

RIKEN clone ID: IRAL007J14

Vector : pOTB7

Gene	ARL4D		
Accession No.	BC000043.2	1383 bp	1..1383
	<i>CDS</i>	606 bp	162..767

●Plasmid DNA purification

Date : 10 08 23 Culture : LB (25 ug/ml Chloramphenicol) 10 ml →37°C O/N

Date : 10 08 24 Purification : QIAGEN Miniprep kit→dH₂O 100 ul

●Digestion by restriction enzyme / Concentration calibration

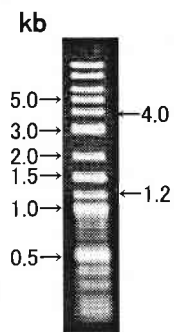
Date : 10 08 24

DNA concentration (O.D.): 166.30 ng/ul

DNA	1 ul
Enzyme (BamHI+Bgl 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 BC000043.2>

1615, 1569 bp

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

Date : 100827 Shipped : 25 ng/ul, 40 ul

Final concentration: 25 ng/ul

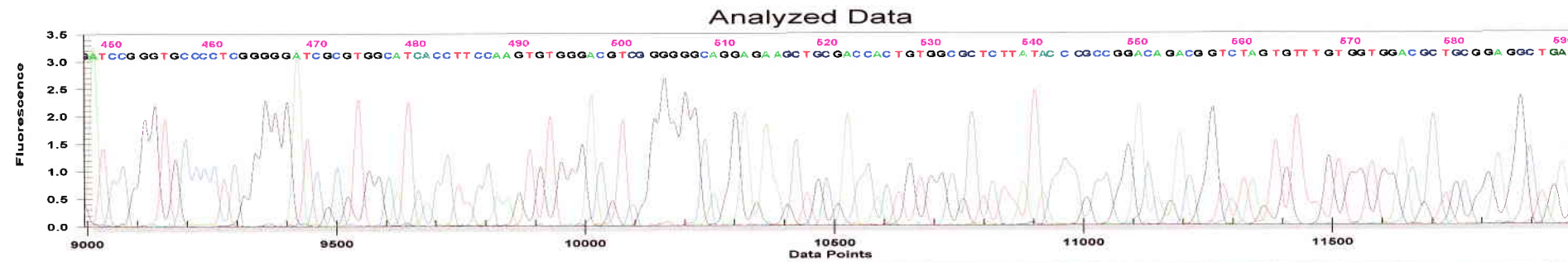
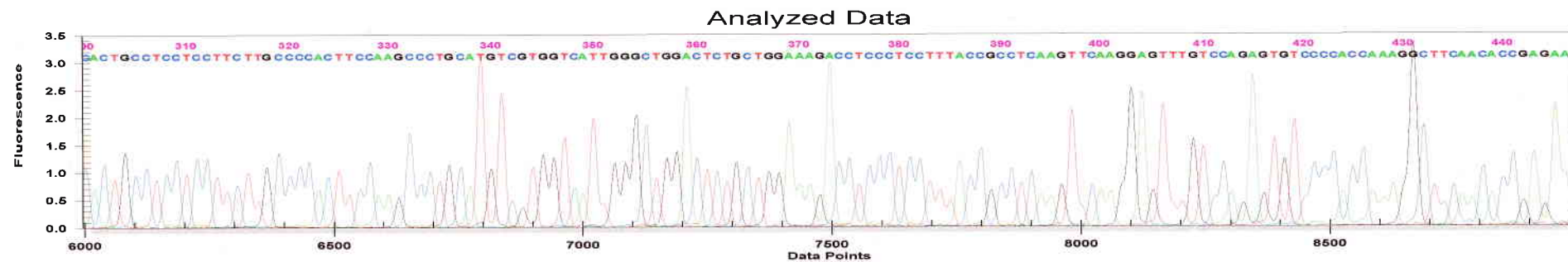
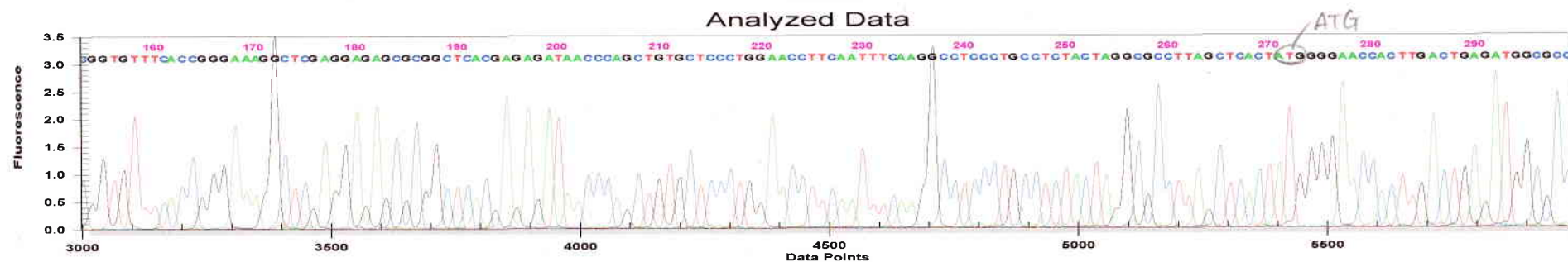
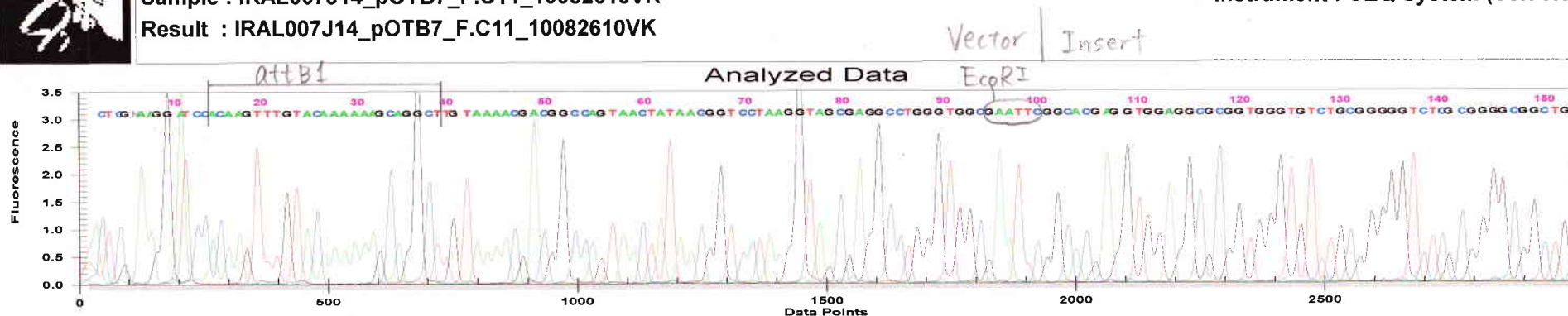
DNA (<u>166.30</u> ng/ul)	<u>80</u> ul
10 × TE	<u>53.2</u> ul
dH ₂ O	<u>398.9</u> ul
Total	<u>532.2</u> ul



Project : GNP
 Sample : IRAL007J14_pOTB7_F.C11_10082610VK
 Result : IRAL007J14_pOTB7_F.C11_10082610VK

System : CEQ System

Operator : 2.100826.furu
 Instrument : CEQ System (Ver. 9.0.25)



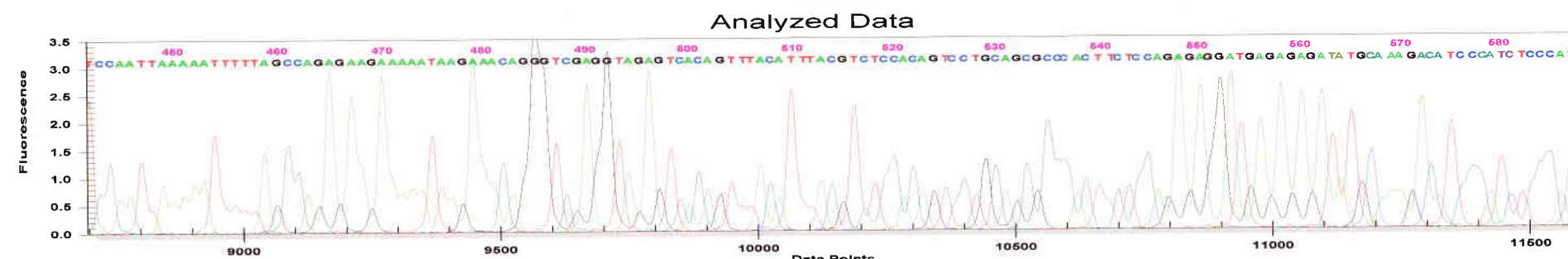
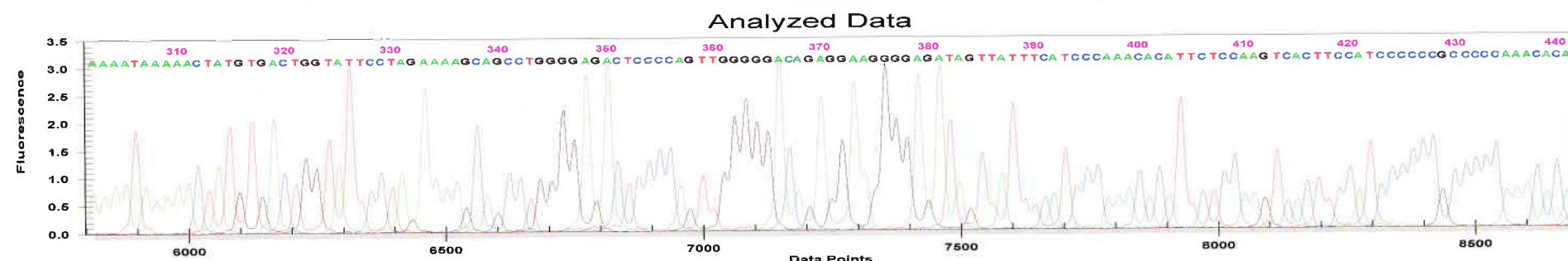
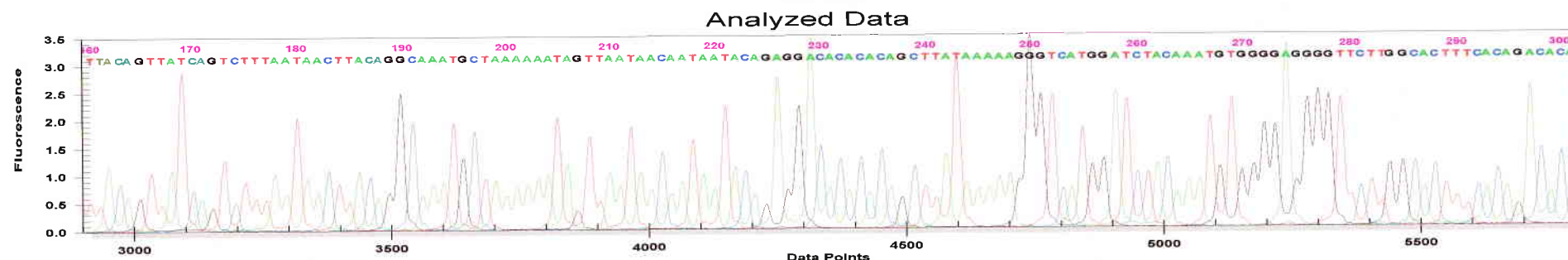
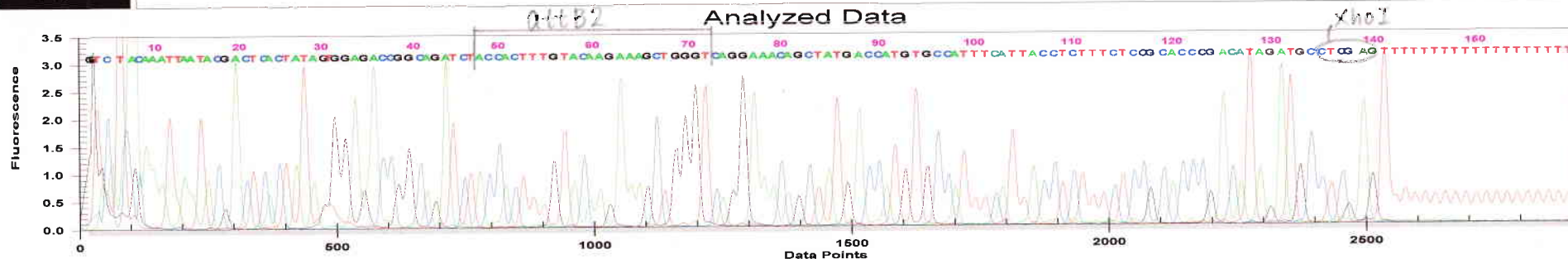


Project : GNP
 Sample : IRAL007J14_pOTB7_R.D11_10082610VK
 Result : IRAL007J14_pOTB7_R.D11_10082610VK

System : CEQ System

Operator : 2.100826.furu
 Instrument : CEQ System (Ver. 9.0.25)

Vector | Insert



[GENETYX : Nucleotide Sequence Homology Data]

Date : 2010.08.26

1st Nucleotide Sequence

File Name : BC000043.2.gnu
Sequence Size : 1383

2nd Nucleotide Sequence

File Name : IRAL007J14_pOTB7_F.C11_10082610VK.fasta
Sequence Size : 595

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

[485 / 485 bp] INT/OPT.Score : < 1940/ 1940 >

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1'                                     TG GAGGCGCGGT
61' ATAACGGTCC TAAGGTAGCG AGGCCTGSGT GGCGAATTCG GCACGAGGTG GAGGCGCGGT
13' GGGTGTCTGC GGGGTCTCG CGGGCGGGCT GCGGTGTTTC ACCGGGAAAG GCTCGAGGAG
*****
121' GGGTGTCTGC GGGGTCTCG CGGGCGGGCT GCGGTGTTTC ACCGGGAAAG GCTCGAGGAG
73' AGCGCGGCTC ACGAGAGATA ACCCAGCTGT GCTCCCTGGA ACCTTCAATT TCAAGGCCCTC
*****
181' AGCGCGGCTC ACGAGAGATA ACCCAGCTGT GCTCCCTGGA ACCTTCAATT TCAAGGCCCTC
133' CCTGCCCTCTA CTAGGCGCCT TAGCTCACTA TGGGAACCA CTTGACTGAG ATGGCGCCCA
*****
241' CCTGCCCTCTA CTAGGCGCCT TAGCTCACTA TGGGAACCA CTTGACTGAG ATGGCGCCCA
193' CTGCCCTCCT CTTCCTGCCC CACTTCCAAG CCCTGCATGT CGTGGTCATT GGGCTGGACT
*****
301' CTGCCCTCCT CTTCCTGCCC CACTTCCAAG CCCTGCATGT CGTGGTCATT GGGCTGGACT
253' CTGCTGGAAA GACCTCCCTC CTTTACCGCC TCAAGTTCAA GGAGTTGTC CAGAGTGTC
*****
361' CTGCTGGAAA GACCTCCCTC CTTTACCGCC TCAAGTTCAA GGAGTTGTC CAGAGTGTC
313' CCACCAAAGG CTTCACACC GAGAAGATCC GGGTGCCCTC CGGGGATCG CGTGGCATCA
*****
421' CCACCAAAGG CTTCACACC GAGAAGATCC GGGTGCCCTC CGGGGATCG CGTGGCATCA
373' CCTTCCAAAGT GTGGGACGTC GGGGGCAGS AGAAGCTGCG ACCACTGTGG CGCTCTTATA
*****
481' CCTTCCAAAGT GTGGGACGTC GGGGGCAGS AGAAGCTGCG ACCACTGTGG CGCTCTTATA
433' CCCGCCGGAC AGACGGTCTA GTGTTTGTGG TGGACGCTGC GGAGGCTGAG CGGCTGGAGG
*****
541' CCCGCCGGAC AGACGGTCTA GTGTTTGTGG TGGACGCTGC GGAGGCTGAG CGGGG

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1st Nucleotide Sequence

File Name : BC000043.2.gnu
Sequence Size : 1383

2nd Nucleotide Sequence

File Name : IRAL007J14_pOTB7_R.D11_10082610VK.fasta (Complementary)
Sequence Size : 611

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

[471 / 471 bp] INT/OPT.Score : < 1884/ 1884 >

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901' TGGGGTGTCC CGTTTGTGTG CCACACTGGG GTGGGGATGG GAGATGGGAT GTCTTTGCAT
*****
1' TTTTGTGGTG CCACACTGGG GTGGGGATGG GAGATGGGAT GTCTTTGCAT
961' ATCTCTCTCA TCCTCTCTGG AGAAGTGGGC GCTGCAGGAC TGTGGAGACC TAAATGTAAA
*****
50' ATCTCTCTCA TCCTCTCTGG AGAAGTGGGC GCTGCAGGAC TGTGGAGACC TAAATGTAAA
1021' CTGTGACTCT ACCTCGACCC TGTTCCTTAT TTTCTCTCTC TGGCTAAAAA TTTTAAATFG
*****
110' CTGTGACTCT ACCTCGACCC TGTTCCTTAT TTTCTCTCTC TGGCTAAAAA TTTTAAATFG
1081' GATGTGTTTG GGGGCGGGG GATGGAAGTG ACTTGGAGAA TGTGTTTGGG ATGAAATAAC
*****
170' GATGTGTTTG GGGGCGGGG GATGGAAGTG ACTTGGAGAA TGTGTTTGGG ATGAAATAAC
1141' TATCTCCCTT TCCTCTGTCC CCCAACTGGG GAGTCTCCCT AGGCTGCTTT TCTAGGAATA
*****
230' TATCTCCCTT TCCTCTGTCC CCCAACTGGG GAGTCTCCCT AGGCTGCTTT TCTAGGAATA
1201' CCAGTCACAT AGTTTTTATT TTTGTGCTCG TGAAAGTGCC AAGAACCCTT CCCACATTT
*****
290' CCAGTCACAT AGTTTTTATT TTTGTGCTCG TGAAAGTGCC AAGAACCCTT CCCACATTT
1261' GTAGATCCAT GACCCTTTTT ATAAGCTGTG TGTGTCTCTT GTATTATGT TATTAACTAT
*****
350' GTAGATCCAT GACCCTTTTT ATAAGCTGTG TGTGTCTCTT GTATTATGT TATTAACTAT
1321' TTTTTAGCAT TTGCCTGTAA GTTATTAAG ACTGATAACT GTAAAAAAA AAAAAAAA
*****
410' TTTTTAGCAT TTGCCTGTAA GTTATTAAG ACTGATAACT GTAAAAAAA AAAAAAAA
1381' AAA
***
470' AAATCTGAGG CATCTATGTC GGGTGGGAG AAAGAGGTAA TGAAATGGCA CATGGTCATA

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