

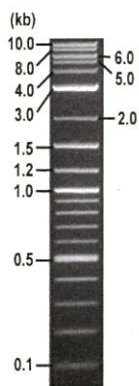


RIKEN DNA BANK

clone name : pENTER-EGFR C797S/T790M/del19

- Clone ID : RDB_15492
- Lot : 15492_A7K8
- DNA Concentration : 25 nanogram/microliter
- Volume : 40 microliter
- Form : DNA solution in TE buffer
- Host : DH5 alpha
- Culture : LB medium
- Antibiotics : 25 microgram/ml kanamycin
- 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	
EcoRV	6.2	kbp
EcoRI	3.6, 1.8, 0.8	kbp
BamHI	4.6, 1.0, 0.5	kbp
		kbp

● Confirmation of the insertion sequence

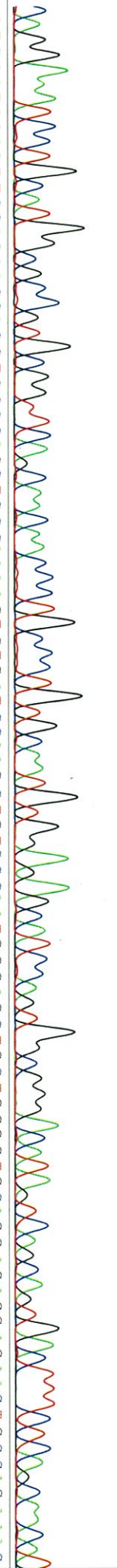
Please be sure to check our sequence analysis results before your request.

Sequence name	Primer ID	Primer name	Confirmed feature
Sequence - A	Pr0531	rrnBT1ter_F2	rrnB T1 ter, attL1, insert 5'
Sequence - B	Pr0071	pDONR_R	attL2, insert 3'
Sequence - C	Pr0313	EGFR-F5	insert middle region (C797S, T790M, del19)
Sequence - D	-	-	-
Sequence - E	-	-	-
Sequence - F	-	-	-
Sequence - G	-	-	-
Sequence - H	-	-	-

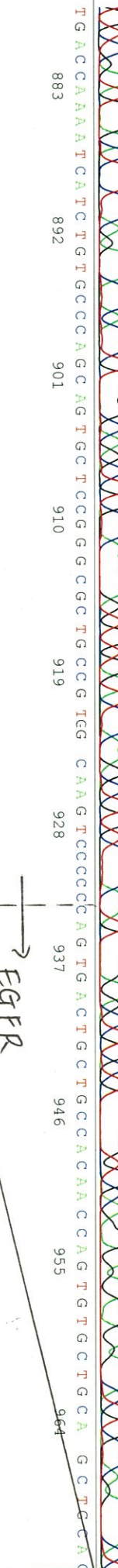
APPROVED BY :



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

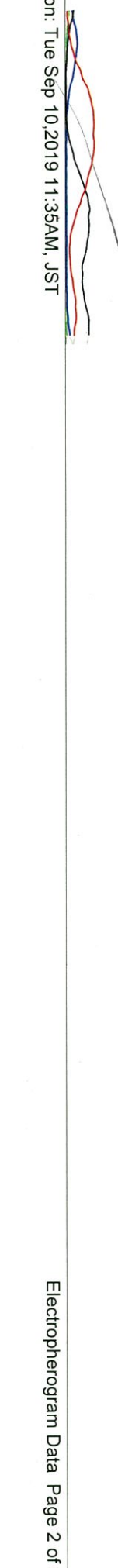


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A G G G C C C C C G G G A G A G C G A C T G C C C T G G T C T G C C G C A A A T T C C C G A G A C G A A G C C A C G T G C A A A G G A C A C C T G C C C C C C C A C T T

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

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



S/N G:685 A:397 T:394 C:421

primer name β : pDONR_R

D04925A5_A7K8_2_pDONR_R

Dec 13, 2017 02:22PM, JST

KB.bcp

5'-GTACATCAGAGATTGGAGACAC-3'

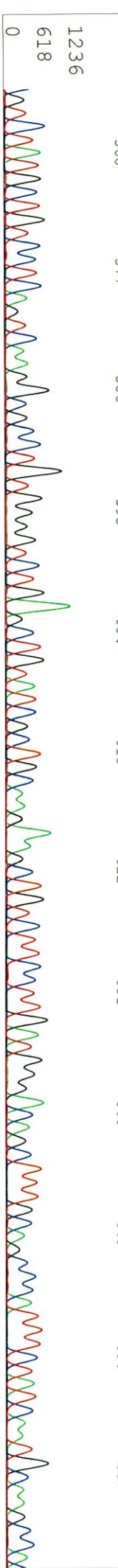
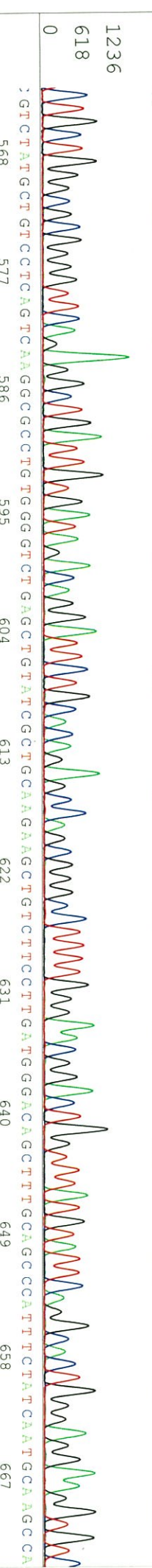
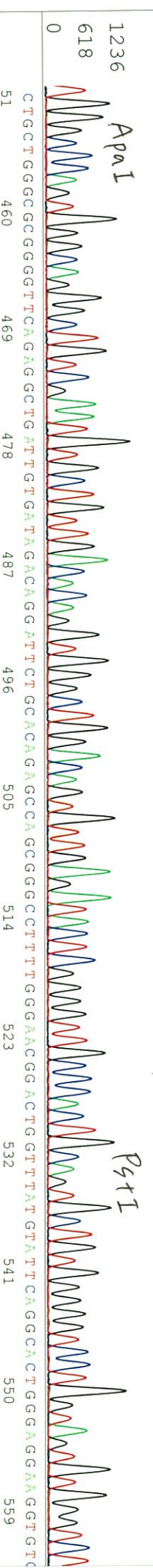
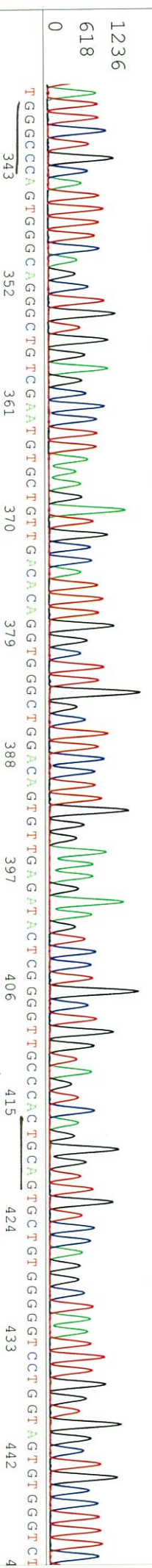
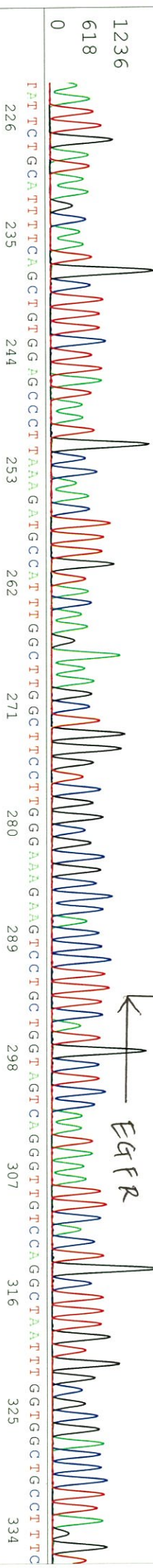
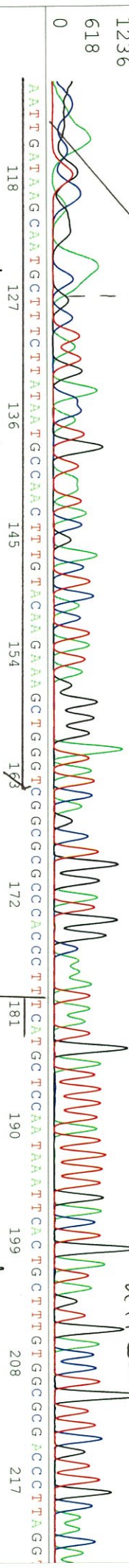
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Dec 13, 2017 03:03PM, JST

KB 1.4.1.8 Cap:14

Pls 1492 to 12648 Pk1 Loc:1469

Spacing:11.34 Pts/Panel1350



Sac I

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

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

AGCGCTGGGGGGTCTCCGGGGCCATTTTGGAGAAATTCGATGATCAACCTCAACGGAACTTTGGGGCGACTATCTGCCCTATAATCCAGCAACGCACTTTGA
883 892 901 910 919 928 937 946 955 964

EGFR ←

CCATGATCATGTAGACATCGATGGTACATAATGGGTGGCTGGAAGGCGTTTCCTCCTTTCATCGGATGGACGAT
973 982 991 1000 1009 1018 1027 1036 1045

TTC CGGCTGGGCAGGGATTTCCGTCATAATGACTTGGAAATTCATAAGGGTCTCAAATCCAACTTTCC
1054 1063 1072 1081 1090 1099

CAAAACCG

1236
618
0

S/N G:500 A:418 T:302 C:426

primer name C : EGFR-F5

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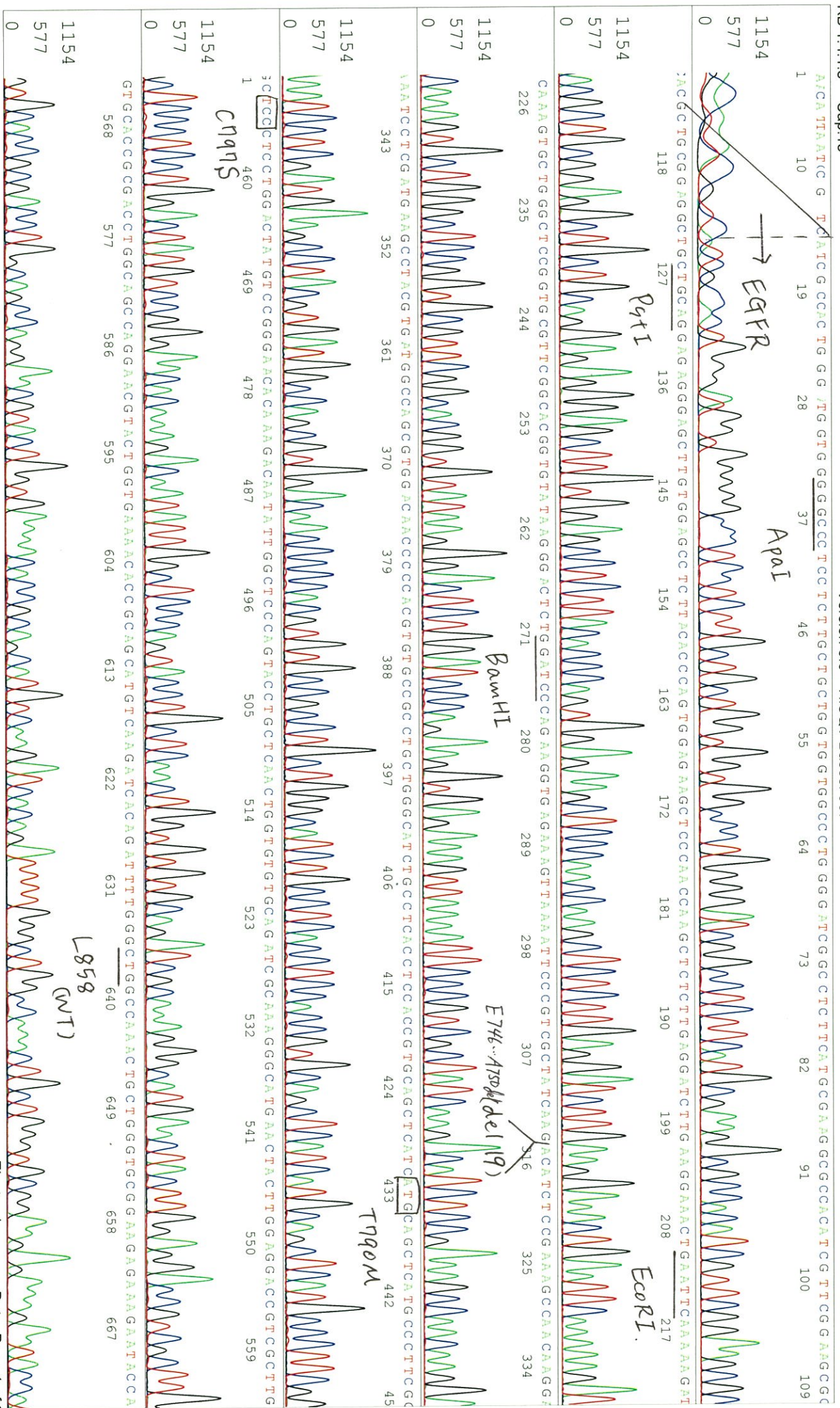
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KB 1.4.1.8 Cap:15

5-CAGGTCCTTGAAGGCTGTC-3'

Version 6.0 HISQV Bases: 967

Plate Name: 20171213 Kitaku



S/N G:500 A:418 T:302 C:426

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Dec 13,2017 03:03PM, JST

KB.bcp

Pls 1500 to 12594 Pk1 Loc:1477

Spacing:11.2 Pls/Panel1350

KB 1.4.1.8 Cap:15

Version 6.0 HISQV Bases: 967

Plate Name: 20171213 Kitaku

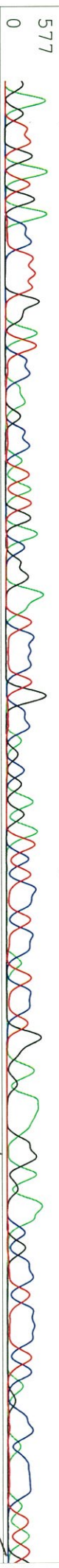
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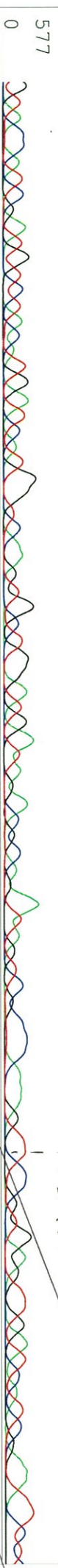
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784 793 802 811 820 829 838 847 856 865 874



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

883 892 901 910 919 928 937 946 955 964



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

973 982 991 1000 1009 1018 1027 1036 1045



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

1054 1063 1072 1081 1090 1099



G G A A T G T

1154 577



Clal

EGFR

BamHI

NdeI

BglII

NdeI