

RIKEN clone ID: M01C008M03

Vector : pDONR221

Gene	AFF4	
Accession No.	AK126818 .1	1451 bp 1..1451
	<i>CDS</i>	257 bp 612..869
	<i>CDS</i> (Delete stop codon)	254 bp 612..866

●Plasmid DNA purification

Date : 110418 Culture : LB (25 ug/ml Kanamycin) 3 ml →37°C O/N

Date : 110419 Purification : QIAGEN Miniprep kit→dH₂O 100 ul

●Digestion by restriction enzyme / Concentration calibration

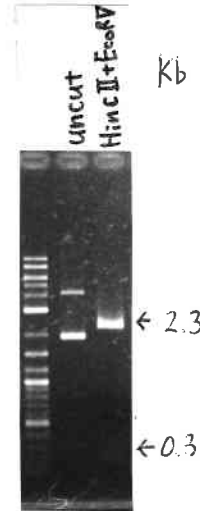
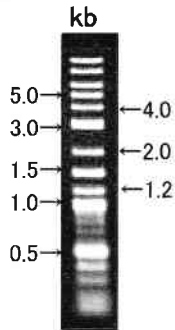
Date : 110419

DNA concentration (O.D.): 82.70 ng/ul

DNA	1 ul
Restriction enzyme (Hinc II +EcoRV)	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 AK126818 .1 CDS>

241, 300, 2263 bp

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

Date : 110422 Shipped : 25 ng/ul, 40 ul

Final concentration: 25 ng/ul

DNA (<u>82.70</u> ng/ul)	<u>84.0</u>	ul
10 × TE	<u>27.8</u>	ul
dH ₂ O	<u>166.1</u>	ul
Total	<u>277.9</u>	ul



Project : GNP

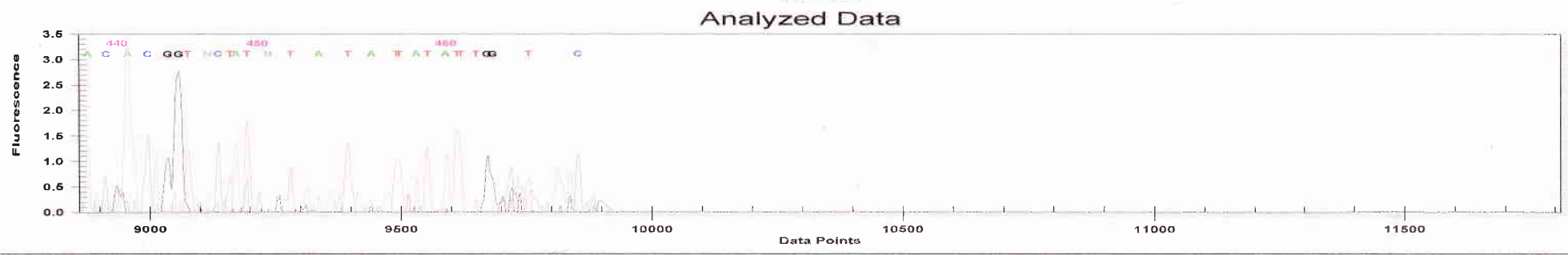
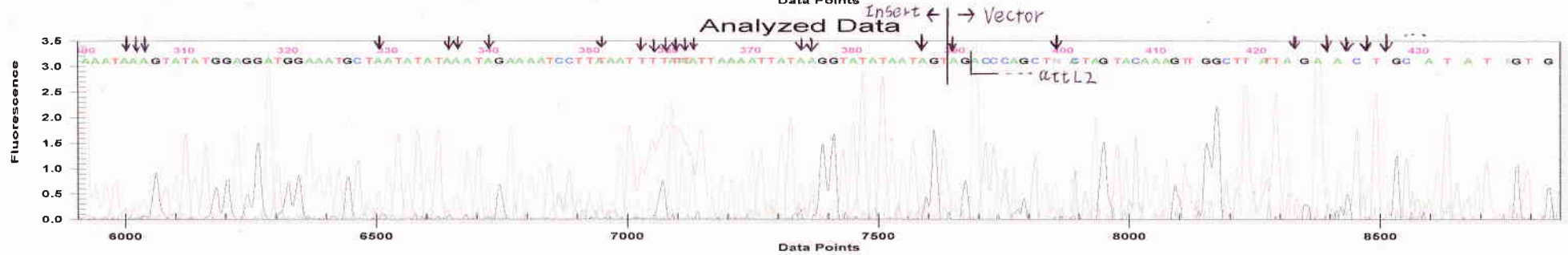
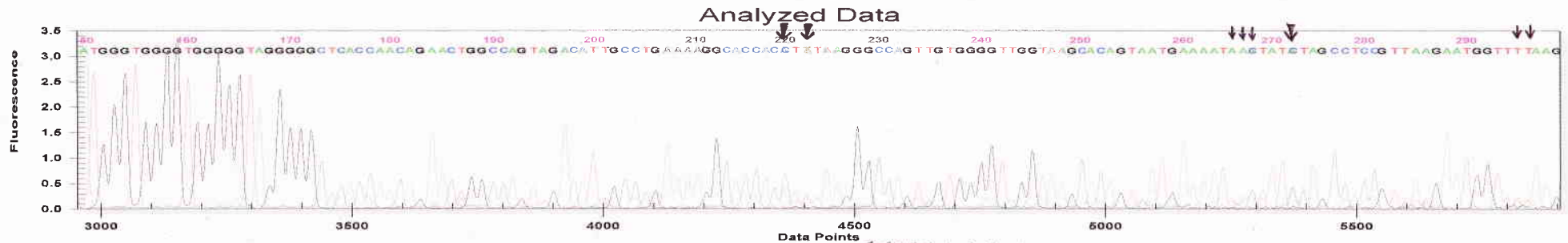
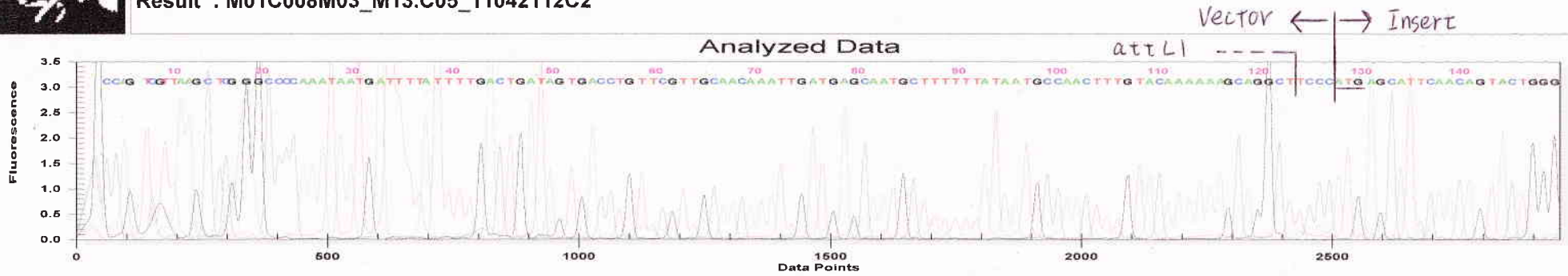
Sample : M01C008M03_M13.C05_11042112C2

Result : M01C008M03_M13.C05_11042112C2

System : System 1

Operator : 1.110421.furu

Instrument : System 1 (Ver. 9.0.25)

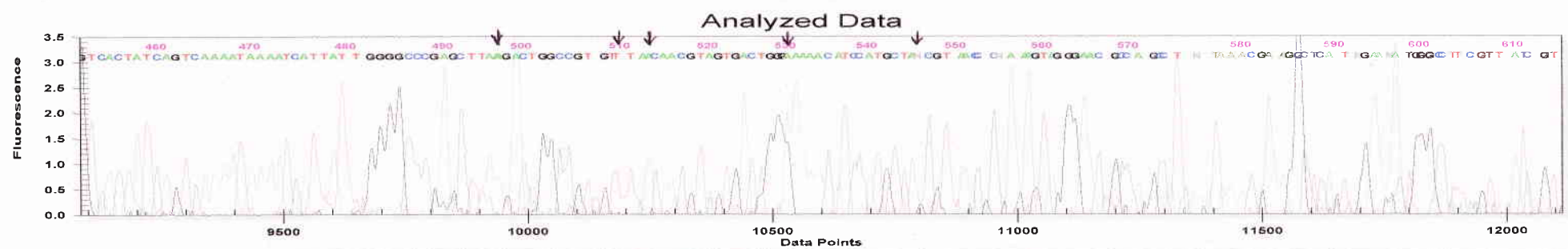
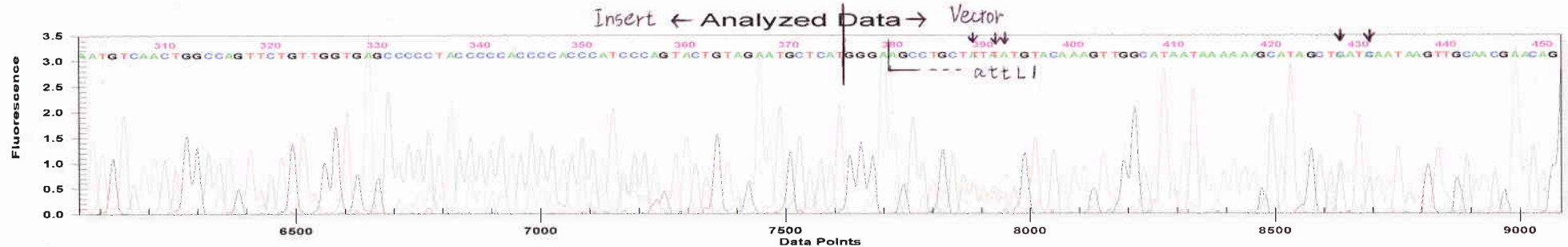
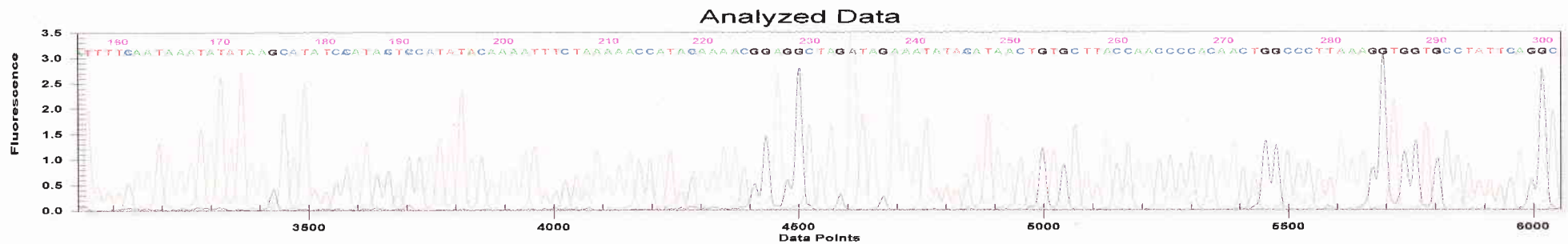
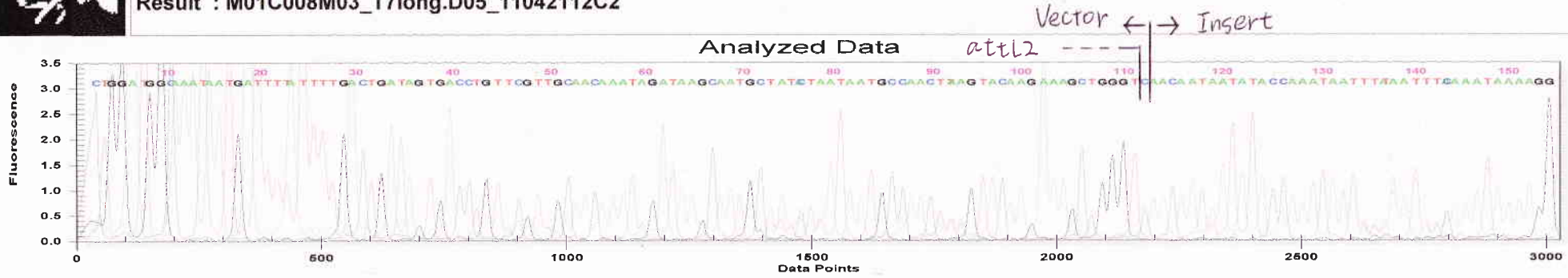




Project : GNP
 Sample : M01C008M03_T7long.D05_11042112C2
 Result : M01C008M03_T7long.D05_11042112C2

System : System 1

Operator : 1.110421.furu
 Instrument : System 1 (Ver. 9.0.25)



[GENETYX : Homology Data]

Date : 2011.04.22

Query Sequence

File Name :
 Sequence Name : AK126818_CDS(612..869)
 Sequence Size : 258

Target Sequence

File Name : M01C008M03_M13.C05_11042112C2
 Sequence Name : M01C008M03_M13.C05_11042112C2
 Sequence Size : 466

Unit Size to Compare = 6

Pick up Location No. = 1

Query Range: 1 - 254

Sbjct Range: 127 - 388

262 bp, INT.Score: 358, OPT.Score: 824

Identity: 234 / 262 (89%)

Strand: Plus / Plus

Query	1	ATGAGCATT	AACAGTACTG	GGATGGGTGG	GGTGGGGGTA	GGGGGCTCAC	CAACAGAACT	60
Sbjct	127	ATGAGCATT	AACAGTACTG	GGATGGGTGG	GGTGGGGGTA	GGGGGCTCAC	CAACAGAACT	186
Query	61	GGCCAGTTGA	CATTGCCTGA	AAAGGCACCA	C-CTT-TAAG	GGCCAGTTGT	GGGGTTGGTA	118
Sbjct	187	GGCCAGTAGA	CATTGCCTGA	AAAGGCACCA	CACTTATAAG	GGCCAGTTGT	GGGGTTGGTA	246
Query	119	AGCACAGTTA	TGAAAAT-TT	CTAT-CTAGC	CTCCGTTTTG	AATGGTTTTA	AGAAATTTTG	176
Sbjct	247	AGCACAGTAA	TGAAAATAAA	CTATACTAGC	CTCCGTTAAG	AATGGTTTTA	AGAAATAAAG	306
Query	177	TATATGGAGG	ATGGAAATGC	TTATATATTT	ATTGAAAATC	CTT----TTA	TTTGAAATTA	232
Sbjct	307	TATATGGAGG	ATGGAAATGC	TAATATATAA	ATAGAAAATC	CTTATAATTT	TATTATATTA	366
Query	233	AAATTATTTG	GTATATAATT	GT	254			
Sbjct	367	AAATTATAAG	GTATATAATA	GT	388			

[GENETYX : Homology Data]

Date : 2011.04.22

Query Sequence

File Name :
 Sequence Name : AK126818_CDS(612..869)
 Sequence Size : 258

Target Sequence

File Name : M01C008M03_T7long.D05_11042112C2
 Sequence Name : M01C008M03_T7long.D05_11042112C2 (complement)
 Sequence Size : 649

Unit Size to Compare = 6

Pick up Location No. = 1

Query Range: 1 - 255

Sbjct Range: 276 - 538

263 bp, INT.Score: 508, OPT.Score: 870

Identity: 246 / 263 (93%)

Strand: Plus / Minus

Query	1	ATGAGCATT	AACAGTACT	GGATGGGT	GGTGGGGT	GGGGGCT	CAACAGAA	60
Sbjct	276	ATGAGCATT	TACAGTACT	GGATGGGT	GGTGGGGT	GGGGGCT	CAACAGAA	335
Query	61	GGCCAGTT	CATTGCCT	AAAGGCAC	CCTTTAAG	CCAGTTGT	GGTTGGTA	120
Sbjct	336	GGCCAGTT	CATTGCCT	ATAGGCAC	CCTTTAAG	CCAGTTGT	GGTTGGTA	395
Query	121	CACAGTTA	-AAAATTT	ATCTAGCC	CG-TTTTG	TGGTTTTA	AAATTTTG	178
Sbjct	396	CACAGTTA	TTATATTT	ATCTAGCC	CGTTTTTG	TGGTTTTT	AAATTTTG	455
Query	179	TATG-GAG	-G ATG-GAA	ATG CTTATA	TATTG-AAA	TCCTTTT	TATTG-AA	232
Sbjct	456	TATGTGAG	TATGATAT	G CTTATA	TATTGAAAA	TCCTTTT	TATTGAA	515
Query	233	AAATTATTT	GTATATA	AATT GTT	255			
Sbjct	516	AAATTATTT	GTATATT	AATT GTT	538			