

RIKEN clone ID: IRAK133F23

Vector : pBluescriptR

Gene	GOLGA3		
Accession No.	BC060826.1	2776 bp	1..>2776
	<i>CDS</i>	2531 bp	246..>2776

●Plasmid DNA purification

Date : 10 11 29 Culture : LB (100 ug/ml Ampicillin) 3 ml →37°C O/N

Date : 10 11 30 Purification : QIAGEN Miniprep kit →dH₂O ⁸⁰~~100~~ ul

●Digestion by restriction enzyme / Concentration calibration

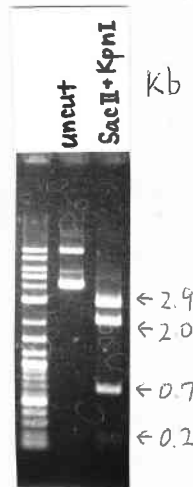
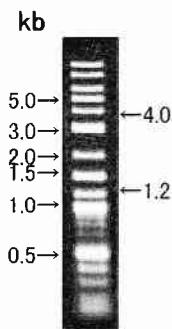
Date : 10 11 30

DNA concentration (O.D.): 272.28 ng/ul

DNA	0.5 ul
Enzyme (Sac II +KpnI)	0.5+0.5 ul
Buffer L	1 ul
dH ₂ O	7.5 ul
Total	10 ul

Electrophoresis: 1% agarose gel, 1 × TAE Buffer

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



<Expected digestion pattern from BC060826.1 >

168, 674, 2062, 2862 bp

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

Date : 10/20/01 Shipped : 25 ng/ul, 40 ul

Final concentration: 25 ng/ul

DNA (<u>272.28</u> ng/ul)	70.0 ul
10 × TE	76.2 ul
dH ₂ O	616.2 ul
Total	762.4 ul



Project : GNP

System : CEQ System

Operator : 3.101201.furu

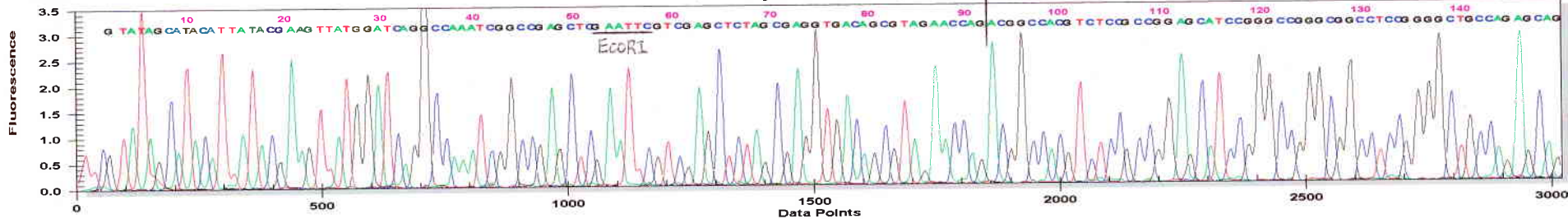
Sample : IRAK133F23_T7.C07_10120110S6

Instrument : CEQ System (Ver. 9.0.25)

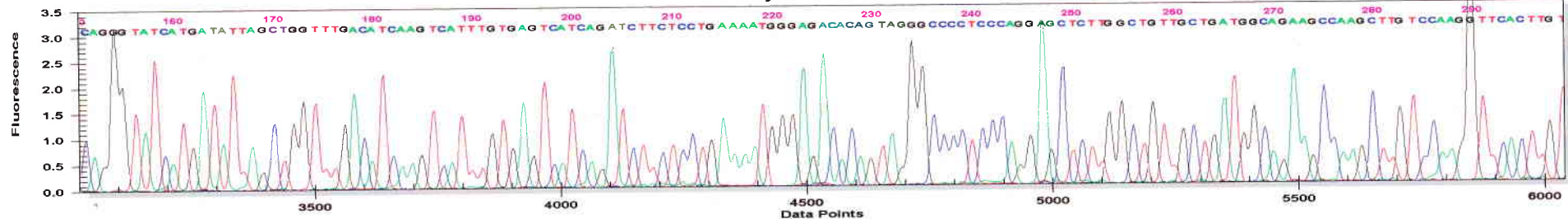
Result : IRAK133F23_T7.C07_10120110S6

Vector ← → Insert

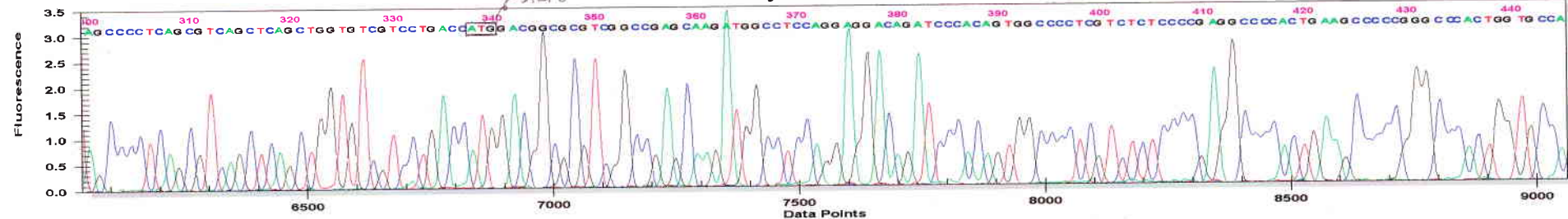
Analyzed Data



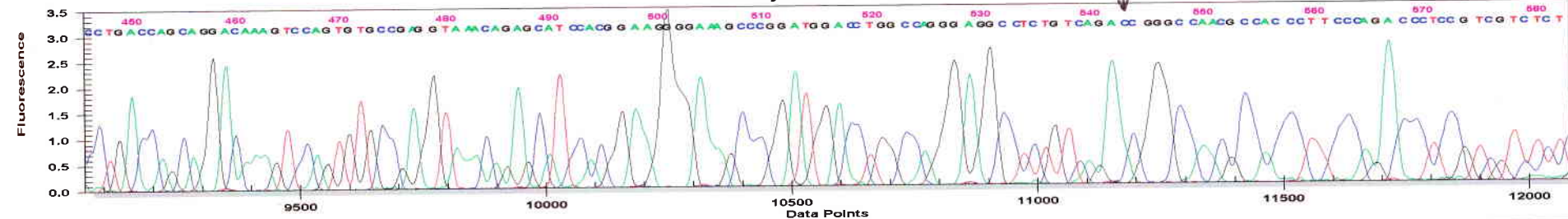
Analyzed Data



Analyzed Data



Analyzed Data





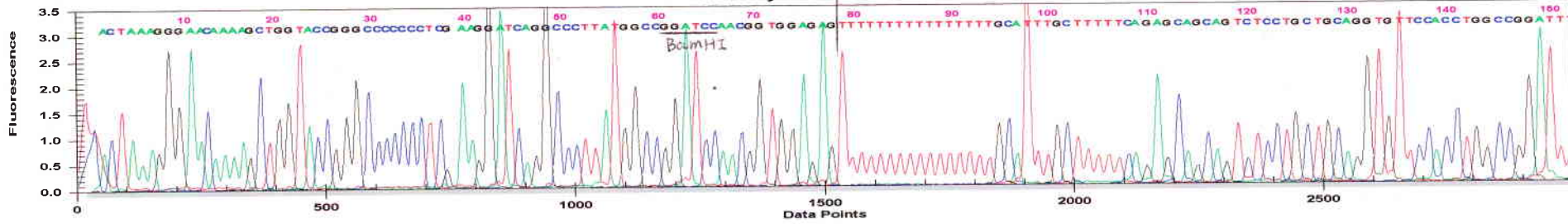
Project : GNP
Sample : IRAK133F23_Reverse2.D07_10120110S6
Result : IRAK133F23_Reverse2.D07_10120110S6

System : CEQ System

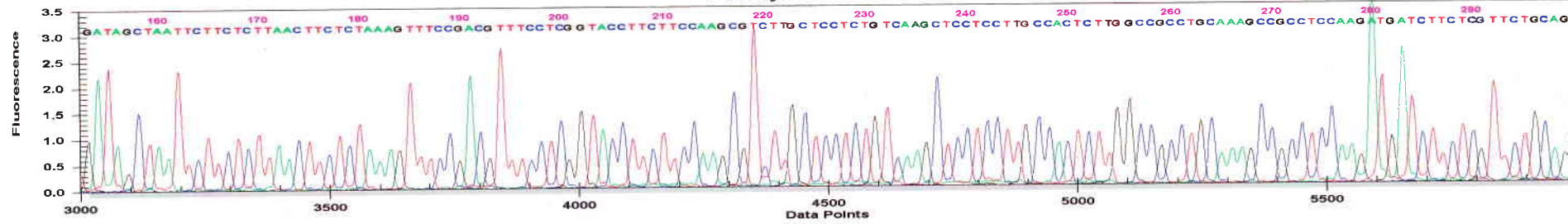
Operator : 3.101201.furu
Instrument : CEQ System (Ver. 9.0.25)

Vector ← → Insert

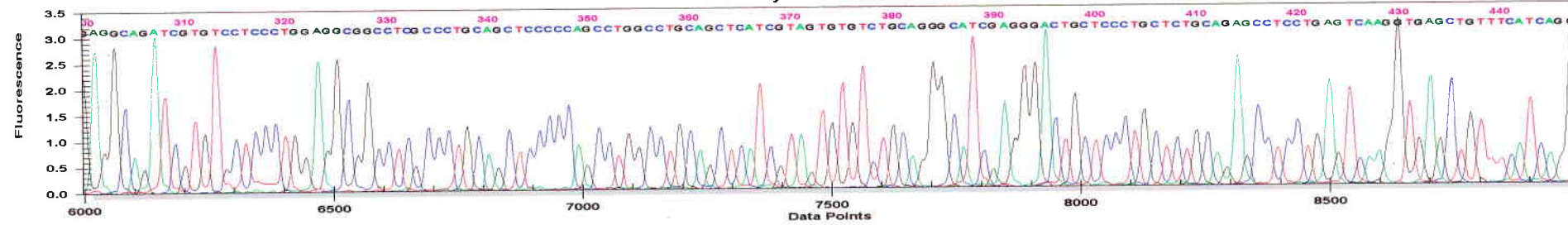
Analyzed Data



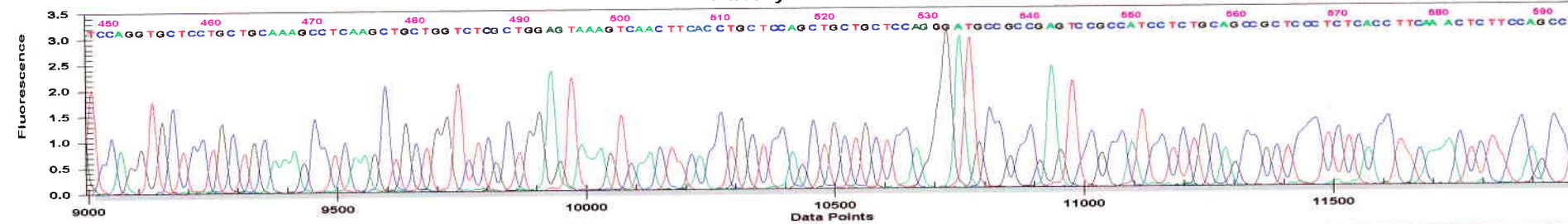
Analyzed Data



Analyzed Data



Analyzed Data



[GENETYX : Homology Data]

Date : 2010.12.01

Query Sequence
File Name :
Sequence Name : BC060826.1
Sequence Size : 2776

Target Sequence
File Name : IRAK133F23_T7.C07_10120110S6.seq
Sequence Name : IRAK133F23_T7.C07_10120110S6
Sequence Size : 656

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

Query Range: 1 - 562
Sbjct Range: 92 - 654
563 bp, INT.Score: 2010, OPT.Score: 2212
Identity: 558 / 563 (99%)
Strand: Plus / Plus

Query 1 ACGGCCACGT CTCGCCGGA GCATCCGGG CCGGCCGCT CCGGGCTGC CAGAGCAGCA 60
Sbjct 92 ACGGCCACGT CTCGCCGGA GCATCCGGG CCGGCCGCT CCGGGCTGC CAGAGCAGCA 151
Query 61 GGGTATCATG ATATTAGCTG GTTTGACATC AAGTCATTTG TGAGTCATCA GATCTTCTCC 120
Sbjct 152 GGGTATCATG ATATTAGCTG GTTTGACATC AAGTCATTTG TGAGTCATCA GATCTTCTCC 211
Query 121 TGAAAATGGG AGACACAGTA GGGCCCTCC CAGGAGCTCT TGGCTGTGC TGATGCCAGA 180
Sbjct 212 TGAAAATGGG AGACACAGTA GGGCCCTCC CAGGAGCTCT TGGCTGTGC TGATGCCAGA 271
Query 181 AGCCAAGCTT GTCCAAGGTT CACTTGTAGC CCTCAGCGT CAGCTCAGCT GGTSTCGTCC 240
Sbjct 272 AGCCAAGCTT GTCCAAGGTT CACTTGTAGC CCTCAGCGT CAGCTCAGCT GGTSTCGTCC 331
Query 241 TGACCATGGA CGGCGCTCG GCCGAGCAAG ATGGCCTCCA GGAGGACAGA TCCCACAGTG 300
Sbjct 332 TGACCATGGA CGGCGCTCG GCCGAGCAAG ATGGCCTCCA GGAGGACAGA TCCCACAGTG 391
Query 301 GCCCCTCGTC TCTCCCGAG GCCCCACTGA AGCCCCGGG CCCACTGGTG CCACCTGACC 360
Sbjct 392 GCCCCTCGTC TCTCCCGAG GCCCCACTGA AGCCCCGGG CCCACTGGTG CCACCTGACC 451
Query 361 AGCAGGACAA AGTCCAGTGT GCCGAGGTAA ACAGAGCATC CACGGAAGGG GAAAGCCCGG 420
Sbjct 452 AGCAGGACAA AGTCCAGTGT GCCGAGGTAA ACAGAGCATC CACGGAAGGG GAAAGCCCGG 511
Query 421 ATGGACCTGG CCAGGAGGC CTCTGTGAGA ACGGGCCAAC GCCACCTTC CCAGACCTTC 480
Sbjct 512 ATGGACCTGG CCAGGAGGC CTCTGTGAGA ACGGGCCAAC GCCACCTTC CCAGACCTTC 571
Query 481 CGTCGTCTCT CGATCCCACC AC-AAGCCCA GTGGGCCCTG ATGCCTCTCC AGTGTGGCT 539
Sbjct 572 CGTCGTCTCT CGATCCCACC ACAAGCCCA GTGGGCCCTG ATGCCTCTCC AGTGTGGCT 631
Query 540 GGTTCCTATG ACAACCTAAG GAA 562
Sbjct 632 GGTTCCTATG ACAACCTAAG GAA 654

Query Sequence
File Name :
Sequence Name : BC060826.1
Sequence Size : 2776

Target Sequence
File Name : IRAK133F23_Reverse2.D07_10120110S6.seq
Sequence Name : IRAK133F23_Reverse2.D07_10120110S6 (complement)
Sequence Size : 698

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

Query Range: 2156 - 2776
Sbjct Range: 2 - 621
621 bp, INT.Score: 2326, OPT.Score: 2462
Identity: 619 / 621 (99%)
Strand: Plus / Minus

Query 2156 CATCGCGGCA CAGCTGCAGG GCATTGAGGC TGACATGTTG GATCAGGAAG CAGCCTTCAT 2215
Sbjct 2 CATCGCGGCA CAGCTGCAGG GCATTGAGGC TGACATG-TG GATCAGGAAG CAGCCTTCAT 60
Query 2216 GCAGATTCAG GAGGCAAAGA CGATGGTGGG GGAGGACCTT CAGAGGAGGC TGGAAAGAGTT 2275
Sbjct 61 GCAGATTCAG GAGGCAAAGA CGATGGTGGG GGAGAACCTT CAGAGGAGGC TGGAAAGAGTT 120
Query 2276 TGAAGGTGAG AGGGAGCGGC TGCAGAGGAT GCGGACTCG GCGGCATCCC TGGAGCAGCA 2335
Sbjct 121 TGAAGGTGAG AGGGAGCGGC TGCAGAGGAT GCGGACTCG GCGGCATCCC TGGAGCAGCA 180
Query 2336 GCTGGAGCAG GTGAAGTTGA CTTTACTCCA GCGAGACCAG CAGCTTGAGG CTTTGCAGCA 2395
Sbjct 181 GCTGGAGCAG GTGAAGTTGA CTTTACTCCA GCGAGACCAG CAGCTTGAGG CTTTGCAGCA 240
Query 2396 GGAGCACCTG GACCTGATGA AACAGCTCAC CTTGACTCAG GAGGCTCTGC AGAGCAGGGA 2455
Sbjct 241 GGAGCACCTG GACCTGATGA AACAGCTCAC CTTGACTCAG GAGGCTCTGC AGAGCAGGGA 300
Query 2456 GCAGTCCCTC GATGCCCTGC AGACACACTA CGATGAGCTG CAGGCCAGGC TGGGGGAGCT 2515
Sbjct 301 GCAGTCCCTC GATGCCCTGC AGACACACTA CGATGAGCTG CAGGCCAGGC TGGGGGAGCT 360
Query 2516 GCAGGGCGAG GCGCCCTCCA GGGAGGACAC GATCTGCCTC CTGCAGAACG AGAAGATCAT 2575
Sbjct 361 GCAGGGCGAG GCGCCCTCCA GGGAGGACAC GATCTGCCTC CTGCAGAACG AGAAGATCAT 420
Query 2576 CTTGGAGGGG GCTTTGCAGG CCGCCAAGAG TGGCAAGGAG GAGCTTGACA GAGGAGCAAG 2635
Sbjct 421 CTTGGAGGGG GCTTTGCAGG CCGCCAAGAG TGGCAAGGAG GAGCTTGACA GAGGAGCAAG 480
Query 2636 ACGCTTGGAA GAAGGTACC GGAACCGTC GGAAACTTTA GAGAAGTTAA GAGAAGAATT 2695
Sbjct 481 ACGCTTGGAA GAAGGTACC GGAACCGTC GGAAACTTTA GAGAAGTTAA GAGAAGAATT 540
Query 2696 AGCTATCAA TCCGGCCAGG TGGAACACCT GCAGCAGGAG ACTGCTGCTC TGAAAAAGCA 2755
Sbjct 541 AGCTATCAA TCCGGCCAGG TGGAACACCT GCAGCAGGAG ACTGCTGCTC TGAAAAAGCA 600
Query 2756 AATGCAAAAA AAAAAAAAAA A 2776
Sbjct 601 AATGCAAAAA AAAAAAAAAA A 621