

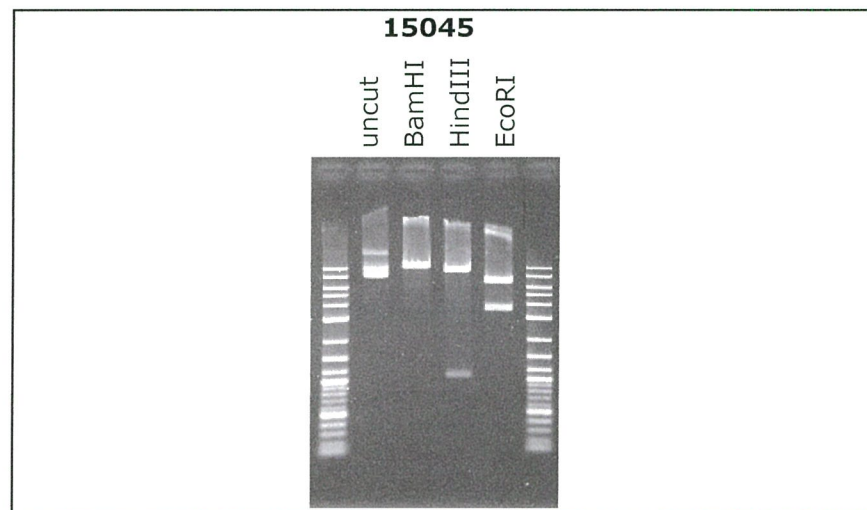
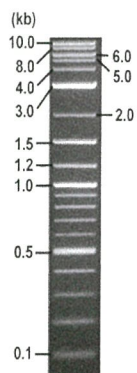


RIKEN DNA BANK

clone name : pK038.CAG-loxP-stop-loxP-EGFP-ires-tTA-WPRE (Supernova)

- Clone ID : RDB\_15045
- Lot : 15045\_A7En
- 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
<b>BamHI</b>	<b>10.3</b> kbp
<b>HindIII</b>	<b>9.2, 1.1</b> kbp
<b>EcoRI</b>	<b>6.8, 3.5</b> 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	Pr0166	pAxCALNLF1	loxP,insert 5'
Sequence - B	Pr0574	mVenus-M_F	insert 3',IRES
Sequence - C	Pr0164	pAxCA_F1	loxP
Sequence - D	Pr0250	PRE_rev	WPRE,tTA Advanceed
Sequence - E	Pr0154	SV40pro_F_V2	NeoR_KanR
Sequence - F	-	-	-
Sequence - G	-	-	-
Sequence - H	-	-	-

APPROVED BY :



S/N G:199 A:237 T:161 C:321

primer name A : paxCALNLF1

KB\_3500\_POP7\_BDTV3.mob

Jul 04 2017 04:00PM, JST

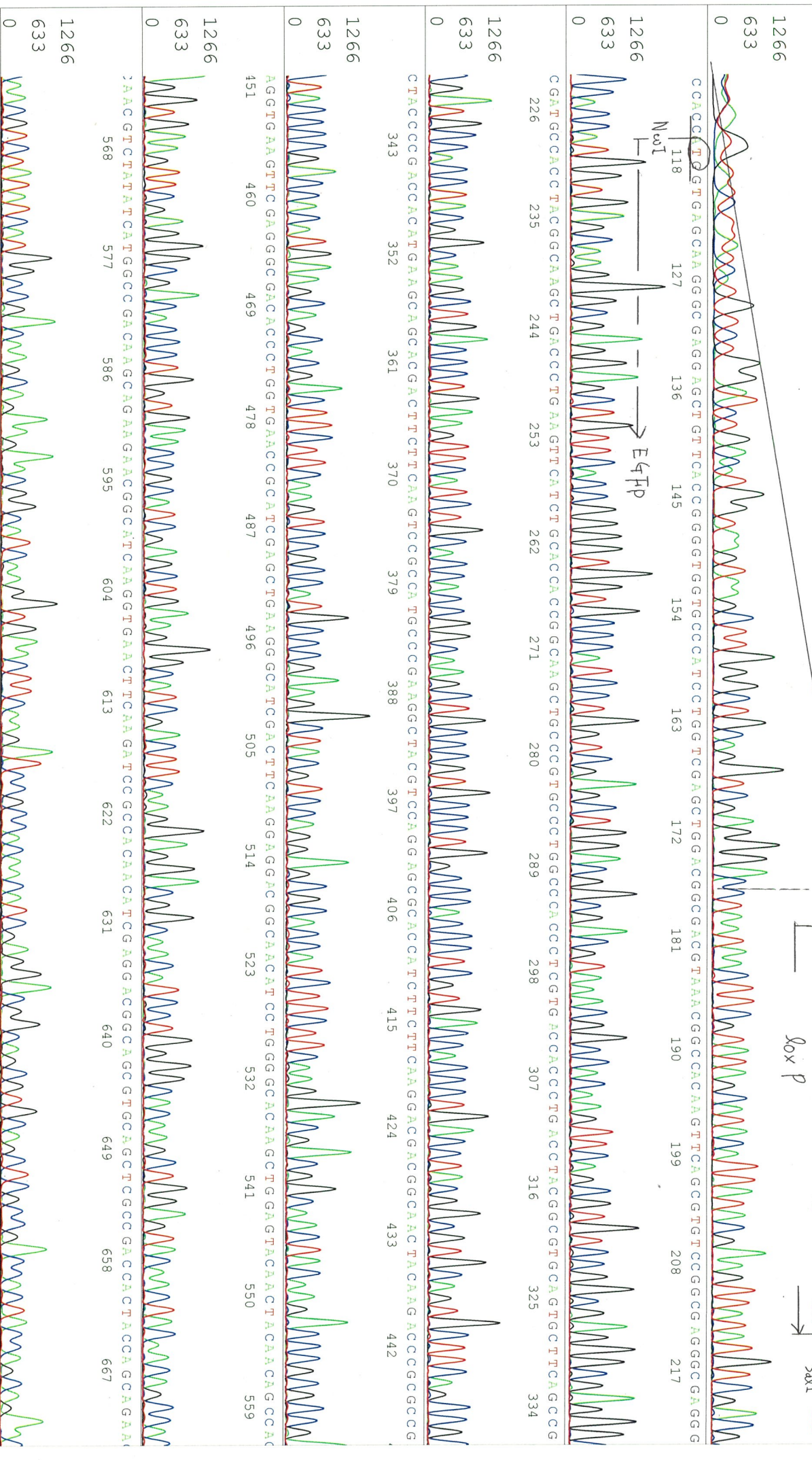
KB:bcpc

5'-CACTGCATTCTAGTTGTTGTC-3'

Pls 1372 to 13275 Pk1 Loc:1349

Spacing:11.78 Pls/Panel1350

KB 1.4.1.8 Cap:7 Version 6.0 HISQV Bases: 924 Plate Name: 20170704 Kitaku





S/N G:199 A:237 T:161 C:321

D04276A3\_A7En\_1\_paxCALNLF1

Jul 04, 2017 03:33PM, JST

KB.bcp

KB\_3500\_POP7\_BDTV3.mob

Jul 04, 2017 04:00PM, JST

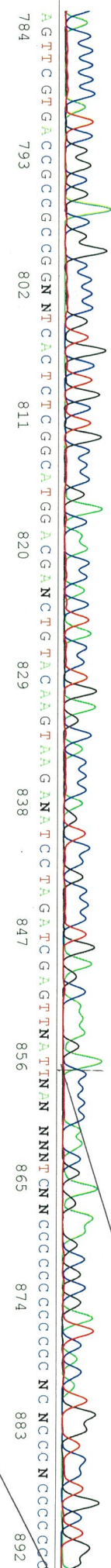
KB 1.4.1.8 Cap:7

Pis 1372 to 13275 Pk1 Loc:1349

Spacing:11.78 Pts/Panel1350

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

EGFP



AGTTCGTGACCGCGCCGCGGNNTCACCTCTCGGCATGGACGANCTGTACAAATAATCCCTAGATCCGAGTTNATTNNNNCNANNGCCGTNTTNGNNNNGNGN  
784 793 802 811 820 829 838 847 856 865 874 883 892

CCCCNAACGTTACNGGNCNAAGCNCCTTGGAAANNNNNGNGGCGTTNGNCNNTTATTTNNNNCNANNGCCGTNTTNGNNNNGNGN  
901 910 919 928 937 946 955 964 973 982 991

NANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGGNNTNNCNNNNNNNGCCGTNTTNGNNNNGNGN  
1000 1009 1018 1027 1036 1045 1054 1063 1072

NN  
1081 1090 1099 1108 1117 1126 1135

NN  
1144 1153



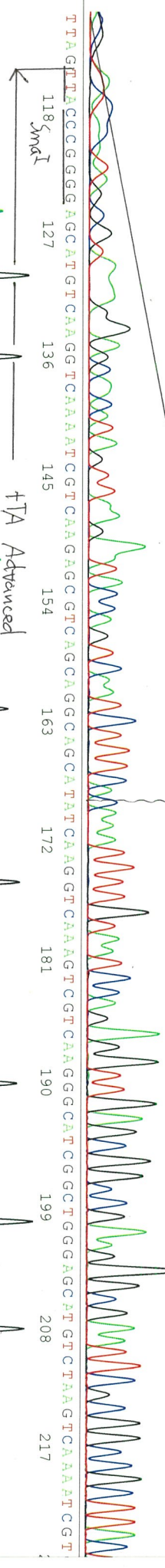






S/N G:427 A:334 T:292 C:370 primer name PRE\_rev : PRE\_rev  
KB.bcp KB\_3500\_POP7\_BDTV3.mob  
KB 1.4.1.8 Cap:14 5'-AGCAATAGCATGATACAAAGGC-3' Pts 1549 to 13591 Pk1 Loc:1526  
Version 6.0 HiSeq Bases: 864

N NN NNNNN N NN N C G NN NN G AN C IN C A T A G T T A A G A A T T A C C A G T C A A T C T T T C N C A A A T T T T G T A A T C C A G A G G T T G A G C C G G C C G A A G G C C G A A T T C G C C G C C G C T T A C  
1 10 19 28 37 46 55 64 73 82 91 100 109  
← PRE → E48I M11



T T A G T T A C C C G G G G A G C A T G T C A A G G T C A A A A T C G T C A A G A G C G T C A G C A G G C A G C A T A T C A A G G T C A A A G T C G T C A A G G C A T C G C T G G G A G C A T G T C T A A G T C A A A A T C G T  
118 bp del +1A Advanced  
C A A G G G C T C G G C C G C C C G C C G C C T T C G C A C T T T A G C T G T T C C A G G C C A C A T A T G A T T A G T T C C A G G C C G A A A A G G A A G G C A G G T C G G C T C C C T G A T G G T C G A A C A G C T C  
226 235 244 253 262 271 280 289 298 307 316 325 334  
Ndel

A A T T G C T T G T C T C A G A A G T G G G G C A T A G A A T C G G T G G T A G G T G T C T C T T T C C T C T T T G C T A C T T G A T G C T C C T G A T C C T C C A A T A C G C A G C C A G T G T A A A G T G G C C C A C  
343 352 361 370 379 388 397 406 415 424 433 442 451

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

C A C T T T A G C C C C G T C C G G A T G T G A G A G G A G A G C A C C G G A A T G A C T T G G C C G A A A G T C T T G C C A T G A C T C C C C T T C C A G G G G C C A G A A G T G G G T A T G A T  
568 577 586 595 604 613 622 631 640 649 658 667

