

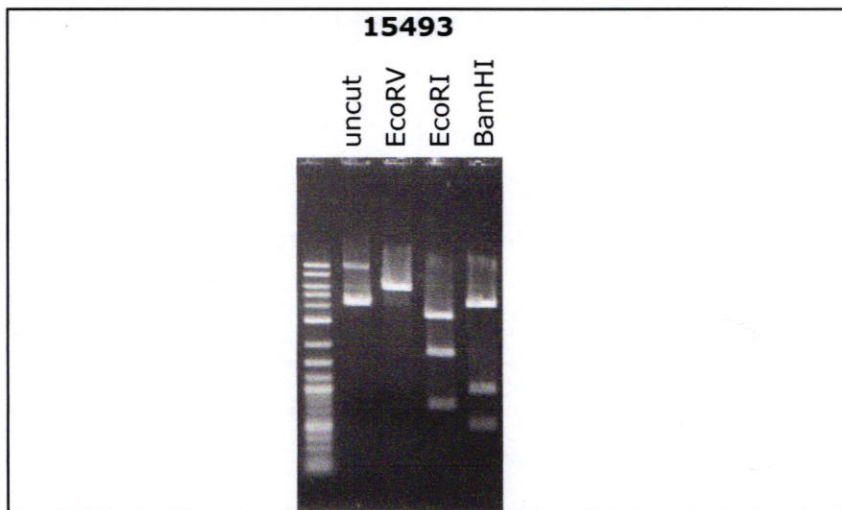
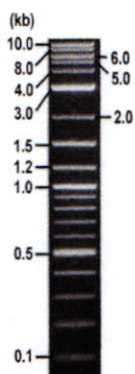


RIKEN DNA BANK

clone name : pENTER-EGFR L858R

- Clone ID : RDB_15493
- Lot : 15493_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
<u>EcoRV</u>	<u>6.2</u> kbp
<u>EcoRI</u>	<u>3.6, 1.8, 0.8</u> kbp
<u>BamHI</u>	<u>4.6, 1.0, 0.5</u> kbp
	kbp

● Confirmation of the insertion sequence

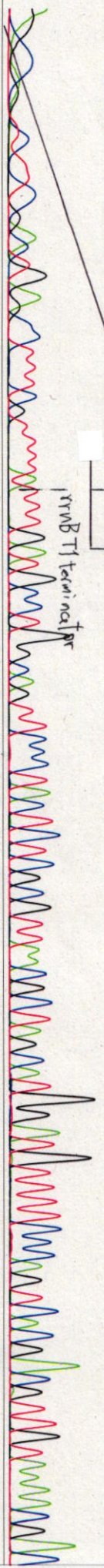
Please be sure to check our sequence analysis results before your request.

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 mid (L858R)
Sequence - D	-	-	-
Sequence - E	-	-	-
Sequence - F	-	-	-
Sequence - G	-	-	-
Sequence - H	-	-	-

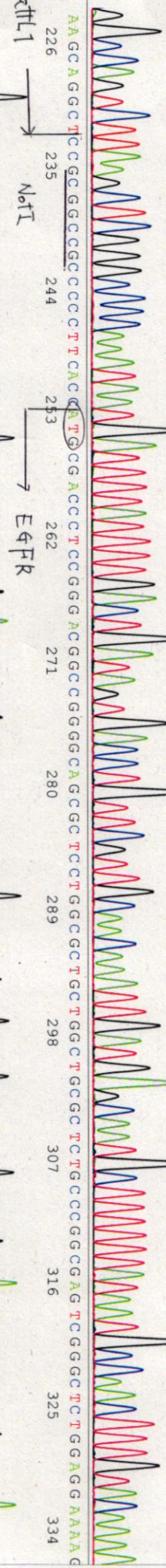
APPROVED BY :



1 NN NNNN NNN NNN N NN NN NN CCT T TCCGTTT TTTTGTGAT GCCCTGGCGAG T TCCCTACTCTCCGGCTTAA CCGCTAGCATGG ATGTTTCCCAAG TCACGAGCTTGTAA A A C G A C
 10 19 28 37 46 55 64 73 82 91 100 109



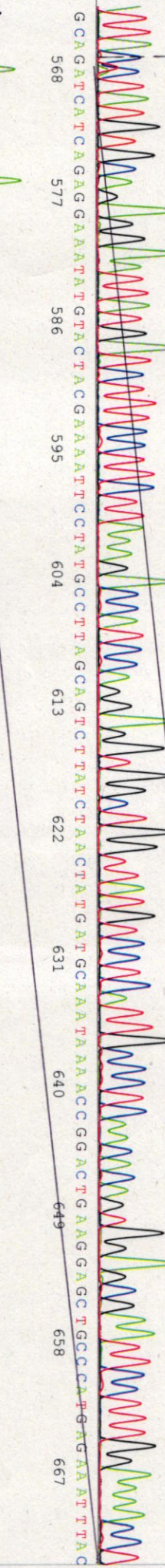
1166
583
0
 :G G C C A G T C T T A A G C C T C G G C C C C C A A A T A A T G A T T T A T T T T G A C T G A T A G C C T G T T C G T T G C A C A C A A A T T G A T G A G C A A T G C T T T T A A T G C C A C T T T G T A C A A A
 118 127 *ApaI* 136 145 *attL1* 154 163 172 181 190 199 208 217



1166
583
0
 A A G C A G G C T C C G C G G C C C C C C C C T T C A C C T G C G A C C C T C C G G G A C G G C C G G G C A G C G C C T C C T G G C C T G C C C G G C G A G T C G G G C T C T G C C C G G C G A G T C G G G C T C T G G A G G A A A A C
 226 235 *NotI* 244 253 262 271 280 289 298 307 316 325 334



1166
583
0
 A T T A N N N A T G T G C A G A G G A A T T A T G A T C T T C C T T C T T A A A G A C C A T C C A G A G G T G G C T G G T T A T G T C C A T T T G C C C T C A A C A C A G T G G A G C G A A T T C C T T T G A A A C C T
 343 352 361 370 379 388 397 406 415 424 433 442 459



1166
583
0
 G C A G A T C A T C A G A G A A A T A T G T A C T A C G A A A A T T C C T A T G C C T T A G C A G T C T T A A C T A T G A T G C A A A T A A A A C C G G A C T G A A G A G C T G C C C A A T G A A A T T T A C
 460 469 478 487 496 505 514 523 532 541 550 559

S/N G:473 A:378 T:352 C:363 Primer name β : pDONR_R

D04925A6_A7K8_2_pDONR_R

Dec 12, 2017 02:58PM, JST

KB bcp
KB 1.4.1.8 Cap:23
5'-GTAACATCAGAGATTTTGAGACAC-3'

KB_3500_POP7_BDTV3.mob
Pts 1465 to 12648 PK1 Loc:1442
Version 6.0 HISQV Bases: 899

Dec 12, 2017 03:38PM, JST
Spacing:11.39 Pts/Panel1350
Plate Name: 20171212 Kitaku



CGGTGGAAATTGTTGCTGGTTGCCACTCAGAGAGCCTCANNGANGGAGTCCCGTGAACGTGGANGGGCTGGCTGAANAAGCCCTGCTGGGANGANGTACTCGTCGGCAATC

E4FR

CACCAAGTGGTCCATGTCCTCTTCATCCNCCNCGNCAAGTTGGANTCTGTANGANTTNNCAAAATGCATCTCTTCCNTCCCCCCNGANTGANNAAGG

ANCGCTNNGGGGTCNCCGGGCCNNTTNGGANNNATGANCNNTCNNNNGNANNNTTNGGNANNAATCTGCNCTATNNNNNNNNNNNNNNNNNN

NCNNNGNNGNNGNNGNNGNNGNNGNNGNNGNNGNNGNNGNNGNNGNNGNNGN

INN>NN

NN>NN

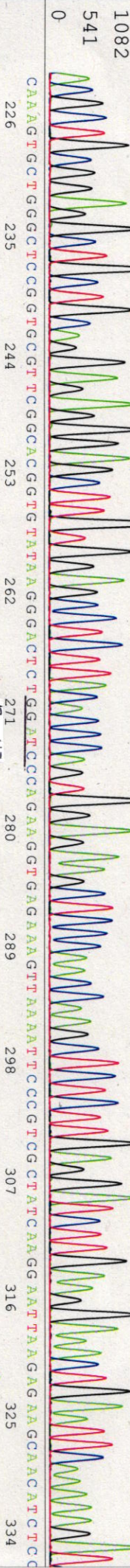
NN>NN



1 NNNNN ANN N N INNNNN NNN NN NN G G IN G GT G G G G C C C T C C T C T G C T G C T G G T G G T G G C C C C T G C G G IN CG G C C C T C T T C A T G C G G A A G G C C C C A C A T C G T T C G G A A G C C



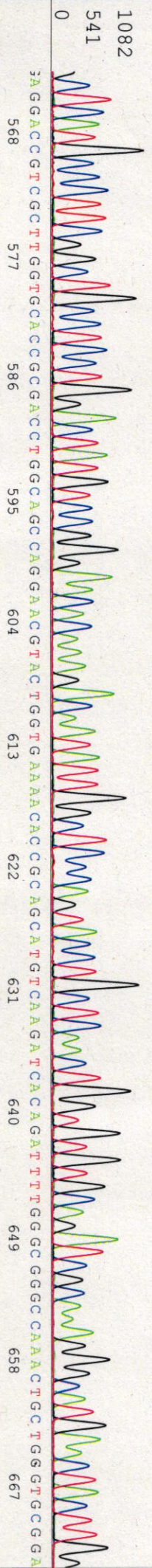
9 ACCGCTGCGGAGGCTGCTGGCAGGAGGAGGAGGCTTGTTGGAGCCTCTTACACCAGTTGGAGAAAGCTCCCAACCAAGCTCTTGAGGATCTGAAAGAAACTGAAATCAAAAAGAT



CAAAGTGTGGGCTCCGGTCCGGTTCGGCACCAGGTGTTATAAGGACTCTGGATCCCAAGAAAGTTAAATTCCTCGCTATCAAGGAAATAAGAGAAACAATCTCC



GAAAGCCAA CAA GG AAAT CCTCGATGAAGCC TACC GTGATGGCCAGCGTGAGACAA CCCCAGTGTGCCCGCTGGGCA TCTGCCCTCACTCCACC GTGCAACTCATCGCA



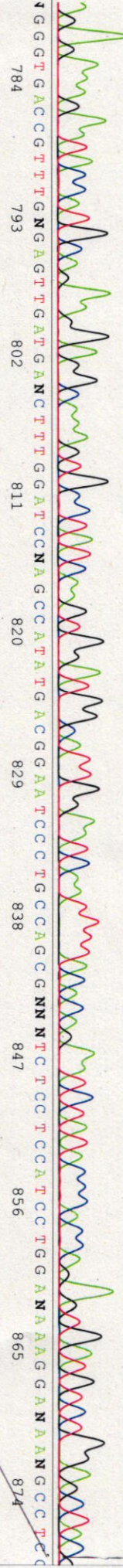
GCTCATGCCCTTCGGCTGCCCTCCCTGGACTATGTCCGGGAAACCAAGACAATATTGGCTCCCAGTACCTGCTCAACTGGTGTGCAAGATCGCAAGGGCATGAATCACTTG



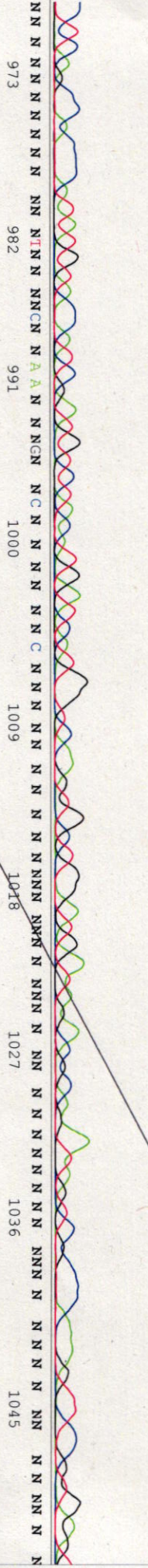
TAGGACCGCTCGCTTGGTGCA CCGCGAACCTGGCAAGCAGGAACGTA CTGGTGA AAAACAC CGCAGCATGTCAAGATCA CAGATTTTGGGCGGGCCAAACTGCTGGGTGGCGA

EGFR

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



CTCANNCCCAATATNNAACCATCNCNTGTCTACNTNNCCTGGNCAANNNTNNNGNNANCGNNNANTCCNNAANNNTNNNN
883 892 901 910 919 928 937 946 955 964



NNNNNNNNNNNTNNNNCNANNGNCCNN
973 982 991 1000 1009 1018 1027 1036 1045



NNNN N N N
1054 1063 1072 1081 1090 1099 1108 1117