

RIKEN clone ID: IRAK064G23

Vector : pCMV-SPORT6

Gene	PARP1		
Accession No.	BC037545.1	3677 bp	1..3677
	<i>CDS</i>	3045 bp	145..3189

● Plasmid DNA purification

Date : 10/007 Culture : LB (100 ug/ml Ampicillin) 3 ml →37°C O/N

Date : 10/008 Purification : QIAGEN Miniprep kit →dH₂O 100 ul

● Digestion by restriction enzyme / Concentration calibration

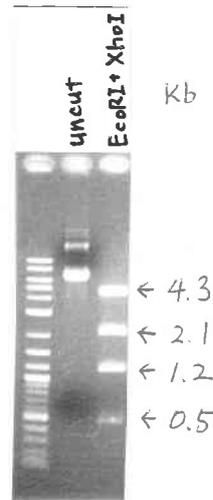
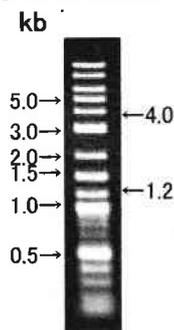
Date : 10/008

DNA concentration (O.D.): 197.99 ng/ul

DNA	1 ul
Enzyme (EcoRI+XhoI)	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 BC037545.1>

4339, 1178, 2074, 468

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

Date : 10/012 Shipped : 25 ng/ul, 40 ul

Final concentration : 25 ng/ul

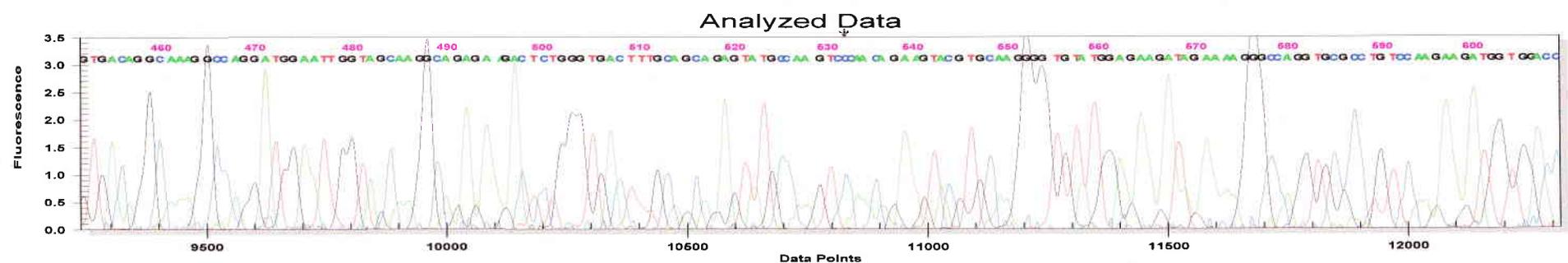
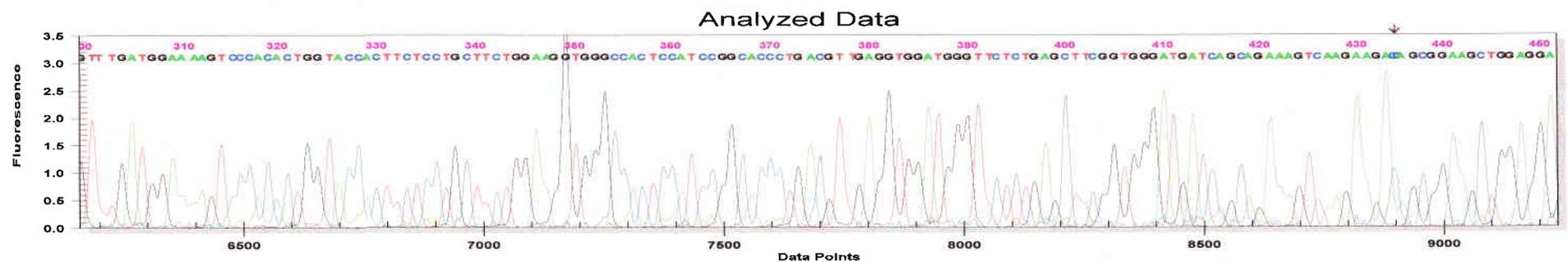
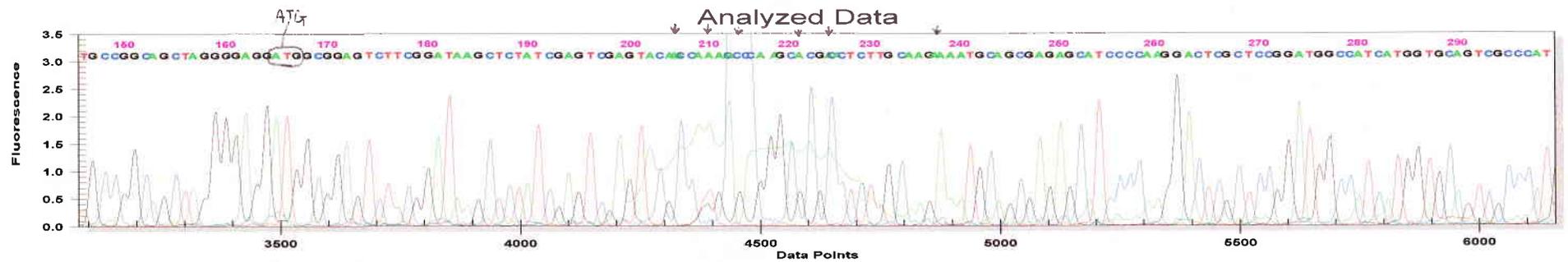
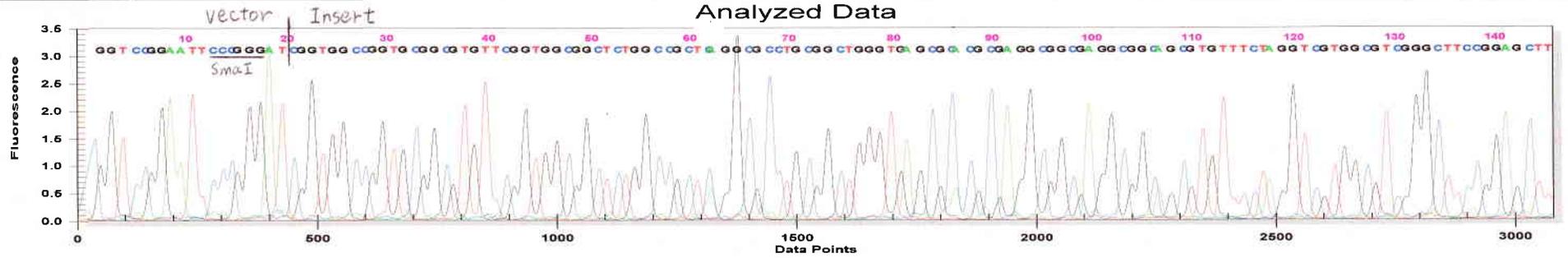
DNA (<u>197.99</u> ng/ul)	82	ul
10 × TE	64.9	ul
dH ₂ O	502.5	ul
Total	649.4	ul



Project : GNP
Sample : IRAK064G23_Reverse2.A08_10101210NX
Result : IRAK064G23_Reverse2.A08_10101210NX

System : CEQ System

Operator : 2.101012.furu
Instrument : CEQ System (Ver. 9.0.25)

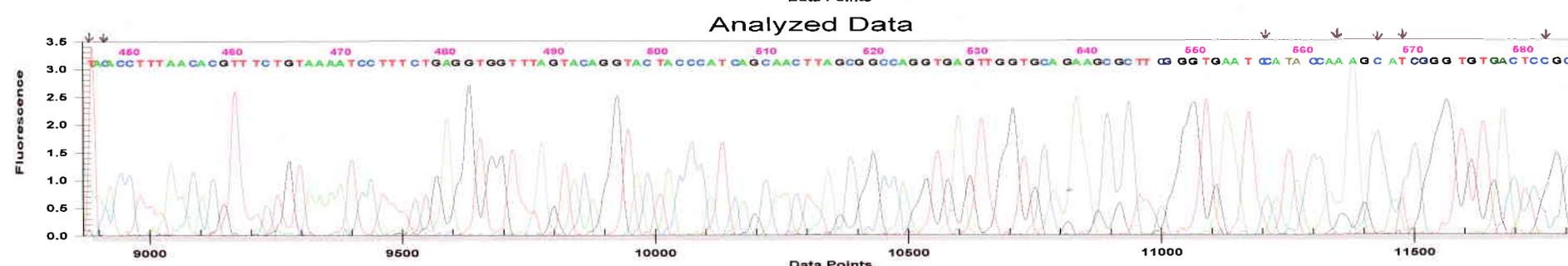
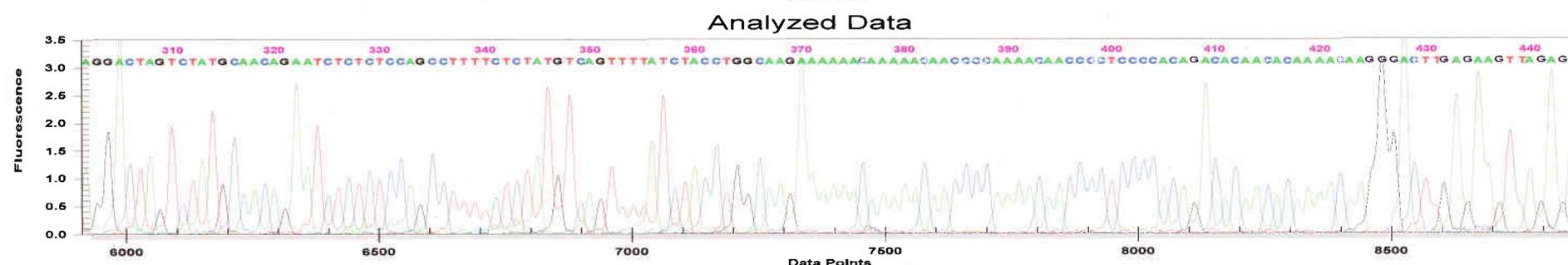
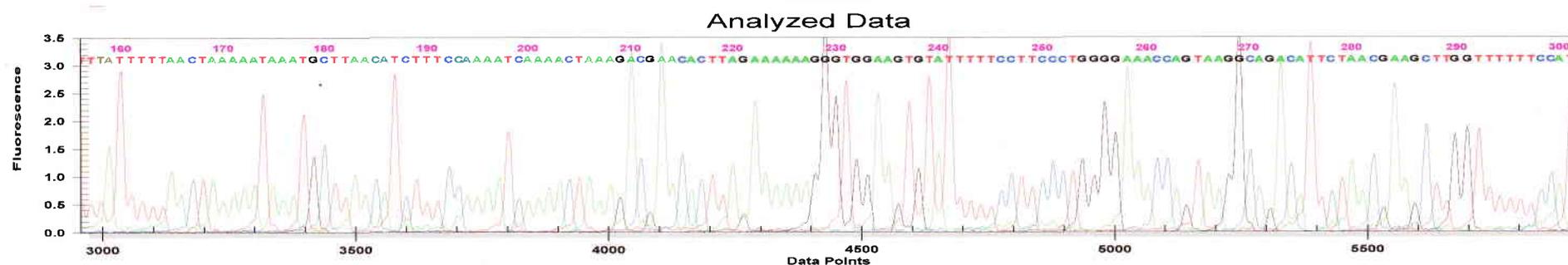
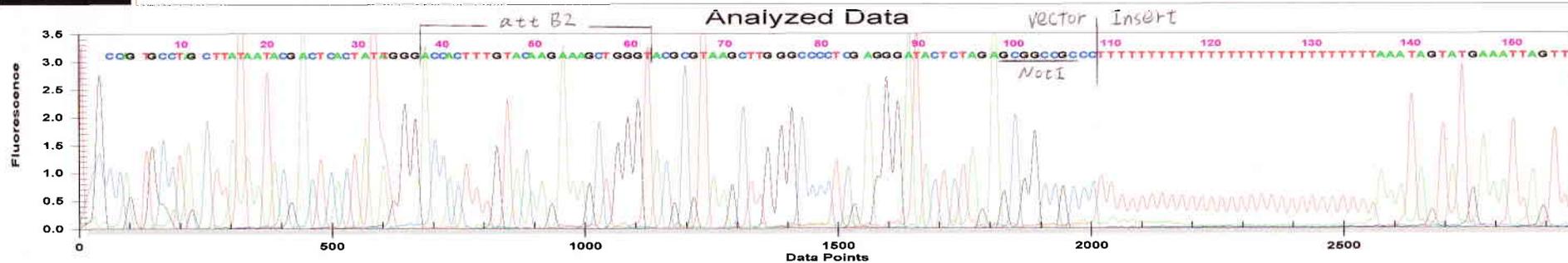




Project : GNP
Sample : IRAK064G23_M13.B08_10101210NX
Result : IRAK064G23_M13.B08_10101210NX

System : CEQ System

Operator : 2.101012.furu
Instrument : CEQ System (Ver. 9.0.25)



[GENETYX : Homology Data]

Date : 2010.10.12

Query Sequence

File Name :
Sequence Name : BC037545.1
Sequence Size : 3677

Target Sequence

File Name : IRAK064G23_Reverse2.A08_10101210NX.fasta
Sequence Name : IRAK064G23_Reverse2.A08_10101210NX
Sequence Size : 676

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

Query Range: 1 - 651
Sbjct Range: 20 - 676
660 bp, INT.Score: 788, OPT.Score: 2394
Identity: 635 / 660 (96%)
Strand: Plus / Plus

Query 1 CGGTGGCCGG TCGCGCGTGT TCGGTGGCGG CTCTGGCCGC TCAGGCGCCT GCGGCTGGGT 60
Sbjct 20 CGGTGGCCGG TCGCGCGTGT TCGGTGGCGG CTCTGGCCGC TCAGGCGCCT GCGGCTGGGT 79
Query 61 GAGCGCACGC GAGGCGGCGA GCGGCGCAGC TGTTCCTAGG TCGTGGCGTC GGGCTTCCGG 120
Sbjct 80 GAGCGCACGC GAGGCGGCGA GCGGCGCAGC TGTTCCTAGG TCGTGGCGTC GGGCTTCCGG 139
Query 121 AGCTTTGCCG GCAGCTAGGG GAGGATGGCG GAGTCTTCGG ATAAGCTCTA TCGAGTCGAG 180
Sbjct 140 AGCTTTGCCG GCAGCTAGGG GAGGATGGCG GAGTCTTCGG ATAAGCTCTA TCGAGTCGAG 199
Query 181 TAC---GCCA AGA-GCGGGC GCG--CCTCT TGCAAG-AAA TGCAGCGAGA GCATCCCCAA 233
Sbjct 200 TACAAACCAA ACACCCAAGC ACGACACTCT TGCAAGAAAA TGCAGCGAGA GCATCCCCAA 259
Query 234 GGAAGTGGG TCGATGGCCA TCATGGTGA GTCGCCCATG TTTGATGGAA AAGTCCCACA 293
Sbjct 260 GGAAGTGGG TCGATGGCCA TCATGGTGA GTCGCCCATG TTTGATGGAA AAGTCCCACA 319
Query 294 CTGGTACCAC TTCTCTGAGC TTCGGTGGGA TGATCAGCAG AAAGTCAAGA AGA-CAGCGG 412
Sbjct 320 CTGGTACCAC TTCTCTGAGC TTCGGTGGGA TGATCAGCAG AAAGTCAAGA AGA-CAGCGG 439
Query 413 AAGCTGGAGG AGTGACAGGC AAAGGCCAGG ATGGAATTGG TAGCAAGGCA GAGAAGACTC 472
Sbjct 440 AAGCTGGAGG AGTGACAGGC AAAGGCCAGG ATGGAATTGG TAGCAAGGCA GAGAAGACTC 499
Query 473 TGGGTGACTT TGCAGCAGAG TATGCCAAGT -CCAACAGAA GTACGTGCAA GGGGTGTATG 531
Sbjct 500 TGGGTGACTT TGCAGCAGAG TATGCCAAGT CCAACAGAA GTACGTGCAA GGGGTGTATG 559
Query 532 GAGAAGATAG AAAAGGGCCA GGTGCGCCTG TCCAAGAAGA TGGTGGACCC GGAGAAGCCA 591
Sbjct 560 GAGAAGATAG AAAAGGGCCA GGTGCGCCTG TCCAAGAAGA TGGTGGACCC GGAGAAGCCA 619
Query 592 CAGCTAGGCA TGATTGACCG CTGGTACCAT CCAGGCTGCT TTGTCAAGAA CAGGGAGGAG 651
Sbjct 620 CAGCTAGGCA TGATTGACCG CTGGT-CCAT TCAGGCTGCT TGGT-TAG-A CAGGGAGGG 676

Query Sequence

File Name :
Sequence Name : BC037545.1
Sequence Size : 3677

Target Sequence

File Name : IRAK064G23_M13.B08_10101210NX.fasta
Sequence Name : IRAK064G23_M13.B08_10101210NX (complement)
Sequence Size : 696

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

Query Range: 3089 - 3677
Sbjct Range: 1 - 589
592 bp, INT.Score: 1540, OPT.Score: 2212
Identity: 576 / 592 (97%)
Strand: Plus / Minus

Query 3089 CCTCTCTACT ATATAAC-GA GTACATTGTC TATGATATTG CTCAGGTAAA TCTGAAGTAT 3147
Sbjct 1 CCTCTCTACT ATATAACCGA GACTTGTGTC TATGATATTG CTCGGGTAAA TCTGAAGTAT 60
Query 3148 CTGCTGAAAC TGAATTC-CA TTTTAAAGACC T-CCCTGTGG TAATTTGGGAG AGGTAGCCGA 3206
Sbjct 61 CTGCTGAAAC TG-AATTC-A TTTTAAAGACC TCCCTGTGG TAATTTGGGAG AGGTAGCCGA 118
Query 3207 GTCACACCCG GTGGCTCTGG TATGAATCA CCCGAAGCGC TTCTGCACCA ACTCACCTGG 3266
Sbjct 119 GTCACACCCG AT-GCTTTGG TATGGATCA CCCGAAGCGC TTCTGCACCA ACTCACCTGG 177
Query 3267 CCGCTAAGTT GCTGATGGGT AGTACCTGTA CTAACCACC TCAGAAAGGA TTTTACAGAA 3326
Sbjct 178 CCGCTAAGTT GCTGATGGGT AGTACCTGTA CTAACCACC TCAGAAAGGA TTTTACAGAA 237
Query 3327 ACGTGTAAA GGT-TTCTC TAACCTCTCA AGTCCCTTGT TTTGTGTTGT GTCTGTGGGG 3385
Sbjct 238 ACGTGTAAA GGTGTATCT TAACCTCTCA AGTCCCTTGT TTTGTGTTGT GTCTGTGGGG 297
Query 3386 AGGGGTGTGT TTGGGGTTGT TTTTGTTTT TCTTGCACAG TAGATAAAAC TGACATAGAG 3445
Sbjct 298 AGGGGTGTGT TTGGGGTTGT TTTTGTTTT TCTTGCACAG TAGATAAAAC TGACATAGAG 357
Query 3446 AAAAGGCTGG AGAGAGATTC TGTTCATAG ACTAGTCCTA TGGAAAAAAC CAAGCTTCGT 3505
Sbjct 358 AAAAGGCTGG AGAGAGATTC TGTTCATAG ACTAGTCCTA TGGAAAAAAC CAAGCTTCGT 417
Query 3506 TAGAATGTCT GCCTTACTGG TTTCCCAGG GAAGGAAAA TACACTTCCA CCCTTTTTTC 3565
Sbjct 418 TAGAATGTCT GCCTTACTGG TTTCCCAGG GAAGGAAAA TACACTTCCA CCCTTTTTTC 477
Query 3566 TAAGTGTTCG TCTTTAGTTT TGATTTTGA AAGATGTTAA GCATTTATTT TTAGTTAAAA 3625
Sbjct 478 TAAGTGTTCG TCTTTAGTTT TGATTTTGA AAGATGTTAA GCATTTATTT TTAGTTAAAA 537
Query 3626 ATAAAACTA ATTTTCATACT ATTTAAAAA AAAAAAAAAA AAAAAAAAAA AA 3677
Sbjct 538 ATAAAACTA ATTTTCATACT ATTTAAAAA AAAAAAAAAA AAAAAAAAAA AA 589