

RIKEN clone ID: IRAL008L10

Vector : pOTB7

Gene	SSBP3		
Accession No.	BC003605.1	1372 bp	1..1372
	<i>CDS</i>	1107 bp	27..1133

● Plasmid DNA purification

Date : ~~100810~~ ¹⁰⁰⁸¹⁶ Culture : LB (25 ug/ml Chloramphenicol) 10 ml → 37°C O/N

Date : ~~100811~~ ¹⁰⁰⁸¹⁷ Purification : QIAGEN Miniprep kit → dH₂O 100 ul

● Digestion by restriction enzyme / Concentration calibration

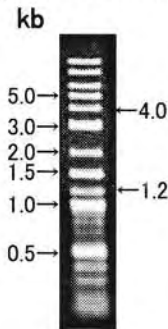
Date : ~~100811~~ ¹⁰⁰⁸¹⁷

DNA concentration (O.D.): 118.52 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 BC003605.1 >

1615, 613, 945 bp

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

Date : 100823 Shipped : 25 ng/ul, 40 ul

Final concentration: 25 ng/ul

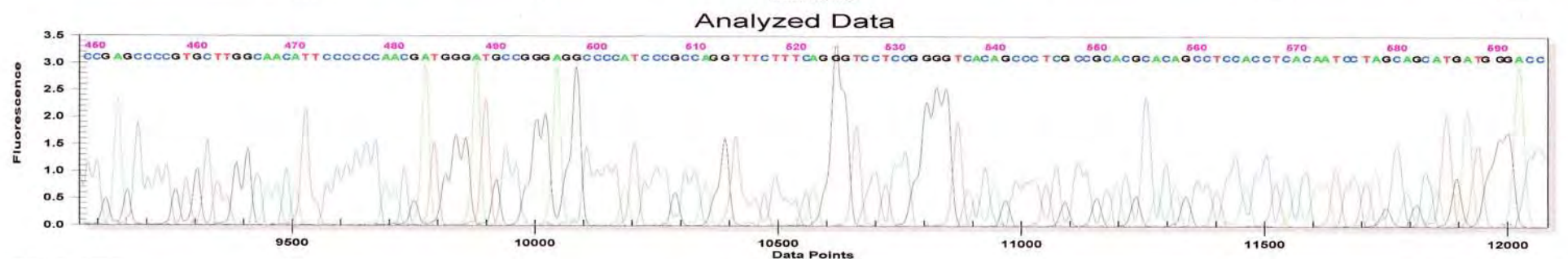
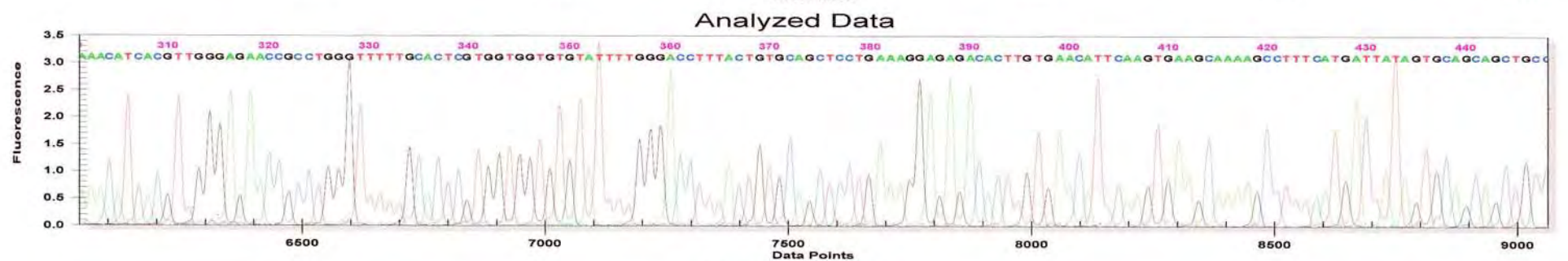
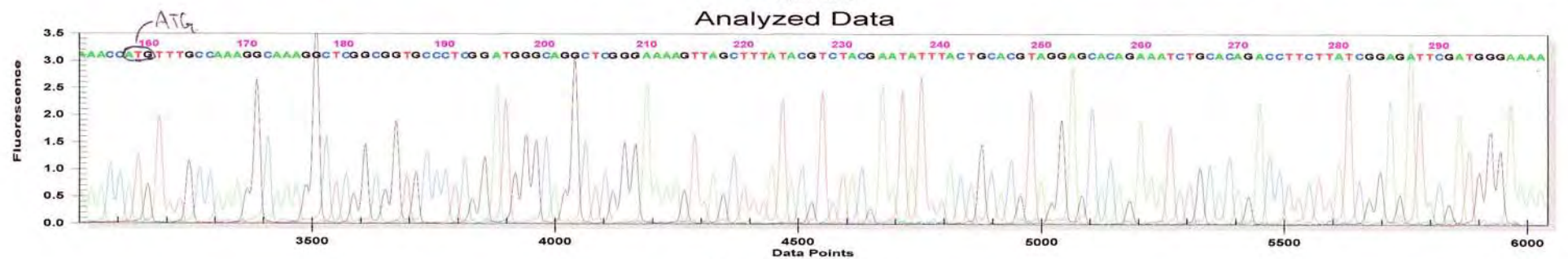
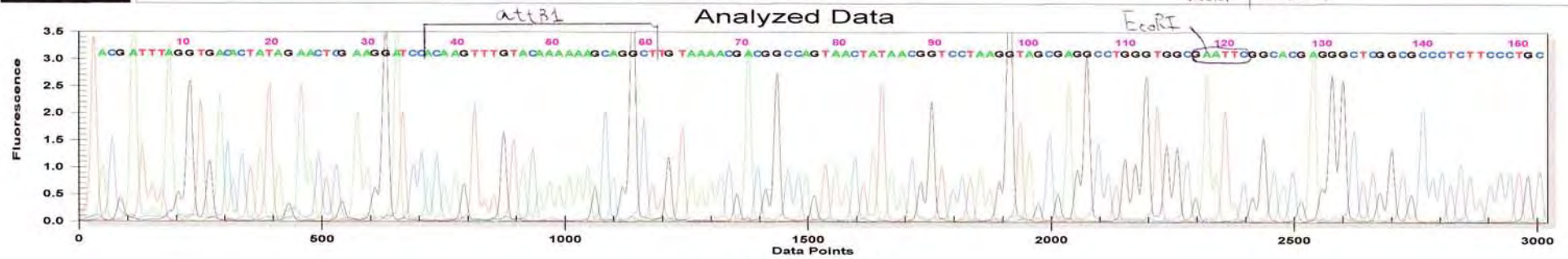
DNA (<u>118.52</u> ng/ul)	81 ul
10 × TE	384 ul
dH ₂ O	2646 ul
Total	3540 ul



Project : GNP
Sample : IRAL008L10_pOTB7_F_3.G10_10081812FM
Result : IRAL008L10_pOTB7_F_3.G10_10081812FM

System : CEQ System

Operator : 2.100818.furu
Instrument : CEQ System (Ver. 9.0.25)

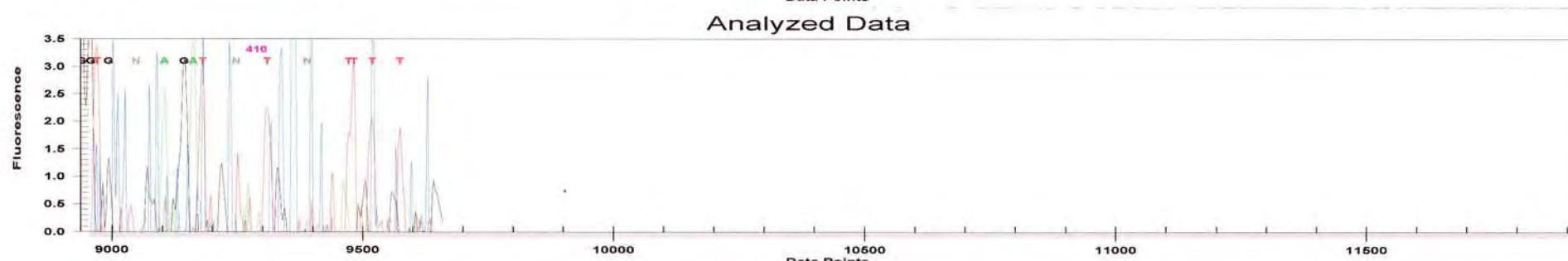
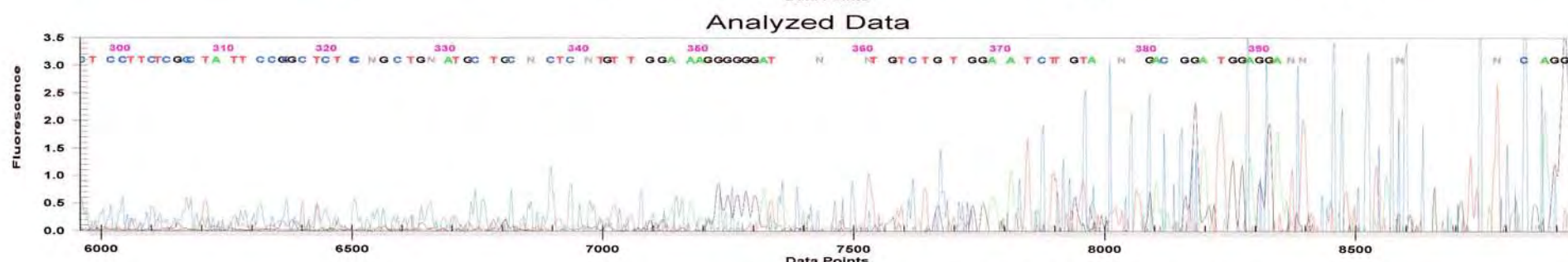
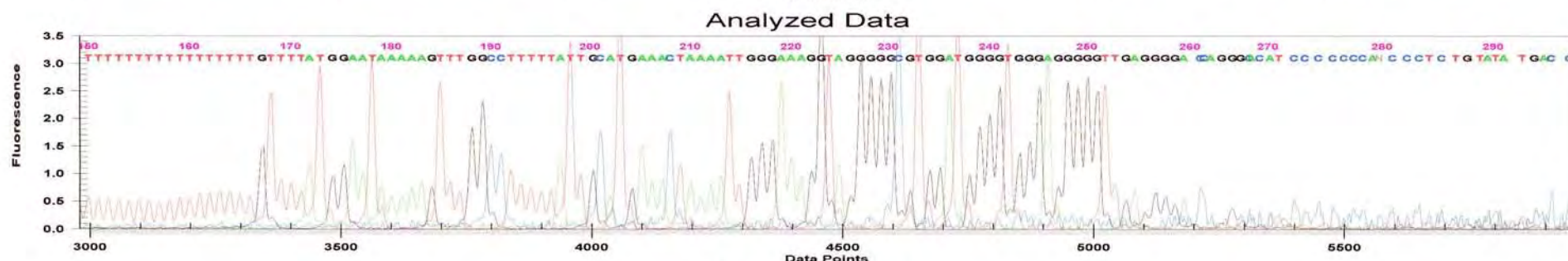
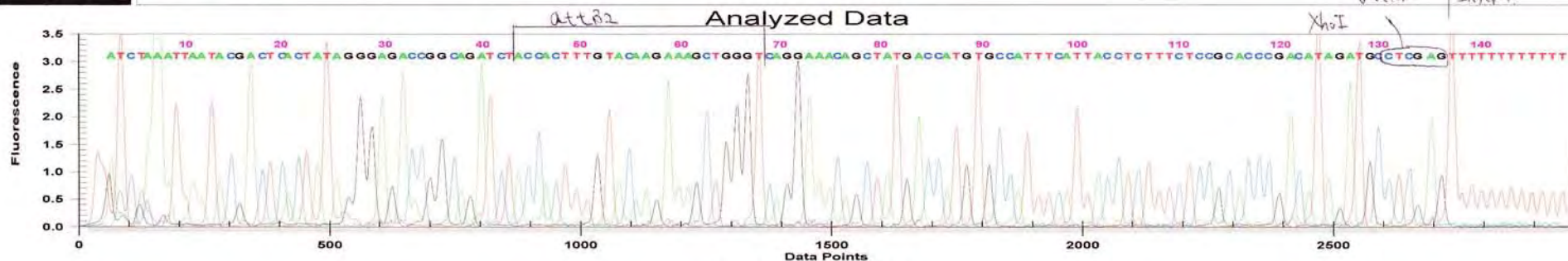




Project : GNP
Sample : IRAL008L10_pOTB7_R_3.H10_10081812FM
Result : IRAL008L10_pOTB7_R_3.H10_10081812FM

System : CEQ System

Operator : 2.100818.furu
Instrument : CEQ System (Ver. 9.0.25)



[GENETYX : Nucleotide Sequence Homology Data]

Date : 2010.08.23

1st Nucleotide Sequence

File Name : BC003605.1.gnu
Sequence Size : 1372

2nd Nucleotide Sequence

File Name : IRAL008L10_pOTB7_F_3.G10_10081812FM.fasta
Sequence Size : 721

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

[587 / 590 bp] INT/OPT.Score : < 2156/ 2332 >

1' GCTCGGCGCC CTCTTCCCTG CAAACCATGT TTGCCAAAGG CAAAGGCTCG
121" CGGCACGAGG GCTCGGCGCC CTCTTCCCTG CAAACCATGT TTGCCAAAGG CAAAGGCTCG
51' GCGGTGCCCT CGGATGGGCA GGCTCGGGAA AAGTTAGCTT TATACGTCTA CGAATATTTA
181" GCGGTGCCCT CGGATGGGCA GGCTCGGGAA AAGTTAGCTT TATACGTCTA CGAATATTTA
111' CTGCACGTAG GAGCACAGAA ATCTGCACAG ACCTTCTTAT CGGAGATTGC ATGGGAAAAA
241" CTGCACGTAG GAGCACAGAA ATCTGCACAG ACCTTCTTAT CGGAGATTGC ATGGGAAAAA
171' AACATCACGT TGGGAGAACC GCCTGGGTTT TTGCACTCGT GGTGGTGTGT ATTTTGGGAC
301" AACATCACGT TGGGAGAACC GCCTGGGTTT TTGCACTCGT GGTGGTGTGT ATTTTGGGAC
231' CTTTACTGTG CAGCTCCTGA AAGGAGAGAC ACTTGTGAAC ATTC AAGTGA AGCAAAAGCC
361" CTTTACTGTG CAGCTCCTGA AAGGAGAGAC ACTTGTGAAC ATTC AAGTGA AGCAAAAGCC
291' TTTCATGATT ATAGTGCAGC AGCTGCCCGG AGCCCGGTGC TTGGCAACAT TCCCCCAAC
421" TTTCATGATT ATAGTGCAGC AGCTGCCCGG AGCCCGGTGC TTGGCAACAT TCCCCCAAC
351' GATGGGATGC CGGGAGGCC CATCCGCCA GGTTCCTTC AGGCTCCTCC GGGGTACAG
481" GATGGGATGC CGGGAGGCC CATCCGCCA GGTTCCTTC AGGCTCCTCC GGGGTACAG
411' CCCTCGCGC ACGCACAGCC TCCAGCTCAC AATCCTAGCA GCATGATGG ACCCCACAGT
541" CCCTCGCGC ACGCACAGCC TCCAGCTCAC AATCCTAGCA GCATGATGG ACCCCACAGT
471' CAGCCTCCGG GAGGAGTTC TGGGACACAG CCATTGCTGC CCAATTCAT GGATCCCACA
601" CAGCCTCCGG GAGGAGTTC TGGGACACAG CCATTGCTGC CCAATTCAT GGATCCCACA
531' CGACAAC-AA GCCACCCCA ACATGGGAGG ATCAATGCAG AGAATGAACC CTCCCCGAGG
661" CGACAACAAA GCCACCCCC ACATGGGAGG ATCCATGCAG AGAATGAACC CTCCCCGAGG
590' CATGGGGCCC ATGGGTCCC GCCACAGAA TTACGGCAGC GGCATGAGAC CACCACCCAA
721" G

1st Nucleotide Sequence

File Name : BC003605.1.gnu
Sequence Size : 1372

2nd Nucleotide Sequence

File Name : IRAL008L10_pOTB7_R_3.H10_10081812FM.fasta (Complementary)
Sequence Size : 415

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

[223 / 293 bp] INT/OPT.Score : < 496/ 627 >

1021' GTGGCATTAG CAATCCTCCA GGCACCCCTC GAGATGACGG CGAGCTAGGA GGGAACTTCC
1" AAAANANATC
1081' TCCACTCCTT TCAGAACGAC AATTATTCTC CAAGCATGAC GATGAGTGTG TGATCCCCC
11" TNCACCCCTG NNNNTCCTCC ATCCGTCNTA CAAG-ATTCC ACAGA---CA NNATCCCCC
1141' TTCTCCGAGA CGCTGAGAGA GCASGCATTG CAGGCGGGAA GATGCCAGAA ATTATGCAAG
67" TT-TCCAACA NG----AGN GCA-GCA-TN CA-GCNGG-A GA-GCGCGA A-TAGGCGAG
1201' AAGTGAGGTG TCATTATCCA GGAGCTGGTG GGGAGGCAT CTCCCTGCTC CCCTCAACCC
115" AAG-GAGG-G TCA-TATACA -GAG--GGNT GGGGGGGATG TGCCCTGGTC CCCTCAACCC
1261' CCTCCACCC CATCCACGCC CCTACCTTT CCAATTTTA GTTTCATGCA ATAAAAAGGC
169" CCTCCACCC CATCCACGCC CCTACCTTT CCAATTTTA GTTTCATGCA ATAAAAAGGC
1321' CAACTTTT ATTCCATAAA ACAAAAAAAA AAAAAAAA AAAAAAAA AA
229" CAACTTTT ATTCCATAAA ACAAAAAAAA AAAAAAAA AAAAAAAA AACTCGAGGC