC033714.1
Sequence Size : 1738

Target Sequence
File Name : IRAK068E12\_Reverse2.C12\_10102212IK.seq
Sequence Name : IRAK068E12\_Reverse2.C12\_10102212IK
Sequence Size : 701

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

Query Range: 1 - 604
Sbjct Range: 97 - 700
604 bp, INT.Score: 2392, OPT.Score: 2398
Identity: 601 / 604 (99%)
Strand: Plus / Plus

Query 1 CCACGCGTCC GCGAAGAAGC ATCGTTAAAG TCTCTCTTCA CCCTGCCGTC ATGTCTAAGT 60
Sbjct 97 CCACGCGTCC GCGAAGAAGC ATCGTTAAAG TCTCTCTTCA CCCTGCCGTC ATGTCTAAGT 156
Query 61 CAGAGTCTCC TAAAGAGCCC GAACAGCTGA GGAAGCTCTT CATTGGAGGG TTGAGCTTTG 120
Sbjct 157 CAGAGTCTCC TAAAGAGCCC GAACAGCTGA GGAAGCTCTT CATTGGAGGG TTGAGCTTTG 216
Query 121 AAACAACTGA TGAGAGCCTG AGGAGCCATT TTGAGCAATG GGAACCGCTC ACGSACTGTG 180
Sbjct 217 AAACAACTGA TGAGAGCCTG AGGAGCCATT TTGAGCAATG GGAACCGCTC ACGSACTGTG 276
Query 181 TGGAATAGAG AGATCCAAAC ACCAAGCGCT CCAGGGGCTT TGGGTTTGTG ACATATGCCA 240
Sbjct 277 TGGAATAGAG AGATCCAAAC ACCAAGCGCT CCAGGGGCTT TGGGTTTGTG ACATATGCCA 336
Query 241 CTGTGGAGGA GGTGGATGCA GCTATGAATG CAAGGCCACA CAAGGTGGAT GGAAGAGTTG 300
Sbjct 337 CTGTGGAGGA GGTGGATGCA GCTATGAATG CAAGGCCACA CAAGGTGGAT GGAAGAGTTG 396
Query 301 TGGAAACAAA GAGAGCTGTC TCCAGAGAAG ATTCTCAAAG ACCAGGTGCC CACTTAACTG 360
Sbjct 397 TGGAAACAAA GAGAGCTGTC TCCAGAGAAG ATTCTCAAAG ACCAGGTGCC CACTTAACTG 456
Query 361 TGAAAAAGAT ATTTGTTGGT GGCATTAAAG AAGACTCTGA AGAACATCAC CTAAGAGATT 420
Sbjct 457 TGAAAAAGAT ATTTGTTGGT GGCATTAAAG AAGACTCTGA AGAACATCAC CTAAGAGATT 516
Query 421 ATTTTGAACA GTATGGAAAA ATTGAAGTGA TTGAAATCAT GACTGACCGA GGCAGTGGGA 480
Sbjct 517 ATTTTGAACA GTATGGAAAA ATTGAAGTGA TTGAAATCAT GACTGACCGA GGCAGTGGGA 576
Query 481 AGAAAAGGGG CTTTGCCTTT GTAACCTTTG ACGACCATGA CTCGGTGGAT AAGATTGTCA 540
Sbjct 577 AGAAAAGGGG CTTTGCCTTT GTAACCTTTG ACGACCATGA CTCGGTGGAT AAGATTGTCA 636
Query 541 TTCAGAAATA CCATACCTGTG AATGGCCACA ACTGTGAAGT TAGAAAAGCC CTGTCAAAGC 600
Sbjct 637 TTCAGAAATA CCATACCTGTG AATGGCCACA ACTGTGAAGT TAGAAAAGCC CTGTCAAAGC 696
Query 601 AAGA 604
Sbjct 697 CAGA 700

Query Sequence
File Name :
Sequence Name : BC033714.1
Sequence Size : 1738

Target Sequence
File Name : IRAK068E12\_M13.D12\_10102212IK.seq
Sequence Name : IRAK068E12\_M13.D12\_10102212IK (complement)
Sequence Size : 724

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

Query Range: 1135 - 1738
Sbjct Range: 2 - 617
616 bp, INT.Score: 1478, OPT.Score: 2120
Identity: 575 / 616 (93%)
Strand: Plus / Minus

Query 1135 ACATGTTTTA GACAAATACT CATGTGTATG GCCAAAAAAC TCGA-GGA-- CTGTA--TTT 1189
Sbjct 2 AAATAACTTT CAATGGTGGT AATGGGGGCA AAAAAAAACT TCGAGGGACC CTGTATTTTT 61
Query 1190 GTG-ACTAA- TTGTATAA-C A-GGTTA-TT TTAGTTTCTG TTCTGTGGAA AGTGTAAAGC 1244
Sbjct 62 GTGAACCTAT TTGTATNACC AGGTTTATTT TTAGTTTCTG TTCTGTGGAA AGTGTAAAGC 121
Query 1245 ATTCCAACAA AGGGTTTTAA TGTAGATTTT TTTTTTTGCA CCCCATGCTG TTGATTGCTA 1304
Sbjct 122 ATTCCCACAA AGGGTTTTAA TGTAGATTTT TTTTTTTGCA CCCCATGCTG TTGATTGCTA 181
Query 1305 AATGTAACAG TCTGATCGTG ACGCTGAATA AATGCTTTTT TTTT-AAATG TCTGTGTAAA 1363
Sbjct 162 AATGTAACAG TCTGATCGTG ACGCTGAATA AATGCTTTTT TTTTAAATG TCTGTGTAAA 241
Query 1364 GTT-AGTCTA CTCTTAAGCC ATCTTGGTAA ATTTCCCAA CAGTGTGAAG TTAGAATTCC 1422
Sbjct 242 GTTAAAGTCTA CTCTTAAGCC ATCTTGGTAA ATTTCCCAA CAGTGTGAAG TTAGAATTCC 301
Query 1423 TTCAGGGTGA TCCAGGTTTC TATTTGGAAT TTATATACAA CCTGCTTGGG TGGAGAAGCC 1482
Sbjct 302 TTCAGGGTGA TCCAGGTTTC TATTTGGAAT TTATATACAA CCTGCTTGGG TGGAGAAGCC 361
Query 1483 ATTTGCTTTCG GAAACCTTGG TGTAGTTGAA CTGATAGTTA CTGTTGTGAC CTGAAGTTCA 1542
Sbjct 362 ATTTGCTTTCG GAAACCTTGG TGTAGTTGAA CTGATAGTTA CTGTTGTGAC CTGAAGTTCA 421
Query 1543 CCATTAAAAG GGATTACCCA AGCAAAATCA TGGAAATGTT ATAAAAGTGA TTGTTGGCAC 1602
Sbjct 422 CCATTAAAAG GGATTACCCA AGCAAAATCA TGGAAATGTT ATAAAAGTGA TTGTTGGCAC 481
Query 1603 ATCCTATGCA ATATATCTAA ATTGAATAAT GGTACCAGAT AAAATTATAG ATGGGAATGA 1662
Sbjct 482 ATCCTATGCA ATATATCTAA ATTGAATAAT GGTACCAGAT AAAATTATAG ATGGGAATGA 541
Query 1663 AGCTTGTGTA TCCATTATCA TGTGTAATCA ATAAACGATT TAATCTCTT GAAAAAATA 1722
Sbjct 542 AGCTTGTGTA TCCATTATCA TGTGTAATCA ATAAACGATT TAATCTCTT GAAAAAATA 601
Query 1723 AAAAAAAAAA AAAAAA 1738
Sbjct 602 AAAAAAAAAA AAAAAA 617