

RIKEN clone ID: IRAK020H22

Vector : pCMV-SPORT6

●プラスミド抽出

作業日: 100331 培養方法: LB (100 ug/ml Ampicillin) 3 ml →37°C O/N

作業日: 100401 抽出方法: QIAGEN Miniprep kit→dH₂O 100 ul

●構造確認・濃度測定

作業日: 100401

DNAの濃度(O.D.): 74.53 ng/ul

DNA	1.5	ul

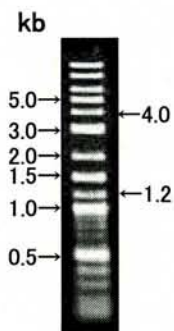
Enzyme (EcoRI+XhoI)	0.5+0.5	ul

Buffer H	1	ul

dH ₂ O	6.5	ul
=====		
Total	10	ul

電気泳動: 1% Agarose gel, 1 × TAE Buffer

使用marker: 2-Log DNA Ladder (NEB#N3200L)



<予想サイズ> BC01845.1 2y

1132, 4339 bp

●濃度調製

作業日: 100407

最終濃度: 25 ng/ul

DNA (74.53 ng/ul)	84	ul

10 × TE	25	ul

dH ₂ O	141.38	ul
=====		
Total	250.42	ul

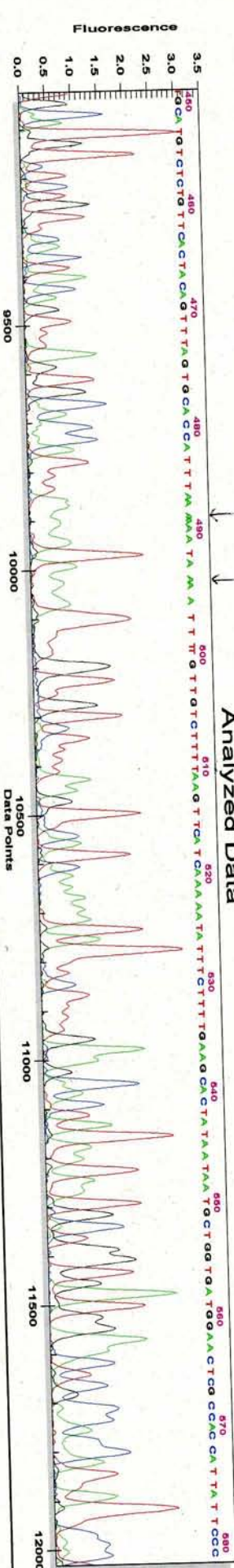
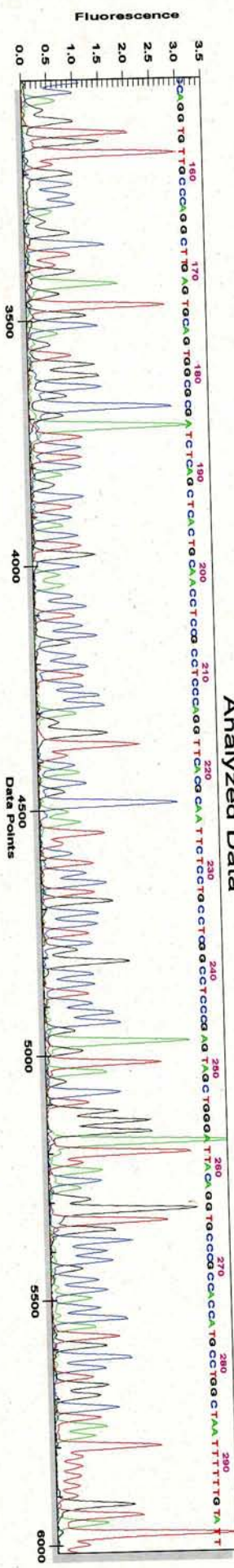
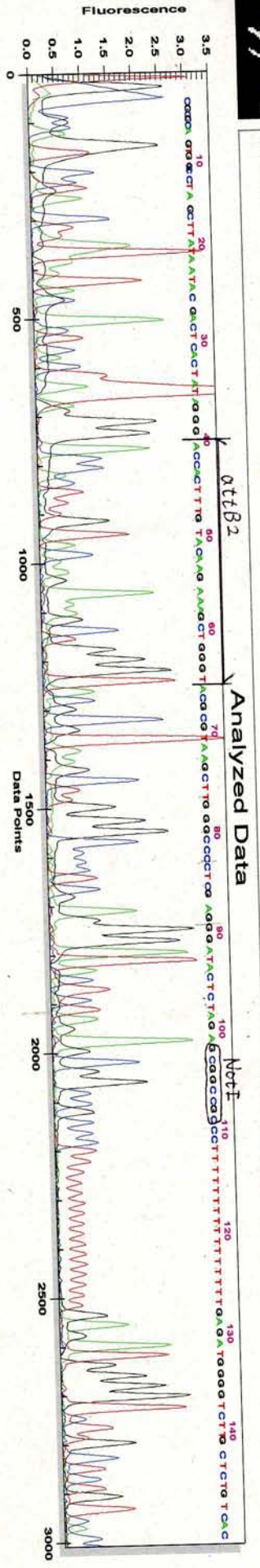


Project : GNP
Sample : IRAK020H22_M13.A03_10040510NC
Result : IRAK020H22_M13.A03_10040510NC

System : CEQ System

Operator : 3.100405.furu
Instrument : CEQ System (Ver. 9.0.25)

Vector Insert



[GENETYX : Nucleotide Sequence Homology Data]

Date : 2010.04.07

1st Nucleotide Sequence
File Name : BC018145.1.gnu
Sequence Size : 1076

2nd Nucleotide Sequence
File Name : IRAK020H22_Reverse2_B03_10040510NC.fasta
Sequence Size : 619

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

[534 / 539 bp] INT/OPT.Score : < 1580/ 2094 >

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1'
61' ATGTGTGACC CACGGCTCG AGAAGCTTGA GGGCACAGAGT CCGGTCCTGA GACGAGGTCC
    *
41' TCAGCCAGCA GAGCCAGCTT CCTTATGAGC ACCGTGGGTT TATTTGATTT TCCTACACCA
    *
121' TCAGCCAGCA GAGCCAGCTT CCTTATGAGC ACCGTGGGTT TATTTGATTT TCCTACACCA
    *
101' CTGACCCGAA TATGCCCGGC GCCATGGGGA CTCGGGCTTT GGGAGAAAGT GACGTTGTTA
    *
181' CTGACCCGAA TATGCCCGGC GCCATGGGGA CTCGGGCTTT GGGAGAAAGT GACGTTGTTA
    *
161' TCCCCAGGAA TAGTGTGAC TCCGGTCCAG ATGGCAGGCA AGAAGGACTA CCTCCTACTG
    *
241' TCCCCAGGAA TAGTGTGAC TCCGGTCCAG ATGGCAGGCA AGAAGGACTA CCTCCTACTG
    *
221' CTTTCCTTGG ATGAGAATGA ACTCGAAGAG CAGTTTGTGA AAGGACACGG TCACAGGGGGC
    *
301' CTTTCCTTGG ATGAGAATGA ACTCGAAGAG CAGTTTGTGA AAGGACACGG TCACAGGGGGC
    *
281' CAGGCAACCA ACAAAAACCAG CAACTGCGTG GTGCTGAAGC ACATCCCTTC AGGCATCGTT
    *
361' CAGGCAACCA ACAAAAACCAG CAACTGCGTG GTGCTGAAGC ACATCCCTTC AGGCATCGTT
    *
341' GTAAGTGGC ATCAGACAAG ATCAGTTGAT CAGAACAGAA AGCTAGCTCG G--AAAATCC
    *
421' GTAAGTGGC ATCAGACAAG ATCAGTTGAT CAGAACAGAA AGCTAGCTCG GAAAATTC
    *
399' T-AC-AAAAG AAGTAGATG TTTTCTACAA TGGTGAAGC AGTCCCTTTC ACAAAAGAAA
    *
481' TAACAAGAG AAGTAGATG TTTTCTACAA TGGTGAAGC AGTCCCTTTC ACAAAAGAAA
    *
457' ACGAAGAGC GGAAGAAAA AACAAAGAA GAAAAAAGA GCAAAAGAAA CCTTGAAAA
    *
541' ACGAAGAGC GGAAGAAAA AACAAAGAA GAAAAAAGA GCAAAAGAAA CCTTGAAAA
    *
517' AAAGAAGCTA CTTAAAGAAC TGTGGAGTC AAGTAAAAAG GTCCACTGAG AAAAGATTA
    *
601' AAAGAAGCTA CTTAAAGAAC

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1st Nucleotide Sequence
File Name : BC018145.1.gnu
Sequence Size : 1076

2nd Nucleotide Sequence
File Name : IRAK020H22_M13.A03_10040510NC.fasta (Complementary)
Sequence Size : 617

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

[499 / 506 bp] INT/OPT.Score : < 1252/ 1946 >

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541' GGAGTCAAGT AAAAAGTCC ACTGAGAAAA GAATTAGAA TTCCAACTGA CAGAACTGTC
    *
1"
601' CAGAAGCTCC CAGGAAATTA TGGTGGCGAG TTCATCACCC AGCATTAATTA TAGTGTCTTA
    *
26' CAGAACTCC CAGGAAATTA TGGTGGCGAG TTCATCACCC AGCATTAATTA TAGTGTCTTA
    *
661' AAAGAAATAT TTTTGATGAA CTTAAAGAAC AAC--AAATT TA--TTTAA ATGTGTGACT
    *
86' AAAGAAATAT TTTTGATGAA CTTAAAGAAC AACAAATTT TATTTTTPAA ATGTGTGACT
    *
716' AAACCTAGT GACAGAGAC ATGCATGATT CAGAAATPAA ACTCGGCC-G GGCACGGTGG
    *
146' AAACCTAGT GACAGAGAC ATGCATGATT CAGAAATPAA ACTCGGCCGG GGCACGGTGG
    *
775' ACGGTGCTC ACATCTGTA TCCGACACT TTGGGAGGCC GAGGGGGGGG GATCACTTGA
    *
206' ACGGTGCTC ACATCTGTA TCCGACACT TTGGGAGGCC GAGGGGGGGG GATCACTTGA
    *
835' GGTGAGAGT TTGAGACAG CTTGGGCCAAC ATGGTGAAGC CCCGTCTTA CTTAAATATAC
    *
266' GGTGAGAGT TTGAGACAG CTTGGGCCAAC ATGGTGAAGC CCCGTCTTA CTTAAATATAC
    *
895' AAAAATTTAG CCAGGCATGG TGGCGGGCAC CTGTAAATCC AGCTACTCGG GAGGCCGAGG
    *
326' AAAAATTTAG CCAGGCATGG TGGCGGGCAC CTGTAAATCC AGCTACTCGG GAGGCCGAGG
    *
955' CAGGAAATT GCGTAAACT GGGAGGGGGA GGTTCACAGT AGCTGAGATC GGGCCACTGC
    *
386' CAGGAAATT GCGTAAACT GGGAGGGGGA GGTTCACAGT AGCTGAGATC GGGCCACTGC
    *
1015' ACTCAAGCTT GGGCAACAC TGGGTGACAG AGCAAGACC CACTCATAA AAAAAAAAA
    *
446' ACTCAAGCTT GGGCAACAC TGGGTGACAG AGCAAGACC CACTCATAA AAAAAAAAA
    *
1075' AA
    *
506' AAGGGGGCC GCTCTAGAT ATCCCTCGAG GGGCCCAAGC TTAGCGGTAC CCAGCTTCT

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