

RIKEN clone ID: **W01A065A15**

Vector : pENTR/D-TOPO

Gene	TRADD		
Accession No.	AK090673.1	1833 bp	1..1833
	<i>CDS</i>	759 bp	625..1383

●Plasmid DNA purification

Date : 110202

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

Date : 110203

Purification : QIAGEN Miniprep kit→dH₂O 100 ul

●Digestion by restriction enzyme / Concentration calibration

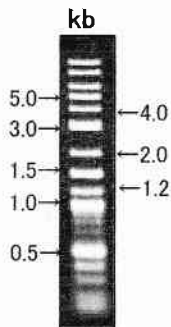
Date : 110203

DNA concentration (O.D.): 86.70 ng/ul

DNA	1 ul
Restriction enzyme (NotI+BssH II)	0.5+0.5 ul
Buffer H	1 ul
dH ₂ O	7 ul
Total	10 ul

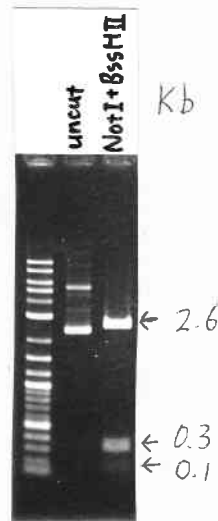
Electrophoresis: 1% agarose gel, 1 × TAE Buffer

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



<Expected digestion pattern from AK090673.1 CDS>

25, 44, 159, 313, 318, 2553 bp



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

Date : 110204

Shipped : 25 ng/ul, 40 ul

Final concentration: 25 ng/ul

DNA (<u>86.70</u> ng/ul)	<u>88.0</u> ul
10 × TE	<u>30.5</u> ul
dH ₂ O	<u>186.7</u> ul
Total	<u>305.2</u> ul



Project : GNP

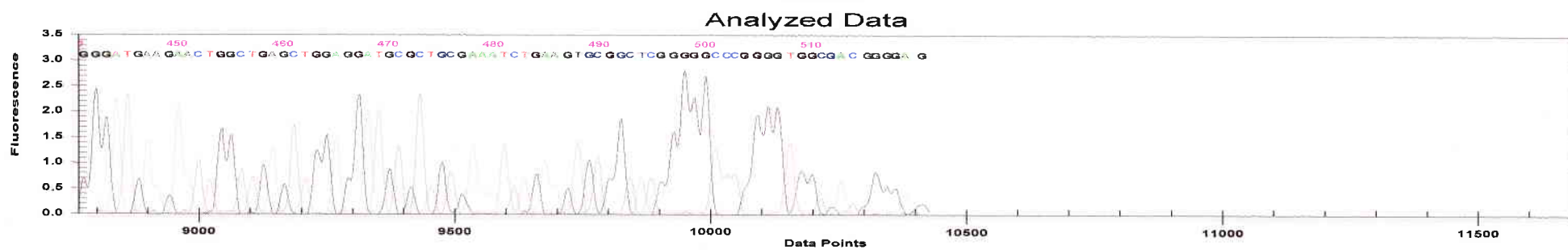
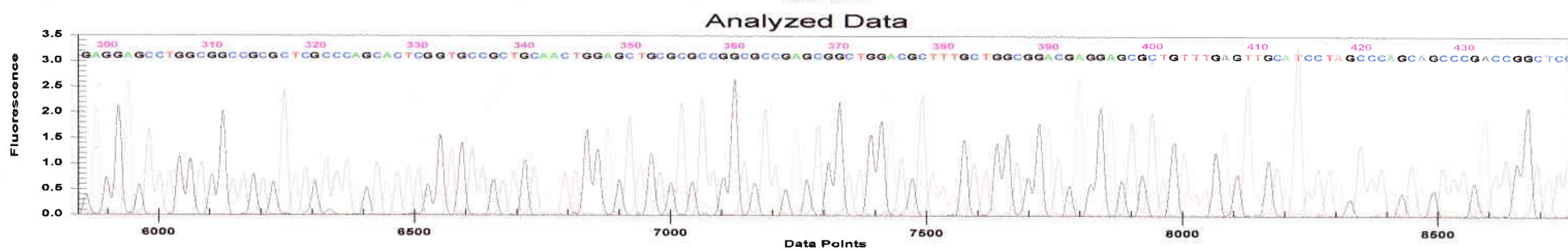
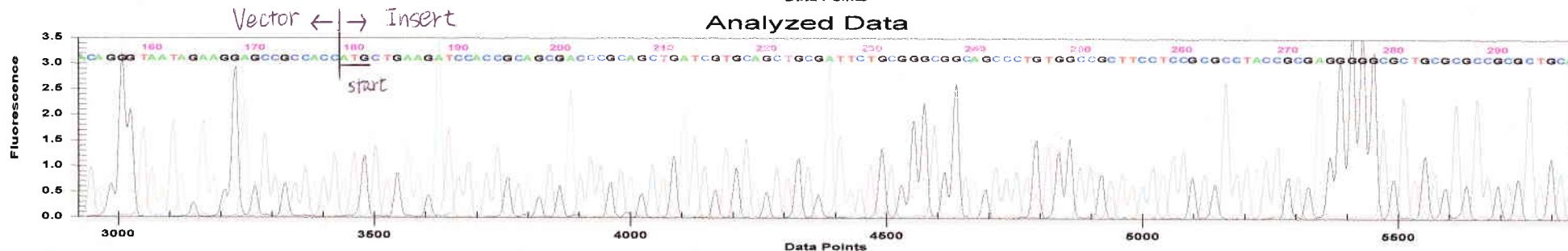
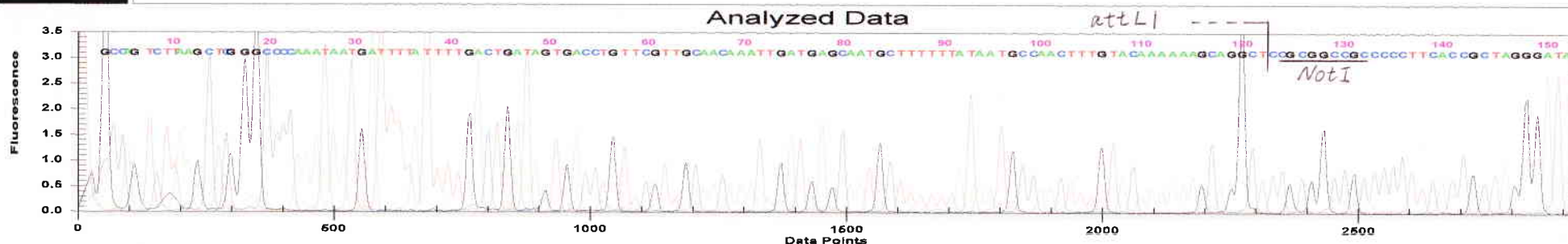
System : System 1

Operator : 1.110204.furu

Sample : W01A065A15_M13.A12_11020410MJ

Instrument : System 1 (Ver. 9.0.25)

Result : W01A065A15_M13.A12_11020410MJ

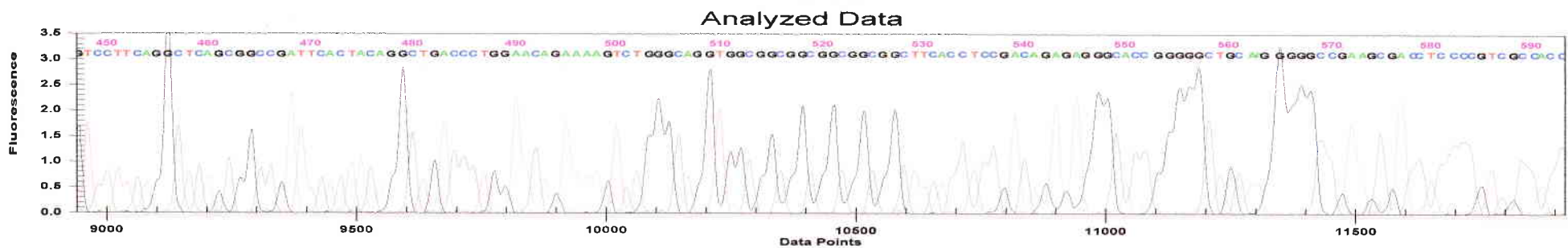
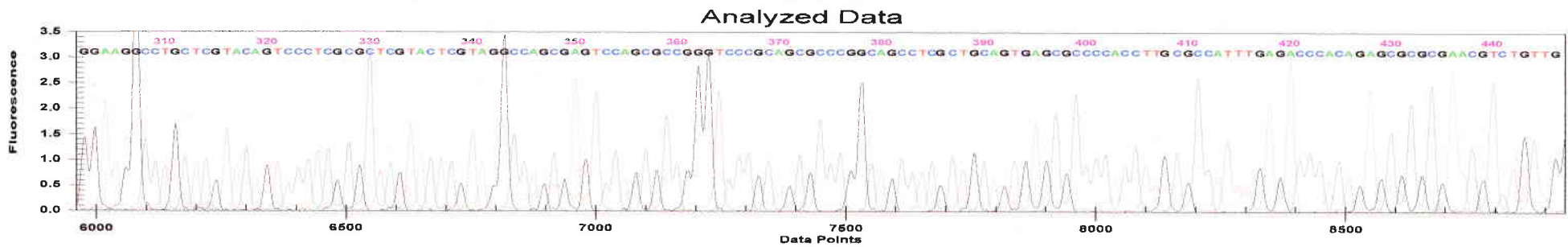
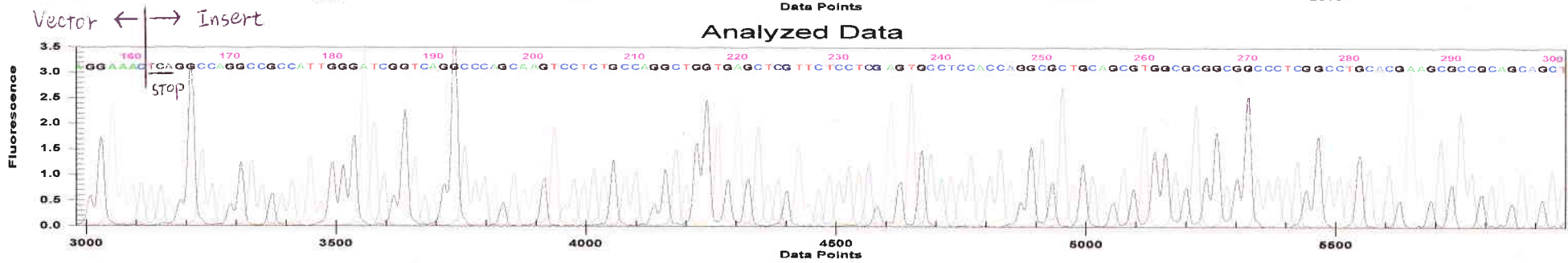
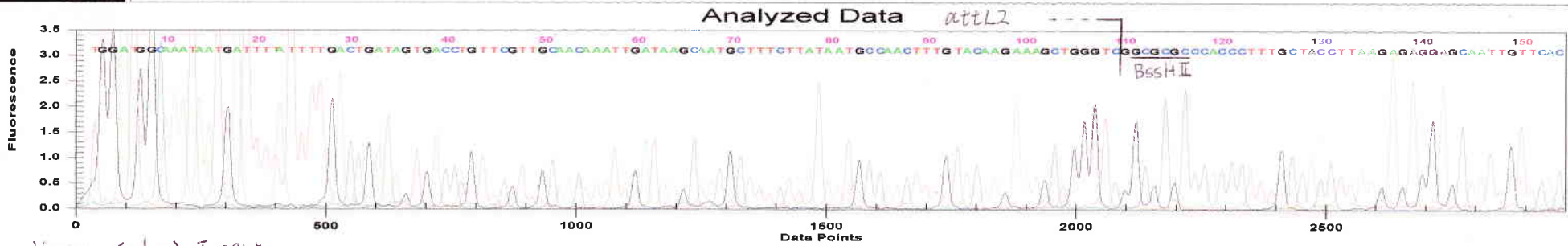




Project : GNP
Sample : W01A065A15_T7long.B12_11020410MJ
Result : W01A065A15_T7long.B12_11020410MJ

System : System 1

Operator : 1.110204.furu
Instrument : System 1 (Ver. 9.0.25)



[GENETYX : Homology Data]

Date : 2011.02.04

Query Sequence

File Name :
 Sequence Name : AK090673_CDS_(625..1383)
 Sequence Size : 759

Target Sequence

File Name : W01A065A15_M13.A12_11020410MJ
 Sequence Name : W01A065A15_M13.A12_11020410MJ
 Sequence Size : 519

Unit Size to Compare = 6

Pick up Location No. = 1

Query Range: 1 - 342

Sbjct Range: 178 - 519

342 bp, INT.Score: 1368, OPT.Score: 1368

Identity: 342 / 342 (100%)

Strand: Plus / Plus

Query	1	ATGCTGAAGA	TCCACCGCAG	CGACCCGCAG	CTGATCGTGC	AGCTGCGATT	CTGCGGGCGG	60
Sbjct	178	ATGCTGAAGA	TCCACCGCAG	CGACCCGCAG	CTGATCGTGC	AGCTGCGATT	CTGCGGGCGG	237
Query	61	CAGCCCTGTG	GCCGCTTCCT	CCGCGCCTAC	CGCGAGGGGG	CGCTGCGCGC	CGCGCTGCAG	120
Sbjct	238	CAGCCCTGTG	GCCGCTTCCT	CCGCGCCTAC	CGCGAGGGGG	CGCTGCGCGC	CGCGCTGCAG	297
Query	121	AGGAGCCTGG	CGGCCGCGCT	CGCCCAGCAC	TCGGTGCCGC	TGCAACTGGA	GCTGCGCGCC	180
Sbjct	298	AGGAGCCTGG	CGGCCGCGCT	CGCCCAGCAC	TCGGTGCCGC	TGCAACTGGA	GCTGCGCGCC	357
Query	181	GGCGCCGAGC	GGCTGGACGC	TTTGCTGGCG	GACGAGGAGC	GCTGTTTGAG	TTGCATCCTA	240
Sbjct	358	GGCGCCGAGC	GGCTGGACGC	TTTGCTGGCG	GACGAGGAGC	GCTGTTTGAG	TTGCATCCTA	417
Query	241	GCCCAGCAGC	CCGACCGGCT	CCGGGATGAA	GAAGTGGCTG	AGCTGGAGGA	TGCGCTGCGA	300
Sbjct	418	GCCCAGCAGC	CCGACCGGCT	CCGGGATGAA	GAAGTGGCTG	AGCTGGAGGA	TGCGCTGCGA	477
Query	301	AATCTGAAGT	GCGGCTCGGG	GGCCCGGGGT	GGCGACGGGG	AG	342	
Sbjct	478	AATCTGAAGT	GCGGCTCGGG	GGCCCGGGGT	GGCGACGGGG	AG	519	

[GENETYX : Homology Data]

Date : 2011.02.04

Query Sequence

File Name :
 Sequence Name : AK090673_CDS_(625..1383)
 Sequence Size : 759

Target Sequence

File Name : W01A065A15_T7long.B12_11020410MJ
 Sequence Name : W01A065A15_T7long.B12_11020410MJ (complement)
 Sequence Size : 680

Unit Size to Compare = 6

Pick up Location No. = 1

Query Range: 242 - 757

Sbjct Range: 3 - 518

516 bp, INT.Score: 2064, OPT.Score: 2064

Identity: 516 / 516 (100%)

Strand: Plus / Minus

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Query  242  CCCAGCAGCC  CGACCGGCTC  CGGGATGAAG  AACTGGCTGA  GCTGGAGGAT  GCGCTGCGAA  301
          |||
Sbjct   3  CCCAGCAGCC  CGACCGGCTC  CGGGATGAAG  AACTGGCTGA  GCTGGAGGAT  GCGCTGCGAA  62

Query  302  ATCTGAAGTG  CGGCTCGGGG  GCCCGGGGTG  GCGACGGGGA  GGTTCGCTTCG  GCCCCCTTGC  361
          |||
Sbjct  63  ATCTGAAGTG  CGGCTCGGGG  GCCCGGGGTG  GCGACGGGGA  GGTTCGCTTCG  GCCCCCTTGC  122

Query  362  AGCCCCCGGT  GCCCTCTCTG  TCGGAGGTGA  AGCCGCCGCC  GCCGCCGCCA  CCTGCCCAGA  421
          |||
Sbjct 123  AGCCCCCGGT  GCCCTCTCTG  TCGGAGGTGA  AGCCGCCGCC  GCCGCCGCCA  CCTGCCCAGA  182

Query  422  CTTTTCTGTT  CCAGGGTCAG  CCTGTAGTGA  ATCGGCCGCT  GAGCCTGAAG  GACCAACAGA  481
          |||
Sbjct 183  CTTTTCTGTT  CCAGGGTCAG  CCTGTAGTGA  ATCGGCCGCT  GAGCCTGAAG  GACCAACAGA  242

Query  482  CGTTCGCGCG  CTCTGTGGGT  CTCAAATGGC  GCAAGGTGGG  GCGCTCACTG  CAGCGAGGCT  541
          |||
Sbjct 243  CGTTCGCGCG  CTCTGTGGGT  CTCAAATGGC  GCAAGGTGGG  GCGCTCACTG  CAGCGAGGCT  302

Query  542  GCCGGGCGCT  GCGGGACCCG  GCGCTGGACT  CGCTGGCCTA  CGAGTACGAG  CGCGAGGGAC  601
          |||
Sbjct 303  GCCGGGCGCT  GCGGGACCCG  GCGCTGGACT  CGCTGGCCTA  CGAGTACGAG  CGCGAGGGAC  362

Query  602  TGTACGAGCA  GGCCTTCCAG  CTGCTGCGGC  GCTTCGTGCA  GGCCGAGGGC  CGCCGCGCCA  661
          |||
Sbjct 363  TGTACGAGCA  GGCCTTCCAG  CTGCTGCGGC  GCTTCGTGCA  GGCCGAGGGC  CGCCGCGCCA  422

Query  662  CGCTGCAGCG  CCTGGTGGAG  GCACTCGAGG  AGAACGAGCT  CACCAGCCTG  GCAGAGGACT  721
          |||
Sbjct 423  CGCTGCAGCG  CCTGGTGGAG  GCACTCGAGG  AGAACGAGCT  CACCAGCCTG  GCAGAGGACT  482

Query  722  TGCTGGGCCT  GACCGATCCC  AATGGCGGCC  TGGCCT  757
          |||
Sbjct 483  TGCTGGGCCT  GACCGATCCC  AATGGCGGCC  TGGCCT  518

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