

RIKEN clone ID: **IRAL016C17**

Vector : pDNR-LIB

Gene	RPA3		
Accession No.	BC005264.1	516 bp	1..516
	<i>CDS</i>	366 bp	46..411

● Plasmid DNA purification

Date : 100809 Culture : LB (25 ug/ml Chloramphenicol) 3 ml → 37°C O/NDate : 100810 Purification : QIAGEN Miniprep kit → dH₂O 100 ul

● Digestion by restriction enzyme / Concentration calibration

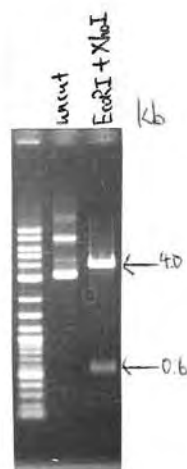
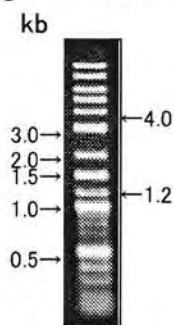
Date : 100810

DNA concentration (O.D.): 84.22 ng/ul

DNA	1 ul
Enzyme (EcoRI+XhoI)	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 BC005264.1>3919, 549bp

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

Date : 100819

Shipped : 25 ng/ul, 40 ul

Final concentration: 25 ng/ul

DNA (<u>84.22</u> ng/ul)	<u>86</u> ul
10 × TE	<u>29.0</u> ul
dH ₂ O	<u>174.7</u> ul
Total	<u>289.7</u> ul



Project : GNP

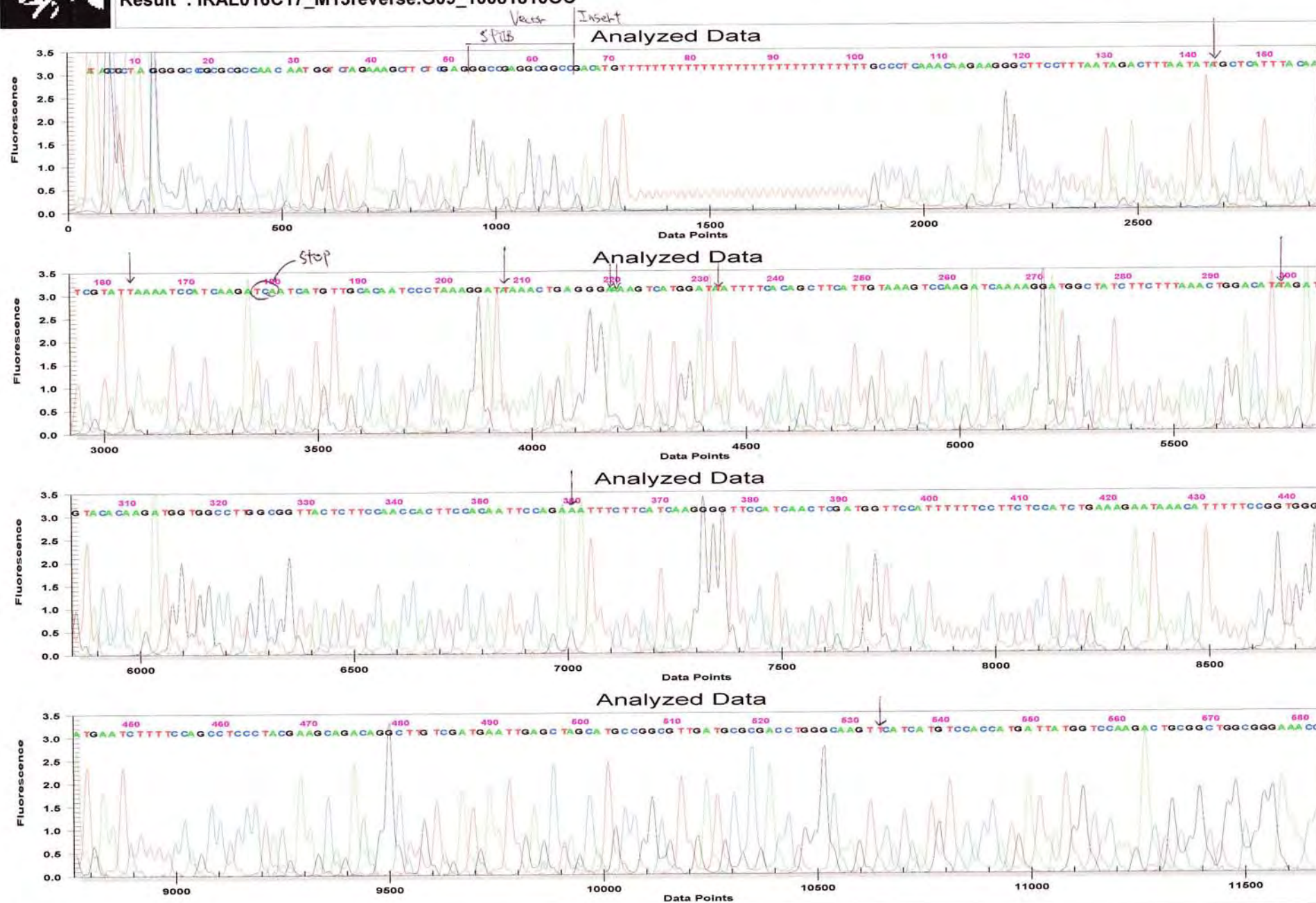
Sample : IRAL016C17_M13reverse.G09_10081810OC

Result : IRAL016C17_M13reverse.G09_10081810OC

System : CEQ System

Operator : 2.100818.furu

Instrument : CEQ System (Ver. 9.0.25)



| GENETYX : Nucleotide Sequence Homology Data |

Date : 2010.08.18

1st Nucleotide Sequence

File Name : BC005264.1.gnu
Sequence Size : 516

2nd Nucleotide Sequence

File Name : IRAL016C17_T7.G03_10081114XC.fasta
Sequence Size : 743Unit Size to Compare = 6
Pick up Location No. = 1

| 513 / 521 bp | INT/OPT.Score : < 1116/ 1987 >

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1'          AGTCG TCCGTGGGTT TCCGCGCAGC CGCAGTCTTG GACCATAATC
*****
121' CCATTACGGC CGGGGAGTCG TCCGTGGGTT TCCGCGCAGC CGCAGTCTTG GACCATAATC

46' ATGGTGGACA TGATGGACTT GCCCAGGTCTG CGCATCAACG CCGGCATGCT AGCTCAATTC
*****
181' ATGGTGGACA TGATGGACTT GCCCAGGTCTG CGCATCAACG CCGGCATGCT AGCTCAATTC

106' ATCGACAAGC CTGTCTGCTT CGTAGGGAGG CTGGAAAAGA TTCATCCAC CGGAAAAATG
*****
241' ATCGACAAGC CTGTCTGCTT CGTAGGGAGG CTGGAAAAGA TTCATCCAC CGGAAAAATG

166' TTTATTCTTT CAGATGSAGA AGGAAAAAAT GGAACCATCG AGTTGATGGA ACCCCTTGAT
*****
301' TTTATTCTTT CAGATGSAGA AGGAAAAAAT GGAACCATCG AGTTGATGGA ACCCCTTGAT

226' GAAGAAATCT CTGGAATTGT GGAAGTGGTT GGAAGAGTAA CCGCCAAGGC CA-CCATCTT
*****
361' GAAGAAATCT CTGGAATTGT GGAAGTGGTT GGAAGAGTAA CCGCCAAGGC CACCCATCTT

285' GTGTACATCT TATGTCCAGT TTAAAGAAGA TAGCCAT-CC TTTTGATCTT GGACTTTACA
*****
421' GTGTACATCT TATGTCCAGT TTAAAGAAGA TAGCCATCCC TTTTGATCTT GGACTTTACA

344' ATGAAGCTGT GAAAATTATC CATGACTT-- CCCTCAGTTT TAT-CCTTTA -GGGATTGTG
*****
481' ATGAAGCTGT GAAAATTATC CATGACTTCC CCCTCAGTTT TATCCCTTTA GGGGATTGTG

400' CAACATGATT GATCTTGATG GATTTTCATA CGATTGTAAA TGAGCTATAT TAAAGTCTAT
*****
541' CAACATGATT GATCTTGATG GATTTTCATA CGATTGTAAA TGAGCTATAT TAAAGTCTAT

460' TAAAGGAAGC CCTTCTTGTT TGAGGGCAAA AAAAAAAAAA AAAAAAAAAA AAAAAAA
*****
601' TAAAGGAAGC CCTTCTGTTT TGAGGGCAAA AAAAAAAAAA AAAAAAAAAA AAAAAACCAT

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1st Nucleotide Sequence

File Name : BC005264.1.gnu
Sequence Size : 516

2nd Nucleotide Sequence

File Name : IRAL016C17_M13reverse.G09_10081810OC.fasta (Complementary)
Sequence Size : 744Unit Size to Compare = 6
Pick up Location No. = 1

| 513 / 522 bp | INT/OPT.Score : < 1164/ 1982 >

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1'          AGTCGTCC GTGGGTTTCC CGCCAGCCGC
*****
121' TATGCCCCGG AATTCGGCCA TTACGGCCGG GGAGTCGTCC GTGGGTTTCC CGCCAGCCGC

29' AGTCTTGGAC CATAATCATG GTGSACATGA TGGACTTGCC CAGGTCGCGC ATCAACGCCG
*****
181' AGTCTTGGAC CATAATCATG GTGSACATGA TGAAC TTGCC CAGGTCGCGC ATCAACGCCG

89' GCATGCTAGC TCAATTATC GACAAGCCTG TCTGCTTCGT AGGGAGGCTG GAAAAGATTC
*****
241' GCATGCTAGC TCAATTATC GACAAGCCTG TCTGCTTCGT AGGGAGGCTG GAAAAGATTC

149' ATCCCACCGG AAAAAATGTTT ATTCTTTCAG ATGGAGAAGG AAAAAATGGA ACCATCGAGT
*****
301' ATCCCACCGG AAAAAATGTTT ATTCTTTCAG ATGGAGAAGG AAAAAATGGA ACCATCGAGT

209' TGATGGAACC CCTTGATGAA GAAATCTCTG GAATTGTGGA AGTGGTTGGA AGAGTAACCG
*****
361' TGATGGAACC CCTTGATGAA GAAATTTCTG GAATTGTGGA AGTGGTTGGA AGAGTAACCG

269' CCAAGGCCAC CATCTTGTGT ACATCT-TAT GTCCAGTTTA AAGAAGATAG CCATCCTTTT
*****
421' CCAAGGCCAC CATCTTGTGT ACATCTATAT GTCCAGTTTA AAGAAGATAG CCATCCTTTT

328' GATCTTGGAC TTTACAATGA AGCTGTGAAA AT-TATCCAT GAC--TTCCC TCAGTTT-TA
*****
481' GATCTTGGAC TTTACAATGA AGCTGTGAAA ATATATCCAT GACTTTTCCC TCAGTTTATA

384' TCCTTTAGGG ATTGTGCAAC ATGATTGATC TTGATGGATT TTCATACGAT TGTAAATGAG
*****
541' TCCTTTAGGG ATTGTGCAAC ATGATTGATC TTGATGGATT TTAATACGAT TGTAAATGAG

444' C-TATATTAA AGTCTATTAA AGGAAGCCCT TCTTGTTTGA GGGCAAAAAA AAAAAAAAAA
*****
601' CATATATTAA AGTCTATTAA AGGAAGCCCT TCTTGTTTGA GGGCAAAAAA AAAAAAAAAA

503' AAAAAAAAAA AAAA
*****
661' AAAAAAAAAA AAAACATGTC GGCCGCTCG GCCTCGAGA AGCTTTCTAG ACCATTGTTG

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