

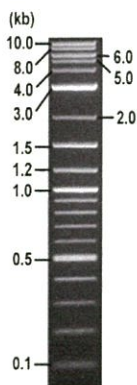


RIKEN DNA BANK

clone name : pCY

- Clone ID : RDB_03031
- Lot : 17446_A9F3
- DNA Concentration : 25 nanogram/microliter
- Volume : 40 microliter
- Form : DNA solution in TE buffer
- Host : DH5 alpha
- Culture : LB medium
- Antibiotics : 100 microgram/ml Ampicillin
- Purification : QIAGEN QIAprep Spin Miniprep kit
- Digestion by restriction enzyme

1 kb Plus DNA Ladder
(NEB#N3200L),
250 ng/well



Electrophoresis : 100 nanogram DNA per lane ; 1% agarose gel , 1 x TAE Buffer

Restriction enzyme	Expected size of fragment
<u>ApaI</u>	<u>7.8</u> kbp
<u>BamHI</u>	<u>5.1, 2.7</u> kbp
<u>PstI</u>	<u>6.8, 1.0</u> kbp
	kbp

● Confirmation of the insertion sequence

Sequence name	Primer name	Sequence name	Primer name
Sequence - A	pUC-CAPbs_up_F	Sequence - E	Jcsp_f4
Sequence - B	pUC-M13_-100	Sequence - F	-
Sequence - C	JCsp_f1	Sequence - G	-
Sequence - D	JCsp_R2	Sequence - H	-

APPROVED BY :



S/N G:103 A:123 T:100 C:111

03031_12319_A9F3_pUC-CAPbs_up_F

Jun 07.2019 02:44PM, JST

KB bcp

KB_3500_POP7_BDTV3.mob

Jun 07.2019 03:24PM, JST

KB 1.4.1.8 Cap:1

Pts 1421 to 13418 PK1 Loc:1398

Spacing:11.65 Pts/Panel1350

Version 6.0 HISQV Bases: 1021

Plate Name: 20190607_mix2

AAAGTTGAGGATGTTTCTTGCCTTATGGGCATGTACTTAAACTTCAAGGAAAAACCACCTGGCAATGCCAAAAAATGTGAAAAAAGAAAGATCAGCCAAATCACCTTAAACAAT

676 685 694 703 712 721 730 739 748 757 766 775
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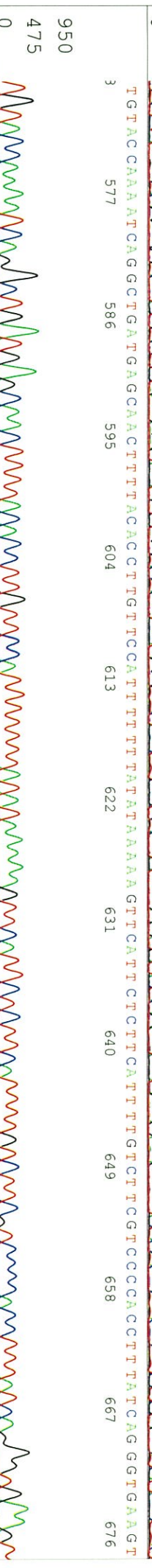
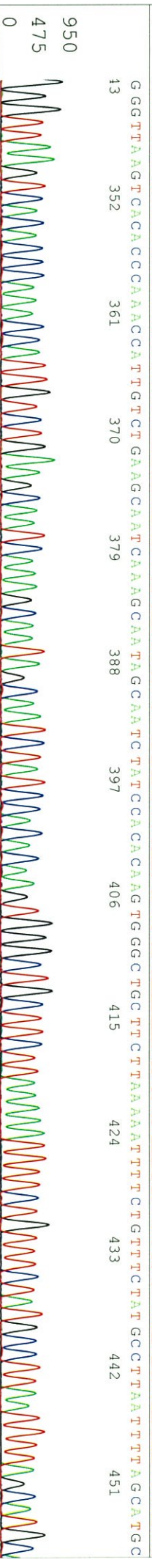
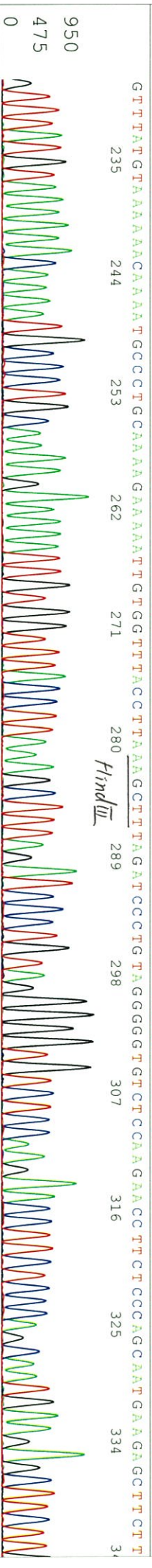
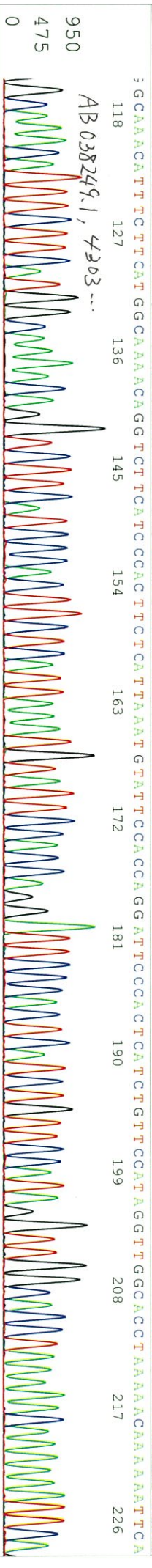
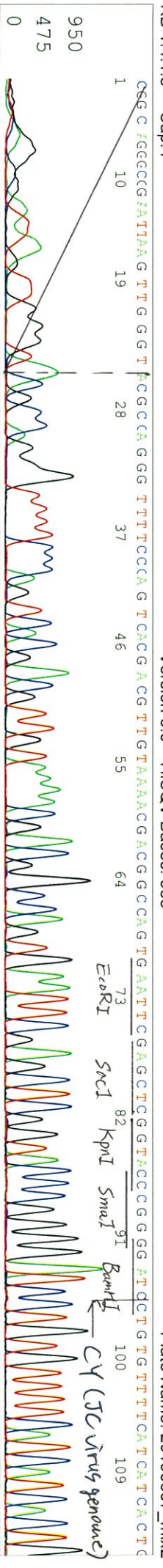
784 793 802 811 820 829 838 847 856 865 874 883
GTTCCATATGAC CAGAGAGAAAAAGTTAGTTGAAA GGTAAATTTTCTTGTATAAAAATGGGACACATGGC CACATGG CAAATGGCTTTTAAAG

892 901 910 919 928 937 946 955 964 973 982
NdeI
3541...
AB...
CY
JTC virus genome

991 1000 1009 1018 1027 1036 1045 1054 1063 1072
3CATAATGGGCTGGCTGGATTCAGATTGATGAGTTCTAAAAATGGCAATTCATTAAT

1081 1090 1099 1108 1117 1126 1135
AAACATCAAAAAAAGTAACTGGCTAAATCCAAAGCAATAAAGTTGCTAAAAATCTAATTAAG

1144 1153
CTGGCAFGGCTGTATACCT



TCTTTGCATT TTTTCAGATAAGCTTTTCTCATGACAGAAATGTTTCCCCATGGCAGATCTATCCAAAGCCCTAA TAAATCCATG AAGCTCCATGGATTCCTCCCTATTCA
 685 694 HindIII 703 712 721 730 BglII 739 748 757 SacI 766 775
 7

GCACTTTGTCCATT TTTGCTTGTGCTTTTGTAGCAAAAAATTAGTGCAAAAAGGAAAACCAAGGAATTCTCCCTGGCCCTCC TAAAAGCC TCCACGCCCTAC TAC
 84 793 802 811 820 829 838 847 856 865 874 883

TTCTGAGTAAAGCTTTGGAGGCCGGAAGCCATCGGCC TCGGCC TCGTATATATAAAAAAAAGGGAA EGTA GGGGAGG AGCTGGCTTAAAAC TGGGATGGGCTGCTC
 892 HindIII 901 910 AB- 919 928 937 946 955 964 973 982
 5/20 AB 038248.1, 1~29
 ← CY (JC Virus Genome)

AGCC AAGCATGAGGCTCATACCTAACCCTAAGGGAGCC AA CCAAGCTGACAGCCAGAGGGAGGCCCTGCTGCATGCTGACCTAC TGA GTG
 991 1000 1009 1018 1027 1036 1045 1054 1063 1072

AAA C C C T C C A T A G T T C T T T A T T C A C A G T T A A C G T T G G G A A G T T G A A A G C A G C
 1081 1090 1099 1108 1117 1126

C C A G G G A C A A T G T
 1135



S/N G:38 A:55 T:37 C:37 primer name C : JCsp_f1

03031_12319_A9F3_JCsp_f1

Jun 17,2019 03:27PM, JST

KB.bcp 5'-CTTTTAGGTTGTACGGGAC-3'

KB_3500_POP7_BDTV3.mob

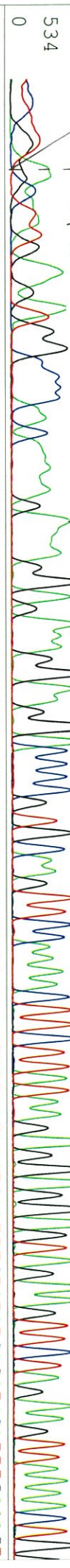
Jun 17,2019 03:53PM, JST

KB 1.4.1.8 Cap:1 1449

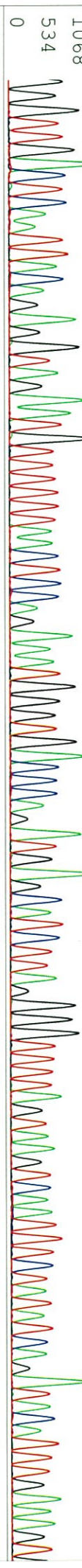
Pis 1407 to 13066 Pk1 Loc:1384

Spacing:1.1.57 Pts/Panel1350

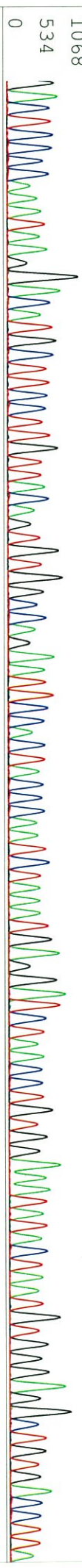
Version 6.0 HiSQV Bases: 935



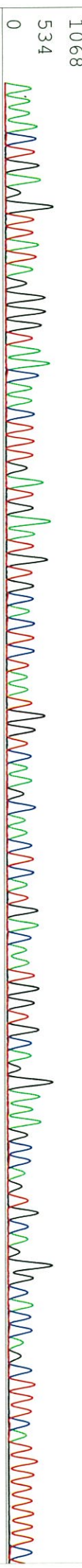
1 TCC TGG TGG CCAATATG AAG ATG GC CCCAA CAAAA G AAAA G GAG AAAAG AAG GACCCCG TGC AAGTTT CCAAAA CTTCTTATA TAA GAGGAG GAGTAA GAA GTTCTAGAA GTTAAACTG



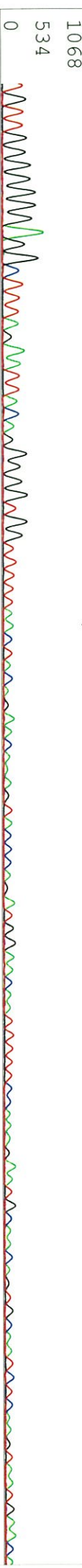
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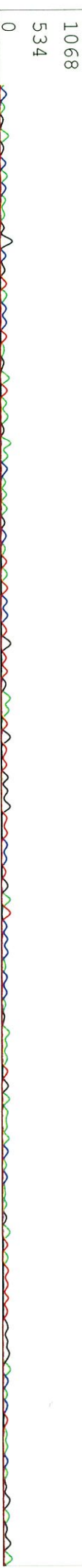
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AAAAC TGAAGT TATAGGGGTAA CAACTTTGATGAATGTGCACTCTAATGGTCAA GCAACTCATG ACAA TGTGCAGAAA GCCAGTGCAGGGCACCAGCTTTCATTTTTC



TGTTGGGGGGGAGGCTTTA GAATTACAGGGGGTGTTTTAACTA CA GAA CAAA GTTACC CA GATGGAACAA TTTTCC PAAAGAA TGCACA CA GTAAATGAAC



VCAGAGCACAAAGCGTACC TAGATAA GAA CAAA GCATATCTCTGTGAA TGTGGGTTCCTGATCCC ACCCAG AAAATGAAAA CACAA GATATTTTGGACAC TAAACAGAGGA

GAATAATGTTCCCTCCAGTTCTTCCATATAACAAA_CACTGCCCAAGAACAGTGGCTGCTTGAATGATTTGGGTGGGCCCACTTTGCAAAAGGTGACAACTTGATTTTGCTGCTT

2152C AB- 2162

CY (JC virus genome)

TTGGATGTTTGTGGCAATGTTTACTAACAGATCTGGTTCCCAAGAGTGGAGAGGACTGTC CAGATAATTTTAAAGTTCAGCTAAGAAAAAEGAGGTTAAAFCCCC

1068
534
0

TAAACCAATTTCTTTCCTTCTTACTAATGATTTAAATAA(A G A AG GAA CCCC T A AATTTGATG GG CC AG C CT A T GT FT GGCCA TG GAATGCCCT CA GGT A GA EGGA GGC

TTA G AG TTT TTT GIAGGGG A AA

1068
534
0

1068
534
0

1068
534
0

TAAAGCCCTCCCCCAACAGAAAAAATGAAAGCTGGTGCCCTGGCACTGGGCTTCCCTGCCACCA TTGTCATGAGTTGGCTTGACCATTAGAGTGCACATTCATCAAAAGT
 676 685 694 703 712 721 730 739 748 757 766 775
 /9/1267

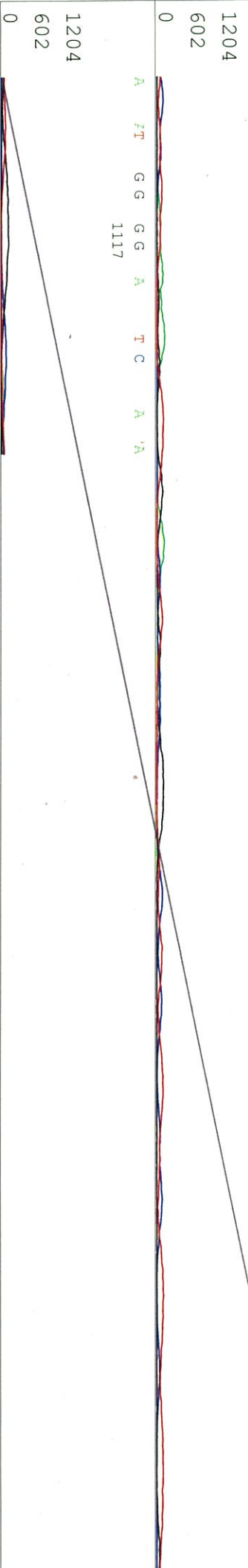
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 784 793 802 811 820 829 838 847 856 865 874 883
 /8/13A /8/5A EcoRI

CTGTAACAAAGGAA GCAATGTCCTTATTTGGGGAGTCCACTTTC AAAATGTTATCTGATAATAGAAATGAC TTACTAAACCCCTAA GATGCTCATCTGGC
 33 892 901 910 919 928 937 946 955 964 973

TCACCCAATTTCTGGAGTTAAAAA CATTCTACTGTATTTGAGTCA CCC CAGTTTTTACCTCTAGAA C TGTACTGCTCC T
 982 991 1000 1009 1018 1027 1036 1045 1054
 AB-1
 (599- → CY (JC virus genome))

TCTCTATATAGAGTTTGGAACTTGGCACTGGGTTCTCATCGATTA GCGATA GCGATTC
 1063 1072 1081 1090 1099 1108

AATGGGATCTAA
 1117



S/N G:267 A:348 T:290 C:318

03031_12319_A9F3_JCsp_f4

Jun 17, 2019 03:27PM, JST

KB bcp

primer name E : Jcsp_f4

KB_3500_POP7_BDTV3.mob

Jun 17, 2019 03:53PM, JST

KB 1.4.1.8 Cap:13

5-CATGACGATCTATCAAGCC-3'

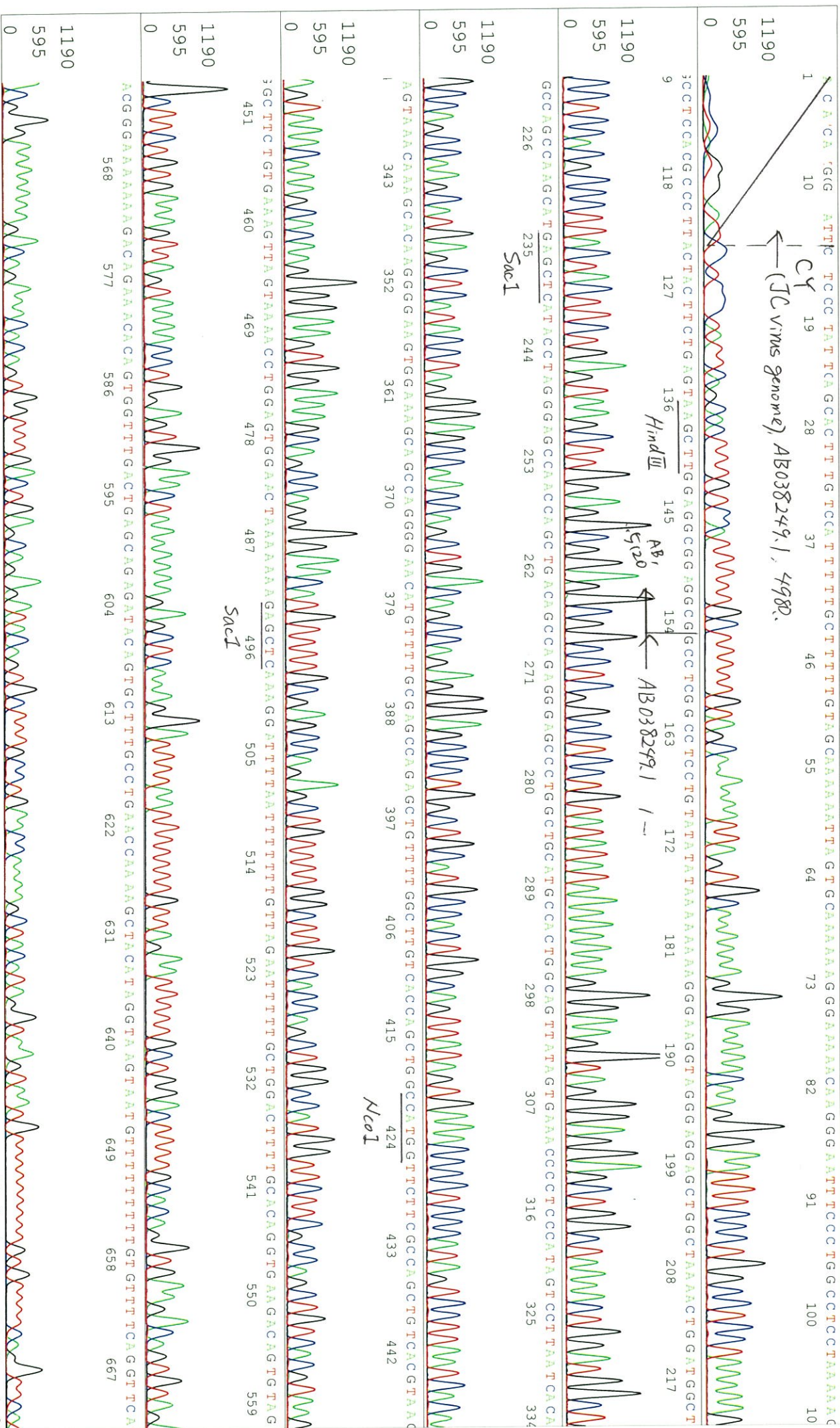
Pts 1392 to 13120 Pk1 Loc:1369

Spacing:11.41 Pts/Panel1350

(JC virus genome), AB038249.1, 4980.

Version 6.0 HISQV Bases: 1007

Plate Name: 20190617_dnabank



S/N G:267 A:348 T:290 C:318

03031_12319_A9F3_JCsp_f4

Jun 17 2019 03:27PM, JST

KB.bcp

KB_3500_POP7_BDTV3.mob

Jun 17 2019 03:53PM, JST

KB 1.4.1.8 Cap:13

Pis 1392 to 13120 PK1 Loc:1369

Spacing:11.41 Pis/Panel1350

Version 6.0 HiSQV Bases: 1007

Plate Name: 20190617_dnabank

TTGGTGC CCGCACTTGCACCTTTGGGGGGAACC TAGTTGCTACTGTTCTGAGGCTGCTGCTGCCACAGGATTTTCAAGTAAAGCTGAATTTGCTGCTAC

676 685 694 703 712 721 730 739 748 757 766 775

1190
595

TATAGAA GTTGAAT TGCACTC CCTTGCTACTGTAGAGGGG/T TACAAGTACCCTGTAGGCTTATA GCTGCTATAG GCCTTAC TCC TGAACAATATGCTGTAATTACT

784 793 802 811 820 829 838 847 856 865 874 883

Kdel

1190
595

GGAGCTCCGGGdgc TGTAGCTGGGTTTGCTGCATTGGTTC A A A C T G T A A C T G T A A C T G G T G T A G T G C T A T T G C C T C A G T T G G A T A T A G A T T T T T T G C T G A C T G G

892 901 910 919 928 937 946 955 964 973 982

SacI

AB

745

CY

(JC virus genome)

1190
595

GATCA TAAA GTTTC AA CA GTTTGGGCTTTTTC A G C A G C A G C T A T G G C T T T A C A G T T A T T T A A T C C C A G A G A C T A C T A T G A T A T T T A

991 1000 1009 1018 1027 1036 1045 1054 1063 1072

1190
595

ATTT C TTGG AG TG AA TG C TT T G A T A C A T A TT CA C T A T T A G A T T C T T A G A A C A T T G G G G C C

1081 1090 1099 1108 1117 1126 1135

1190
595

ATTCG TTTGA AT C T T C G A

1144 1153